



## Sequence Listing

Baker, Kevin P.  
Botstein, David  
Desnoyers, Luc  
Eaton, Dan L.  
Ferrara, Napoleone  
Fong, Sherman  
Gao, Wei-Qiang  
Goddard, Audrey  
Godowski, Paul J.  
Grimaldi, Christopher J.  
Gurney, Austin L.  
Hillan, Kenneth J.  
Pan, James  
Paoni, Nicholas F.

<120> Secreted and Transmembrane Polypeptides and Nucleic  
Acids Encoding the Same

<130> P2830P1C44

<140> 10/015388

<141> 2001-12-11

<150> 60/098716

<151> 1998-09-01

<150> 60/098723

<151> 1998-09-01

<150> 60/098749

<151> 1998-09-01

<150> 60/098750

<151> 1998-09-01

<150> 60/098803

<151> 1998-09-02

<150> 60/098821

<151> 1998-09-02

<150> 60/098843

<151> 1998-09-02

<150> 60/099536

<151> 1998-09-09

<150> 60/099596

<151> 1998-09-09

<150> 60/099598

<151> 1998-09-09

<150> 60/099602

<151> 1998-09-09

<150> 60/099642  
<151> 1998-09-09

<150> 60/099741  
<151> 1998-09-10

<150> 60/099754  
<151> 1998-09-10

<150> 60/099763  
<151> 1998-09-10

<150> 60/099792  
<151> 1998-09-10

<150> 60/099808  
<151> 1998-09-10

<150> 60/099812  
<151> 1998-09-10

<150> 60/099815  
<151> 1998-09-10

<150> 60/099816  
<151> 1998-09-10

<150> 60/100385  
<151> 1998-09-15

<150> 60/100388  
<151> 1998-09-15

<150> 60/100390  
<151> 1998-09-15

<150> 60/100584  
<151> 1998-09-16

<150> 60/100627  
<151> 1998-09-16

<150> 60/100661  
<151> 1998-09-16

<150> 60/100662  
<151> 1998-09-16

<150> 60/100664  
<151> 1998-09-16

<150> 60/100683  
<151> 1998-09-17

<150> 60/100684  
<151> 1998-09-17



<150> 60/100710  
<151> 1998-09-17

<150> 60/100711  
<151> 1998-09-17

<150> 60/100848  
<151> 1998-09-18

<150> 60/100849  
<151> 1998-09-18

<150> 60/100919  
<151> 1998-09-17

<150> 60/100930  
<151> 1998-09-17

<150> 60/101014  
<151> 1998-09-18

<150> 60/101068  
<151> 1998-09-18

<150> 60/101071  
<151> 1998-09-18

<150> 60/101279  
<151> 1998-09-22

<150> 60/101471  
<151> 1998-09-23

<150> 60/101472  
<151> 1998-09-23

<150> 60/101474  
<151> 1998-09-23

<150> 60/101475  
<151> 1998-09-23

<150> 60/101476  
<151> 1998-09-23

<150> 60/101477  
<151> 1998-09-23

<150> 60/101479  
<151> 1998-09-23

<150> 60/101738  
<151> 1998-09-24

<150> 60/101741  
<151> 1998-09-24

<150> 60/101743  
<151> 1998-09-24

<150> 60/101915  
<151> 1998-09-24

<150> 60/101916  
<151> 1998-09-24

<150> 60/102207  
<151> 1998-09-29

<150> 60/102240  
<151> 1998-09-29

<150> 60/102307  
<151> 1998-09-29

<150> 60/102330  
<151> 1998-09-29

<150> 60/102331  
<151> 1998-09-29

<150> 60/102484  
<151> 1998-09-30

<150> 60/102487  
<151> 1998-09-30

<150> 60/102570  
<151> 1998-09-30

<150> 60/102571  
<151> 1998-09-30

<150> 60/102684  
<151> 1998-10-01

<150> 60/102687  
<151> 1998-10-01

<150> 60/102965  
<151> 1998-10-02

<150> 60/103258  
<151> 1998-10-06

<150> 60/103314  
<151> 1998-10-07

<150> 60/103315  
<151> 1998-10-07

<150> 60/103328  
<151> 1998-10-07

<150> 60/103395  
<151> 1998-10-07

<150> 60/103396  
<151> 1998-10-07

<150> 60/103401  
<151> 1998-10-07

<150> 60/103449  
<151> 1998-10-06

<150> 60/103633  
<151> 1998-10-08

<150> 60/103678  
<151> 1998-10-08

<150> 60/103679  
<151> 1998-10-08

<150> 60/103711  
<151> 1998-10-08

<150> 60/104257  
<151> 1998-10-14

<150> 60/104987  
<151> 1998-10-20

<150> 60/105000  
<151> 1998-10-20

<150> 60/105002  
<151> 1998-10-20

<150> 60/105104  
<151> 1998-10-21

<150> 60/105169  
<151> 1998-10-22

<150> 60/105266  
<151> 1998-10-22

<150> 60/105693  
<151> 1998-10-26

<150> 60/105694  
<151> 1998-10-26

<150> 60/105807  
<151> 1998-10-27

<150> 60/105881  
<151> 1998-10-27

<150> 60/105882  
<151> 1998-10-27

<150> 60/106023  
<151> 1998-10-28

<150> 60/106029  
<151> 1998-10-28

<150> 60/106030  
<151> 1998-10-28

<150> 60/106032  
<151> 1998-10-28

<150> 60/106033  
<151> 1998-10-28

<150> 60/106062  
<151> 1998-10-27

<150> 60/106178  
<151> 1998-10-28

<150> 60/106248  
<151> 1998-10-29

<150> 60/106384  
<151> 1998-10-29

<150> 60/108500  
<151> 1998-10-29

<150> 60/106464  
<151> 1998-10-30

<150> 60/106856  
<151> 1998-11-03

<150> 60/106902  
<151> 1998-11-03

<150> 60/106905  
<151> 1998-11-03

<150> 60/106919  
<151> 1998-11-03

<150> 60/106932  
<151> 1998-11-03

<150> 60/106934  
<151> 1998-11-03

<150> 60/107783  
<151> 1998-11-10

<150> 60/108775  
<151> 1998-11-17

<150> 60/108779  
<151> 1998-11-17

<150> 60/108787  
<151> 1998-11-17

<150> 60/108788  
<151> 1998-11-17

<150> 60/108801  
<151> 1998-11-17

<150> 60/108802  
<151> 1998-11-17

<150> 60/108806  
<151> 1998-11-17

<150> 60/108807  
<151> 1998-11-17

<150> 60/108848  
<151> 1998-11-18

<150> 60/108849  
<151> 1998-11-18

<150> 60/108850  
<151> 1998-11-18

<150> 60/108851  
<151> 1998-11-18

<150> 60/108852  
<151> 1998-11-18

<150> 60/108858  
<151> 1998-11-18

<150> 60/108867  
<151> 1998-11-17

<150> 60/108904  
<151> 1998-11-18

<150> 60/108925  
<151> 1998-11-17

<150> 60/113296  
<151> 1998-12-22

<150> 60/114223  
<151> 1998-12-30

<150> 60/129674  
<151> 1999-04-16

<150> 60/141037  
<151> 1999-06-23

<150> 60/144758  
<151> 1999-07-20

<150> 60/145698  
<151> 1999-07-26

<150> 60/162506  
<151> 1999-10-29

<150> 09/218517  
<151> 1998-12-22

<150> 09/284291  
<151> 1999-04-12

<150> 09/403297  
<151> 1999-10-18

<150> 09/872035  
<151> 2001-06-01

<150> 09/882636  
<151> 2001-06-14

<150> 09/946374  
<151> 2001-09-04

<150> PCT/US99/00106  
<151> 1999-01-05

<150> PCT/US99/20111  
<151> 1999-09-01

<150> PCT/US99/21194  
<151> 1999-09-15

<150> PCT/US99/28313  
<151> 1999-11-30

<150> PCT/US99/28551  
<151> 1999-12-02

<150> PCT/US99/30095  
<151> 1999-12-16

<150> PCT/US00/00219  
<151> 2000-01-05

<150> PCT/US00/00376  
<151> 2000-01-06

<150> PCT/US00/03565  
<151> 2000-02-11

<150> PCT/US00/04342  
<151> 2000-02-18

<150> PCT/US00/05004  
<151> 2000-02-24

<150> PCT/US00/05841  
<151> 2000-03-02

<150> PCT/US00/06884  
<151> 2000-03-15

<150> PCT/US00/13705  
<151> 2000-05-17

<150> PCT/US00/14042  
<151> 2000-05-22

<150> PCT/US00/14941  
<151> 2000-05-30

<150> PCT/US00/15264  
<151> 2000-06-02

<150> PCT/US00/23328  
<151> 2000-08-24

<150> PCT/US00/23522  
<151> 2000-08-23

<150> PCT/US00/30873  
<151> 2000-11-10

<150> PCT/US00/30952  
<151> 2000-11-08

<150> PCT/US00/32678  
<151> 2000-12-01

<150> PCT/US01/06520  
<151> 2001-02-28

<150> PCT/US01/06666  
<151> 2001-03-01

<150> PCT/US01/17800  
<151> 2001-06-01

<150> PCT/US01/19692  
<151> 2001-06-20

<150> PCT/US01/21066  
<151> 2001-06-29

<150> PCT/US01/21735

<151> 2001-07-09

<160> 477

<210> 1

<211> 43

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 1

tgtaaacga cggccagtta aatagacctg caattattaa tct 43

<210> 2

<211> 41

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 2

caggaaacag ctatgaccac ctgcacacct gcaaattccat t 41

<210> 3

<211> 1110

<212> DNA

<213> Homo sapiens

<400> 3

ccaatcgccc ggtgcggtgg tgcagggctct cgggctagtc atggcgctccc 50

cgtctcggag actgcagact aaaccagtca ttacttggtt caagagcgtt 100

ctgctaattct acacttttat tttctggatc actggcgtta tccttcttgc 150

agttggcatt tggggcaagg tgagcctgga gaattacttt tctcttttaa 200

atgagaaggc caccaatgtc cccttcgtgc tcattgctac tggtagcgtc 250

attattcttt tgggcacctt tgggtggttt gctacctgcc gagcttctgc 300

atggatgcta aaactgtatg caatgtttct gactctcgtt tttttggtcg 350

aactggtcgc tgccatcgta ggatttggtt tcagacatga gattaagaac 400

agctttaaga ataattatga gaaggctttg aagcagtata actctacagg 450

agattataga agccatgcag tagacaagat ccaaaatacg ttgcattggt 500

gtggtgtcac cgattataga gattggacag atactaatta ttactcagaa 550

aaaggatttc ctaagagttg ctgtaaacct gaagattgta ctccacagag 600



agatgcagac aaagtaaaca atgaagggtg tttataaaag gtgatgacca 650  
 ttatagagtc agaaatggga gtcgttgagc gaatttcctt tggagttgct 700  
 tgcttccaac tgattggaat ctttctcgcc tactgccwct ctcgtgccat 750  
 aacaaataac cagtatgaga tagtgtaacc caatgtatct gtgggcctat 800  
 tcctctctac ctttaaggac atttagggtc cccctgtga attagaaaagt 850  
 tgcttggtg gagaactgac aacactactt actgatagac caaaaaacta 900  
 caccagtagg ttgattcaat caagatgtat gtagacctaa aactacacca 950  
 ataggctgat tcaatcaaga tccgtgctcg cagtgggctg attcaatcaa 1000  
 gatgtatgtt tgctatgttc taagtccacc ttctatcca ttcattgtag 1050  
 atcgttgaaa ccctgtatcc ctctgaaaca ctggaagagc tagtaaattg 1100  
 taaatgaagt 1110

<210> 4  
 <211> 245  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> sig\_peptide  
 <222> 1-42  
 <223> Signal Peptide

<220>  
 <221> TRANSMEM  
 <222> 19-42, 61-83, 92-114, 209-230  
 <223> Transmembrane Domains

<220>  
 <221> misc\_feature  
 <222> 69-80, 211-222  
 <223> Prokaryotic Membrane Lipoprotein Lipid Attachment Site.

<220>  
 <221> misc\_feature  
 <222> 75-81, 78-84, 210-216, 214-220, 226-232  
 <223> N-Myristoylation Site.

<220>  
 <221> misc\_feature  
 <222> 134-138  
 <223> N-Glycosylation Site.

<220>  
 <221> misc\_feature  
 <222> 160-168, 160-169  
 <223> Tyrosine Kinase Phosphorylation Site.

<220>

<221> unsure

<222> 233

<223> unknown amino acid

<400> 4

Met	Ala	Ser	Pro	Ser	Arg	Arg	Leu	Gln	Thr	Lys	Pro	Val	Ile	Thr
1				5					10					15

Cys	Phe	Lys	Ser	Val	Leu	Leu	Ile	Tyr	Thr	Phe	Ile	Phe	Trp	Ile
				20					25					30

Thr	Gly	Val	Ile	Leu	Leu	Ala	Val	Gly	Ile	Trp	Gly	Lys	Val	Ser
				35					40					45

Leu	Glu	Asn	Tyr	Phe	Ser	Leu	Leu	Asn	Glu	Lys	Ala	Thr	Asn	Val
				50					55					60

Pro	Phe	Val	Leu	Ile	Ala	Thr	Gly	Thr	Val	Ile	Ile	Leu	Leu	Gly
				65					70					75

Thr	Phe	Gly	Cys	Phe	Ala	Thr	Cys	Arg	Ala	Ser	Ala	Trp	Met	Leu
				80					85					90

Lys	Leu	Tyr	Ala	Met	Phe	Leu	Thr	Leu	Val	Phe	Leu	Val	Glu	Leu
				95					100					105

Val	Ala	Ala	Ile	Val	Gly	Phe	Val	Phe	Arg	His	Glu	Ile	Lys	Asn
				110					115					120

Ser	Phe	Lys	Asn	Asn	Tyr	Glu	Lys	Ala	Leu	Lys	Gln	Tyr	Asn	Ser
				125					130					135

Thr	Gly	Asp	Tyr	Arg	Ser	His	Ala	Val	Asp	Lys	Ile	Gln	Asn	Thr
				140					145					150

Leu	His	Cys	Cys	Gly	Val	Thr	Asp	Tyr	Arg	Asp	Trp	Thr	Asp	Thr
				155					160					165

Asn	Tyr	Tyr	Ser	Glu	Lys	Gly	Phe	Pro	Lys	Ser	Cys	Cys	Lys	Leu
				170					175					180

Glu	Asp	Cys	Thr	Pro	Gln	Arg	Asp	Ala	Asp	Lys	Val	Asn	Asn	Glu
				185					190					195

Gly	Cys	Phe	Ile	Lys	Val	Met	Thr	Ile	Ile	Glu	Ser	Glu	Met	Gly
				200					205					210

Val	Val	Ala	Gly	Ile	Ser	Phe	Gly	Val	Ala	Cys	Phe	Gln	Leu	Ile
				215					220					225

Gly	Ile	Phe	Leu	Ala	Tyr	Cys	Xaa	Ser	Arg	Ala	Ile	Thr	Asn	Asn
				230					235					240

Gln	Tyr	Glu	Ile	Val
				245

<210> 5

<211> 1218

<212> DNA

<213> Homo sapiens

<400> 5

cccacgcgtc cggcgccgtg gcctcgcgtc catctttgcc gttctctcgg 50  
acctgtcaca aaggagtcgc gccgccgccg ccgccccctc cctccggtgg 100  
gcccgggagg tagagaaagt cagtgccaca gcccgaccgc gctgctctga 150  
gccctgggca cgcggaacgg gagggagtct gagggttggg gacgtctgtg 200  
agggagggga acagccgctc gagcctgggg cgggcggacc ggactggggc 250  
cggggtaggc tctggaaagg gcccgggaga gaggtggcgt tggtcagaac 300  
ctgagaaaca gccgagaggt ttccaccga ggcccgcgct tgagggatct 350  
gaagagggtc ctagaagagg gtgttcctc tttcgggggt cctcaccaga 400  
agaggttctt gggggtcgcc cttctgagga ggctgcggct aacagggcc 450  
agaactgcca ttgatgtcc agaatcccct gtagttgata atgttgggaa 500  
taagctctgc aactttcttt ggcattcagt tgttaaaaac aaataggatg 550  
caaattcctc aactccaggt tatgaaaaca gtacttgga aactgaaaac 600  
tacctaaatg atcgtctttg gttgggccgt gttcttagcg agcagaagcc 650  
ttggccaggg tctgttggtg actctcgaag agcacatagc ccacttcta 700  
gggactggag gtgccgtac taccatgggt aattcctgta tctgccgaga 750  
tgacagtgga acagatgaca gtgttgacac ccaacagcaa caggccgaga 800  
acagtgcagt acccactgct gacacaagga gcccaaccag ggaccctgtt 850  
cggccaccaa ggagggggccg aggacctcat gagccaagga gaaagaaaca 900  
aaatgtggat gggctagtgt tggacacact ggcagtaata cggactcttg 950  
tagataagta agtatctgac tcacggtcac ctccagtgga atgaaaagtg 1000  
ttctgcccg aacctgact ttaggactcc ttcagttcct ttaggacata 1050  
ctcgccaagc cttgtgctca cagggcaaag gagaatattt taatgctccg 1100  
ctgatggcag agtaaatgat aagatttgat gtttttgctt gctgtcatct 1150  
actttgtctg gaaatgtcta aatgtttctg tagcagaaaa cacgataaag 1200  
ctatgatctt tattagag 1218

<210> 6  
<211> 117  
<212> PRT  
<213> Homo sapiens

<220>  
<221> sig\_peptide  
<222> 1-16  
<223> Signal Peptide

<220>  
<221> misc\_feature  
<222> 18-24, 32-38, 34-40, 35-41, 51-57  
<223> N-Myristoylation Site.

<220>  
<221> misc\_feature  
<222> 22-26, 50-54, 113-117  
<223> Casein Kinase II Phosphorylation Site.

<400> 6  
Met Ile Val Phe Gly Trp Ala Val Phe Leu Ala Ser Arg Ser Leu  
1 5 10 15  
Gly Gln Gly Leu Leu Leu Thr Leu Glu Glu His Ile Ala His Phe  
20 25 30  
Leu Gly Thr Gly Gly Ala Ala Thr Thr Met Gly Asn Ser Cys Ile  
35 40 45  
Cys Arg Asp Asp Ser Gly Thr Asp Asp Ser Val Asp Thr Gln Gln  
50 55 60  
Gln Gln Ala Glu Asn Ser Ala Val Pro Thr Ala Asp Thr Arg Ser  
65 70 75  
Gln Pro Arg Asp Pro Val Arg Pro Pro Arg Arg Gly Arg Gly Pro  
80 85 90  
His Glu Pro Arg Arg Lys Lys Gln Asn Val Asp Gly Leu Val Leu  
95 100 105  
Asp Thr Leu Ala Val Ile Arg Thr Leu Val Asp Lys  
110 115

<210> 7  
<211> 756  
<212> DNA  
<213> Homo sapiens

<400> 7  
ggcacgagggc gctgtccacc cgggggcgtg ggagtgaggt accagattca 50  
gcccatttgg ccccgacgcc tctgttctcg gaatccgggt gctgcggatt 100  
gaggtcccgg ttctaacgg actgcaagat ggaggaaggc gggaacctag 150

gaggcctgat taagatggtc catctactgg tcttgtcagg tgcctggggc 200  
 atgcaaagtgt gggtagacatt cgtctcaggc ttcttgcttt tccgaagcct 250  
 tccccgacat accttcggac tagtgcagag caaactcttc cccttctact 300  
 tccacatctc catgggctgt gccttcatca acctctgcat cttggcttca 350  
 cagcatgctt gggctcagct cacattctgg gaggccagcc agctttacct 400  
 gctgttcttg agccttacgc tggccactgt caacgcccgc tggctggaac 450  
 cccgcaccac agctgccatg tgggccctgc aaaccgtgga gaaggagcga 500  
 ggcttgggtg gggaggtacc aggcagccac caggggtccg atccctaccg 550  
 ccagctgcga gagaaggacc ccaagtacag tgctctccgc cagaatttct 600  
 tccgctacca tgggctgtcc tctctttgca atctgggctg cgtcctgagc 650  
 aatgggctct gtctcgctgg ccttgccctg gaaataagga gcctctagca 700  
 tgggccctgc atgctaataa atgcttcttc agaaatgaaa aaaaaaaaaa 750  
 aaaaaa 756

<210> 8  
 <211> 189  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> sig\_peptide  
 <222> 1-24  
 <223> Signal Peptide

<220>  
 <221> misc\_feature  
 <222> 4-10, 5-11, 47-53, 170-176, 176-182  
 <223> N-Myristoylation Site.

<220>  
 <221> misc\_feature  
 <222> 44-85  
 <223> G-protein Coupled Receptors Proteins.

<220>  
 <221> misc\_feature  
 <222> 54-65  
 <223> Prokaryotic Membrane Lipoprotein Lipid Attachment Site.

<220>  
 <221> misc\_feature  
 <222> 82-86  
 <223> Casein Kinase II Phosphorylation Site.

<220>

<221> TRANSMEM  
 <222> 86-103, 60-75  
 <223> Transmembrane Domain

<220>  
 <221> misc\_feature  
 <222> 144-151  
 <223> Tyrosine Kinase Phosphorylation Site.

<400> 8  
 Met Glu Glu Gly Gly Asn Leu Gly Gly Leu Ile Lys Met Val His  
   1                  5                  10                  15  
  
 Leu Leu Val Leu Ser Gly Ala Trp Gly Met Gln Met Trp Val Thr  
                   20                  25                  30  
  
 Phe Val Ser Gly Phe Leu Leu Phe Arg Ser Leu Pro Arg His Thr  
                   35                  40                  45  
  
 Phe Gly Leu Val Gln Ser Lys Leu Phe Pro Phe Tyr Phe His Ile  
                   50                  55                  60  
  
 Ser Met Gly Cys Ala Phe Ile Asn Leu Cys Ile Leu Ala Ser Gln  
                   65                  70                  75  
  
 His Ala Trp Ala Gln Leu Thr Phe Trp Glu Ala Ser Gln Leu Tyr  
                   80                  85                  90  
  
 Leu Leu Phe Leu Ser Leu Thr Leu Ala Thr Val Asn Ala Arg Trp  
                   95                  100                  105  
  
 Leu Glu Pro Arg Thr Thr Ala Ala Met Trp Ala Leu Gln Thr Val  
                   110                  115                  120  
  
 Glu Lys Glu Arg Gly Leu Gly Gly Glu Val Pro Gly Ser His Gln  
                   125                  130                  135  
  
 Gly Pro Asp Pro Tyr Arg Gln Leu Arg Glu Lys Asp Pro Lys Tyr  
                   140                  145                  150  
  
 Ser Ala Leu Arg Gln Asn Phe Phe Arg Tyr His Gly Leu Ser Ser  
                   155                  160                  165  
  
 Leu Cys Asn Leu Gly Cys Val Leu Ser Asn Gly Leu Cys Leu Ala  
                   170                  175                  180  
  
 Gly Leu Ala Leu Glu Ile Arg Ser Leu  
                   185

<210> 9  
 <211> 1508  
 <212> DNA  
 <213> Homo sapiens

<400> 9  
 aattcagatt ttaagcccat tctgcagtgg aatttcatga actagcaaga 50

ggacaccatc ttcttgtatt atacaagaaa ggagtgtacc tatcacacac 100  
agggggaaaa atgctctttt gggtgctagg cctcctaata ctctgtgggt 150  
ttctgtggac tcgtaaagga aaactaaaga ttgaagacat cactgataag 200  
tacattttta tcaactggatg tgactcgggc tttggaaact tggcagccag 250  
aacttttgat aaaaagggat ttcatgtaat cgctgcctgt ctgactgaat 300  
caggatcaac agctttaaag gcagaaacct cagagagact tcgtactgtg 350  
cttctggatg tgaccgaccc agagaatgtc aagaggactg cccagtgggt 400  
gaagaaccaa gttggggaga aaggtctctg gggctctgat aataatgctg 450  
gtgttcccg cgtgctggct cccactgact ggctgacact agaggactac 500  
agagaacctt ttgaagtga cctgtttgga ctcactcagt tgacactaaa 550  
tatgcttcc ttggtcaaga aagctcaagg gagagttatt aatgtctcca 600  
gtgttgagg tcgccttgca atcgttggag ggggctatac tccatccaaa 650  
tatgcagtgg aaggtttcaa tgacagctta agacgggaca tgaaagcttt 700  
tgggtgtcac gtctcatgca ttgaaccagg attgttcaaa acaaacttgg 750  
cagatccagt aaaggtaatt gaaaaaaaaac tcgccatttg ggagcagctg 800  
tctccagaca tcaacaaca atatggagaa ggttacattg aaaaaagtct 850  
agacaaactg aaaggcaata aatcctatgt gaacatggac ctctctccgg 900  
tggtagagt catggaccac gctctaaca gtctcttccc taagactcat 950  
tatgccgctg gaaaagatgc caaaattttc tggatacctc tgtctcacat 1000  
gccagcagct ttgcaagact ttttattgtt gaaacagaaa gcagagctgg 1050  
ctaataccaa ggcagtgtga ctcagctaac cacaatgtc tcctccaggc 1100  
tatgaaattg gccgatttca agaacacatc tccttttcaa cccatttcc 1150  
tatctgctcc aacctggact catttagatc gtgcttattt ggattgcaaa 1200  
agggagtccc accatcgctg gtggtatccc agggtccttg ctcaagtttt 1250  
ctttgaaaag gagggctgga atggtacatc acataggcaa gtcctgccct 1300  
gtatttaggc ttgctgctg tgggtgtgat taagggaat tgaaagactt 1350  
gcccattcaa aatgatcttt accgtggcct gcccattgct tatgggtccc 1400  
agcatttaca gtaacttgtg aatgttaagt atcatctctt atctaaatat 1450  
taaaagataa gtcaacccaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 1500

aaaaaaaa 1508

<210> 10

<211> 319

<212> PRT

<213> Homo sapiens

<220>

<221> sig\_peptide

<222> 1-17

<223> Signal Peptide

<220>

<221> misc\_feature

<222> 36-47, 108-113, 166-171,198-203, 207-212

<223> N-myristoylation Sites.

<220>

<221> misc\_feature

<222> 39-42

<223> Glycosaminoglycan Attachment Site.

<220>

<221> TRANSMEM

<222> 136-152

<223> Transmembrane Domain

<220>

<221> misc\_feature

<222> 161-163, 187-190 and 253-256

<223> N-glycosylation Sites.

<400> 10

Met	Leu	Phe	Trp	Val	Leu	Gly	Leu	Leu	Ile	Leu	Cys	Gly	Phe	Leu
1				5					10					15

Trp	Thr	Arg	Lys	Gly	Lys	Leu	Lys	Ile	Glu	Asp	Ile	Thr	Asp	Lys
				20					25					30

Tyr	Ile	Phe	Ile	Thr	Gly	Cys	Asp	Ser	Gly	Phe	Gly	Asn	Leu	Ala
				35					40					45

Ala	Arg	Thr	Phe	Asp	Lys	Lys	Gly	Phe	His	Val	Ile	Ala	Ala	Cys
				50					55					60

Leu	Thr	Glu	Ser	Gly	Ser	Thr	Ala	Leu	Lys	Ala	Glu	Thr	Ser	Glu
				65					70					75

Arg	Leu	Arg	Thr	Val	Leu	Leu	Asp	Val	Thr	Asp	Pro	Glu	Asn	Val
				80					85					90

Lys	Arg	Thr	Ala	Gln	Trp	Val	Lys	Asn	Gln	Val	Gly	Glu	Lys	Gly
				95					100					105

Leu	Trp	Gly	Leu	Ile	Asn	Asn	Ala	Gly	Val	Pro	Gly	Val	Leu	Ala
				110					115					120



Pro Thr Asp Trp	Leu Thr Leu Glu Asp	Tyr Arg Glu Pro Ile Glu	125	130	135
Val Asn Leu Phe	Gly Leu Ile Ser Val	Thr Leu Asn Met Leu Pro	140	145	150
Leu Val Lys Lys	Ala Gln Gly Arg Val	Ile Asn Val Ser Ser Val	155	160	165
Gly Gly Arg Leu	Ala Ile Val Gly Gly	Gly Tyr Thr Pro Ser Lys	170	175	180
Tyr Ala Val Glu	Gly Phe Asn Asp Ser	Leu Arg Arg Asp Met Lys	185	190	195
Ala Phe Gly Val	His Val Ser Cys Ile	Glu Pro Gly Leu Phe Lys	200	205	210
Thr Asn Leu Ala	Asp Pro Val Lys Val	Ile Glu Lys Lys Leu Ala	215	220	225
Ile Trp Glu Gln	Leu Ser Pro Asp Ile	Lys Gln Gln Tyr Gly Glu	230	235	240
Gly Tyr Ile Glu	Lys Ser Leu Asp Lys	Leu Lys Gly Asn Lys Ser	245	250	255
Tyr Val Asn Met	Asp Leu Ser Pro Val	Val Glu Cys Met Asp His	260	265	270
Ala Leu Thr Ser	Leu Phe Pro Lys Thr	His Tyr Ala Ala Gly Lys	275	280	285
Asp Ala Lys Ile	Phe Trp Ile Pro Leu	Ser His Met Pro Ala Ala	290	295	300
Leu Gln Asp Phe	Leu Leu Leu Lys Gln	Lys Ala Glu Leu Ala Asn	305	310	315
Pro Lys Ala Val					

<210> 11

<211> 2720

<212> DNA

<213> Homo sapiens

<400> 11

gcgggctgtt gacggcgctg cgatggctgc ctgcgagggc aggagaagcg 50

gagctctcgg ttcctctcag tcggacttcc tgacgccgcc agtgggaggc 100

gccccttggg ccgtcgccac cactgtagtc atgtaccac cgccgccgcc 150

gccgcctcat cgggacttca tctcggtgac gctgagcttt ggcgagagct 200

atgacaacag caagagttgg cggcggcgct cgtgctggag gaaatggaag 250  
caactgtcga gattgcagcg gaatatgatt ctcttcctcc ttgcctttct 300  
gctttttctgt ggactcctct tctacatcaa cttggctgac cattggaaag 350  
ctctggcttt caggctagag gaagagcaga agatgaggcc agaaattgct 400  
gggttaaaac cagcaaatcc acccgtctta ccagctcctc agaaggcgga 450  
caccgaccct gagaacttac ctgagatttc gtcacagaag acacaaagac 500  
acatccagcg gggaccacct cacctgcaga ttagaccccc aagccaagac 550  
ctgaaggatg ggaccagga ggaggccaca aaaaggcaag aagcccctgt 600  
ggatccccgc ccggaaggag atccgcagag gacagtcatc agctggaggg 650  
gagcggtgat cgagcctgag cagggcaccg agctcccttc aagaagagca 700  
gaagtgccca ccaagcctcc cctgccaccg gccaggacac agggcacacc 750  
agtgcactcg aactatcgcc agaagggcgt gattgacgtc ttcttgcattg 800  
catggaaagg ataccgcaag tttgcatggg gccatgacga gctgaagcct 850  
gtgtccaggt ccttcagtga gtggtttggc ctcggtctca cactgatcga 900  
cgcgctggac accatgtgga tcttgggtct gaggaagaa tttgaggaag 950  
ccaggaagtg ggtgtcgaag aagttacact ttgaaaagga cgtggacgtc 1000  
aacctgtttg agagcacgat ccgcatactg ggggggctcc tgagtgccta 1050  
ccacctgtct ggggacagcc tcttcctgag gaaagctgag gattttggaa 1100  
atcggtaat gcctgccttc agaacaccat ccaagattcc ttactcggat 1150  
gtgaacatcg gtactggagt tgcccacccg ccacggtgga cctccgacag 1200  
cactgtggcc gaggtgacca gcattcagct ggagttccgg gagctctccc 1250  
gtctcagagg ggataagaag ttccaggagg cagtggagaa ggtgacacag 1300  
cacatccacg gcctgtctgg gaagaaggat gggctggtgc ccatgttcat 1350  
caatacccac agtggcctct tcaccacct gggcgtattc acgctgggcg 1400  
ccagggccga cagctactat gagtacctgc tgaagcagtg gatccagggc 1450  
gggaagcagg agacacagct gctggaagac tacgtggaag ccatcgaggg 1500  
tgtcagaacg cacctgtctg ggcactccga gccagtaag ctcacctttg 1550  
tgggggagct tgcccacggc cgcttcagtg ccaagatgga ccacctggtg 1600  
tgcttctctg cagggacgct ggctctgggc gtctaccacg gcctgcccgc 1650

cagccacatg gagctggccc aggagctcat ggagacttgt taccagatga 1700  
 accggcagat ggagacgggg ctgagtcccg agatcgtgca cttcaacctt 1750  
 tacccccagc cgggccgtcg ggacgtggag gtcaagccag cagacaggca 1800  
 caacctgctg cggccagaga ccgtggagag cctgttctac ctgtaccgcg 1850  
 tcacagggga ccgcaaatac caggactggg gctgggagat tctgcagagc 1900  
 ttcagccgat tcacacgggt cccctcgggt ggctattctt ccatcaacaa 1950  
 tgtccaggat cctcagaagc ccgagcctag ggacaagatg gagagcttct 2000  
 tcctggggga gacgctcaag tatctgttct tgcctttctc cgatgacca 2050  
 aacctgctca gcctggacgc ctacgtgttc aacaccgaag cccaccctct 2100  
 gcctatctgg acccctgcct aggggtggatg gctgctggtg tggggacttc 2150  
 ggggtgggcag aggcaccttg ctgggtctgt ggcatTTTcc aaggggccac 2200  
 gtagcaccgg caaccgcaa gtggcccagg ctctgaactg gctctgggct 2250  
 cctcctcgtc tctgctttaa tcaggacacc gtgaggacaa gtgaggccgt 2300  
 cagtcttggt gtgatgcggg gtgggctggg ccgctggagc ctccgcctgc 2350  
 ttctccaga agacacgaat catgactcac gattgctgaa gcctgagcag 2400  
 gtctctgtgg gccgaccaga ggggggcttc gaggtggtcc ctggtactgg 2450  
 ggtgaccgag tggacagccc aggggtgcagc tctgcccggt ctcgtgaagc 2500  
 ctcatatgc cccaatcaa gggctctggag gggctgccgt gactccagag 2550  
 gcctgagggt ccagggtctg ctctgggtgt tacaagctgg actcagggat 2600  
 cctcctggcc gcccgcagg gggcttggag ggctggacgg caagtccgtc 2650  
 tagctcacgg gccctccag tggaatgggt cttttcgggt gagataaaag 2700  
 ttgatttgct ctaaccgcaa 2720

<210> 12

<211> 699

<212> PRT

<213> Homo sapiens

<220>

<221> TRANSMEM

<222> 21-40 and 84-105

<223> Transmembrane Domain (type II)

<400> 12

Met Ala Ala Cys Glu Gly Arg Arg Ser Gly Ala Leu Gly Ser Ser

1	5	10	15
Gln Ser Asp Phe	Leu Thr Pro Pro Val	Gly Gly Ala Pro Trp	Ala
	20	25	30
Val Ala Thr Thr	Val Val Met Tyr Pro	Pro Pro Pro Pro	Pro
	35	40	45
His Arg Asp Phe	Ile Ser Val Thr Leu	Ser Phe Gly Glu Ser Tyr	
	50	55	60
Asp Asn Ser Lys	Ser Trp Arg Arg Arg	Ser Cys Trp Arg Lys Trp	
	65	70	75
Lys Gln Leu Ser	Arg Leu Gln Arg Asn Met	Ile Leu Phe Leu Leu	
	80	85	90
Ala Phe Leu Leu	Phe Cys Gly Leu Leu	Phe Tyr Ile Asn Leu Ala	
	95	100	105
Asp His Trp Lys	Ala Leu Ala Phe Arg	Leu Glu Glu Glu Gln Lys	
	110	115	120
Met Arg Pro Glu	Ile Ala Gly Leu Lys	Pro Ala Asn Pro Pro Val	
	125	130	135
Leu Pro Ala Pro	Gln Lys Ala Asp Thr	Asp Pro Glu Asn Leu Pro	
	140	145	150
Glu Ile Ser Ser	Gln Lys Thr Gln Arg	His Ile Gln Arg Gly Pro	
	155	160	165
Pro His Leu Gln	Ile Arg Pro Pro Ser	Gln Asp Leu Lys Asp Gly	
	170	175	180
Thr Gln Glu Glu	Ala Thr Lys Arg Gln	Glu Ala Pro Val Asp Pro	
	185	190	195
Arg Pro Glu Gly	Asp Pro Gln Arg Thr	Val Ile Ser Trp Arg Gly	
	200	205	210
Ala Val Ile Glu	Pro Glu Gln Gly Thr	Glu Leu Pro Ser Arg Arg	
	215	220	225
Ala Glu Val Pro	Thr Lys Pro Pro Leu	Pro Pro Ala Arg Thr Gln	
	230	235	240
Gly Thr Pro Val	His Leu Asn Tyr Arg	Gln Lys Gly Val Ile Asp	
	245	250	255
Val Phe Leu His	Ala Trp Lys Gly Tyr	Arg Lys Phe Ala Trp Gly	
	260	265	270
His Asp Glu Leu	Lys Pro Val Ser Arg	Ser Phe Ser Glu Trp Phe	
	275	280	285
Gly Leu Gly Leu	Thr Leu Ile Asp Ala	Leu Asp Thr Met Trp Ile	

	290	295	300
Leu Gly Leu Arg	Lys Glu Phe Glu Glu	Ala Arg Lys Trp Val	Ser
	305	310	315
Lys Lys Leu His	Phe Glu Lys Asp Val	Asp Val Asn Leu Phe	Glu
	320	325	330
Ser Thr Ile Arg	Ile Leu Gly Gly Leu	Leu Ser Ala Tyr His	Leu
	335	340	345
Ser Gly Asp Ser	Leu Phe Leu Arg Lys	Ala Glu Asp Phe Gly	Asn
	350	355	360
Arg Leu Met Pro	Ala Phe Arg Thr Pro	Ser Lys Ile Pro Tyr	Ser
	365	370	375
Asp Val Asn Ile	Gly Thr Gly Val Ala	His Pro Pro Arg Trp	Thr
	380	385	390
Ser Asp Ser Thr	Val Ala Glu Val Thr	Ser Ile Gln Leu Glu	Phe
	395	400	405
Arg Glu Leu Ser	Arg Leu Thr Gly Asp	Lys Lys Phe Gln Glu	Ala
	410	415	420
Val Glu Lys Val	Thr Gln His Ile His	Gly Leu Ser Gly Lys	Lys
	425	430	435
Asp Gly Leu Val	Pro Met Phe Ile Asn	Thr His Ser Gly Leu	Phe
	440	445	450
Thr His Leu Gly	Val Phe Thr Leu Gly	Ala Arg Ala Asp Ser	Tyr
	455	460	465
Tyr Glu Tyr Leu	Leu Lys Gln Trp Ile	Gln Gly Gly Lys Gln	Glu
	470	475	480
Thr Gln Leu Leu	Glu Asp Tyr Val Glu	Ala Ile Glu Gly Val	Arg
	485	490	495
Thr His Leu Leu	Arg His Ser Glu Pro	Ser Lys Leu Thr Phe	Val
	500	505	510
Gly Glu Leu Ala	His Gly Arg Phe Ser	Ala Lys Met Asp His	Leu
	515	520	525
Val Cys Phe Leu	Pro Gly Thr Leu Ala	Leu Gly Val Tyr His	Gly
	530	535	540
Leu Pro Ala Ser	His Met Glu Leu Ala	Gln Glu Leu Met Glu	Thr
	545	550	555
Cys Tyr Gln Met	Asn Arg Gln Met Glu	Thr Gly Leu Ser Pro	Glu
	560	565	570
Ile Val His Phe	Asn Leu Tyr Pro Gln	Pro Gly Arg Arg Asp	Val

	575	580	585
Glu Val Lys Pro	Ala Asp Arg His Asn	Leu Leu Arg Pro	Glu Thr
	590	595	600
Val Glu Ser Leu	Phe Tyr Leu Tyr Arg	Val Thr Gly Asp Arg	Lys
	605	610	615
Tyr Gln Asp Trp	Gly Trp Glu Ile Leu	Gln Ser Phe Ser Arg	Phe
	620	625	630
Thr Arg Val Pro	Ser Gly Gly Tyr Ser	Ser Ile Asn Asn Val	Gln
	635	640	645
Asp Pro Gln Lys	Pro Glu Pro Arg Asp	Lys Met Glu Ser Phe	Phe
	650	655	660
Leu Gly Glu Thr	Leu Lys Tyr Leu Phe	Leu Leu Phe Ser Asp	Asp
	665	670	675
Pro Asn Leu Leu	Ser Leu Asp Ala Tyr	Val Phe Asn Thr Glu	Ala
	680	685	690
His Pro Leu Pro	Ile Trp Thr Pro Ala		
	695		

<210> 13

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 13

cgccagaagg gcgtgattga cgtc 24

<210> 14

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 14

ccatccttct tcccagacag gccg 24

<210> 15

<211> 44

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 15

gaagcctgtg tccaggtcct tcagtgagtg gtttggcctc ggtc 44

<210> 16

<211> 1524

<212> DNA

<213> Homo sapiens

<400> 16

ggcgccgcgt aggcccgga ggccgggccc gccgggctgc gagcgctgc 50  
cccatgcgcc gccgctctc cgacgatgt tcccctcgcg gaggaagcg 100  
gcgcagctgc cctgggagga cggcaggtcc gggttgctct ccggcgccct 150  
ccctcggaag tggtccgtct tccacctgtt cgtggcctgc ctctcgctgg 200  
gcttcttctc cctactctgg ctgcagctca gctgctctgg ggacgtggcc 250  
cgggcagtca ggggacaagg gcaggagacc tcgggccctc cccgtgcctg 300  
ccccccagag ccgccccctg agcactggga agaagacgca tcctggggcc 350  
cccaccgcct ggcaagtgtg gtgcccttcc gcgaacgctt cgaggagctc 400  
ctggtcttcg tgccccacat gcgccgcttc ctgagcagga agaagatccg 450  
gcaccacatc tacgtgtcga accaggtgga ccacttcagg ttcaaccggg 500  
cagcgctcat caacgtgggc ttcttgaga gcagcaacag cacggactac 550  
attgccatgc acgacgttga cctgctccct ctcaacgagg agctggacta 600  
tggttttctc gaggtgggc ccttccacgt ggctccccg gagctccacc 650  
ctctctacca ctacaagacc tatgtcggcg gcctcctgct gctctccaag 700  
cagcactacc ggctgtgcaa tgggatgtcc aaccgcttct ggggctgggg 750  
ccgcgaggac gacgagttct accggcgcat taaggagct gggctccagc 800  
ttttccgcc ctcgggaatc acaactgggt acaagacatt tcgccacctg 850  
catgaccag cctggcgga gagggaccag aagcgcatcg cagctcaaaa 900  
acaggagcag ttcaaggtgg acagggaggg aggcctgaac actgtgaagt 950  
accatgtggc ttcccgact gccctgtctg tgggcggggc cccctgcact 1000  
gtcctcaaca tcatgttga ctgtgacaag accgccacac cctggtgcac 1050  
attcagctga gctggatgga cagtgaggaa gcctgtacct acaggccata 1100  
ttgtcaggc tcaggacaag gcctcaggtc gtgggccag ctctgacagg 1150  
atgtggagt gccaggacca agacagcaag ctacgcaatt gcagccacc 1200  
ggccgccaag gcaggcttg gctgggccag gacacgtgg gtgcctggga 1250

cgctgcttgc catgcacagt gatcagagag aggctggggt gtgtcctgtc 1300  
 cgggaccccc cctgccttcc tgctcaccct actctgacct ccttcacgtg 1350  
 cccaggcctg tgggtagtgg ggagggtga acaggacaac ctctcatcac 1400  
 cctactctga cctccttcac gtgcccaggc ctgtgggtag tggggagggc 1450  
 tgaacaggac aacctctcat ccccccaaa aaaaaaaaaa aaaaaaaaaa 1500  
 aaaaaaaaaa aaaaaaaaaa aaaa 1524

<210> 17  
 <211> 327  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> sig\_peptide  
 <222> 1-42  
 <223> Signal peptide.

<220>  
 <221> misc\_feature  
 <222> 19-25,65-71,247-253,285-291,303-310  
 <223> N-myristoylation site.

<220>  
 <221> misc\_feature  
 <222> 27-31  
 <223> cAMP- and cGMP-dependent protein kinase phosphorylation site.

<220>  
 <221> TRANSMEM  
 <222> 29-49  
 <223> Transmembrane domain (type II).

<220>  
 <221> misc\_feature  
 <222> 154-158  
 <223> N-glycosylation site.

<220>  
 <221> misc\_feature  
 <222> 226-233  
 <223> Tyrosine kinase phosphorylation site.

<400> 17  
 Met Phe Pro Ser Arg Arg Lys Ala Ala Gln Leu Pro Trp Glu Asp  
     1                    5                    10                    15  
 Gly Arg Ser Gly Leu Leu Ser Gly Gly Leu Pro Arg Lys Cys Ser  
                     20                    25                    30  
 Val Phe His Leu Phe Val Ala Cys Leu Ser Leu Gly Phe Phe Ser  
                     35                    40                    45



Leu	Leu	Trp	Leu	Gln	Leu	Ser	Cys	Ser	Gly	Asp	Val	Ala	Arg	Ala
				50					55					60
Val	Arg	Gly	Gln	Gly	Gln	Glu	Thr	Ser	Gly	Pro	Pro	Arg	Ala	Cys
				65					70					75
Pro	Pro	Glu	Pro	Pro	Pro	Glu	His	Trp	Glu	Glu	Asp	Ala	Ser	Trp
				80					85					90
Gly	Pro	His	Arg	Leu	Ala	Val	Leu	Val	Pro	Phe	Arg	Glu	Arg	Phe
				95					100					105
Glu	Glu	Leu	Leu	Val	Phe	Val	Pro	His	Met	Arg	Arg	Phe	Leu	Ser
				110					115					120
Arg	Lys	Lys	Ile	Arg	His	His	Ile	Tyr	Val	Leu	Asn	Gln	Val	Asp
				125					130					135
His	Phe	Arg	Phe	Asn	Arg	Ala	Ala	Leu	Ile	Asn	Val	Gly	Phe	Leu
				140					145					150
Glu	Ser	Ser	Asn	Ser	Thr	Asp	Tyr	Ile	Ala	Met	His	Asp	Val	Asp
				155					160					165
Leu	Leu	Pro	Leu	Asn	Glu	Glu	Leu	Asp	Tyr	Gly	Phe	Pro	Glu	Ala
				170					175					180
Gly	Pro	Phe	His	Val	Ala	Ser	Pro	Glu	Leu	His	Pro	Leu	Tyr	His
				185					190					195
Tyr	Lys	Thr	Tyr	Val	Gly	Gly	Ile	Leu	Leu	Leu	Ser	Lys	Gln	His
				200					205					210
Tyr	Arg	Leu	Cys	Asn	Gly	Met	Ser	Asn	Arg	Phe	Trp	Gly	Trp	Gly
				215					220					225
Arg	Glu	Asp	Asp	Glu	Phe	Tyr	Arg	Arg	Ile	Lys	Gly	Ala	Gly	Leu
				230					235					240
Gln	Leu	Phe	Arg	Pro	Ser	Gly	Ile	Thr	Thr	Gly	Tyr	Lys	Thr	Phe
				245					250					255
Arg	His	Leu	His	Asp	Pro	Ala	Trp	Arg	Lys	Arg	Asp	Gln	Lys	Arg
				260					265					270
Ile	Ala	Ala	Gln	Lys	Gln	Glu	Gln	Phe	Lys	Val	Asp	Arg	Glu	Gly
				275					280					285
Gly	Leu	Asn	Thr	Val	Lys	Tyr	His	Val	Ala	Ser	Arg	Thr	Ala	Leu
				290					295					300
Ser	Val	Gly	Gly	Ala	Pro	Cys	Thr	Val	Leu	Asn	Ile	Met	Leu	Asp
				305					310					315
Cys	Asp	Lys	Thr	Ala	Thr	Pro	Trp	Cys	Thr	Phe	Ser			
				320					325					

<210> 18  
<211> 23  
<212> DNA  
<<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 18  
gcgaacgctt cgaggagtcc tgg 23

<210> 19  
<211> 24  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 19  
gcagtgcggg aagccacatg gtac 24

<210> 20  
<211> 46  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 20  
cttcctgagc aggaagaaga tccggcacca catctacgtg ctcaac 46

<210> 21  
<211> 494  
<212> DNA  
<213> Homo sapiens

<400> 21  
caatgtttgc ctatccacct cccccaagcc cctttaccta tgetgctgct 50  
aacgctgctg ctgctgctgc tgctgcttaa aggctcatgc ttggagtggg 100  
gactgggctgg tgcccagaaa gtctcttctg ccaactgacgc ccccatcagg 150  
gattgggcct tctttccccc ttcctttctg tgtctcctgc ctcatcggcc 200  
tgccatgacc tgcagccaag cccagccccg tggggaaggg gagaaagtgg 250  
gggatggcta agaaagctgg gagataggga acagaagagg gtagtgggtg 300  
ggctaggggg gctgccttat ttaaagtggg tgtttatgat tcttatacta 350  
atttatacaa agatattaag gccctgttca ttaagaaatt gttcccttcc 400  
cctgtgttca atgtttgtaa agattgttct gtgtaaatat gtctttataa 450

taaacagtta aaagctgaaa aaaaaaaaaa aaaaaaaaaa aaaa 494

<210> 22

<211> 73

<212> PRT

<213> Homo sapiens

<220>

<221> sig\_peptide

<222> 1-15

<223> Signal peptide.

<220>

<221> misc\_feature

<222> 3-18

<223> Growth factor and cytokines receptors family.

<400> 22

Met	Leu	Leu	Leu	Thr	Leu	Leu	Leu	Leu	Leu	Leu	Leu	Lys	Gly
1				5				10					15

Ser	Cys	Leu	Glu	Trp	Gly	Leu	Val	Gly	Ala	Gln	Lys	Val	Ser	Ser
			20					25						30

Ala	Thr	Asp	Ala	Pro	Ile	Arg	Asp	Trp	Ala	Phe	Phe	Pro	Pro	Ser
			35					40						45

Phe	Leu	Cys	Leu	Leu	Pro	His	Arg	Pro	Ala	Met	Thr	Cys	Ser	Gln
			50					55						60

Ala	Gln	Pro	Arg	Gly	Glu	Gly	Glu	Lys	Val	Gly	Asp	Gly
			65					70				

<210> 23

<211> 2883

<212> DNA

<213> Homo sapiens

<400> 23

gggacccatg cggccgtgac ccccggtccc ctagaggccc agcgcagccg 50

cagcggacaa aggagcatgt ccgcgcgggg gaaggcccgt cctccggccg 100

ccataaggct ccggtcgccg ctggggccgc gccgcgctcc tgcccgcccg 150

ggctccgggg cggcccgcta ggccagtgcg ccgcgcgtcg ccccgaggcg 200

cccgccccgc agcatggagc caccgggacg ccggcggggc cgcgcgcagc 250

cgccgctgtt gctgccgctc tcgctgttag cgctgctcgc gctgctggga 300

ggcggcgggc gcggcggcgc cgcggcgctg cccgccggct gcaagcacga 350

tgggcggccc cgaggggctg gcagggcggc gggcgccgcc gagggcaagg 400

tgggtgtgcag cagcctggaa ctgcgcgagg tcctgcccc agatactctg 450

cccaaccgca cggtcaccct gattctgagt aacaataaga tatccgagct 500  
gaagaatggc tcattttctg gggttaagtct ccttgaaaga ttggacctcc 550  
gaaacaatct tattagtagt atagatccag gtgccttctg gggactgtca 600  
tctctaaaaa gattggatct gacaaacaat cgaataggat gtctgaatgc 650  
agacatattt cgaggactca ccaatctggg tccgctaaac ctttcgggga 700  
atttgttttc ttcattatct caaggaactt ttgattatct tgcgtcatta 750  
cggctcttgg aattccagac tgagtatctt ttgtgtgact gtaacatact 800  
gtggatgcat cgctgggtaa aggagaagaa catcacggta cgggatacca 850  
gggtgtgttta tcctaagtca ctgcaggccc aaccagtcac aggcgtgaag 900  
caggagctgt tgacatgcga ccctccgctt gaattgccgt ctttctacat 950  
gactccatct catcgccaag ttgtgtttga aggagacagc cttcctttcc 1000  
agtgcattggc ttcatatatt gatcaggaca tgcaagtgtt gtggtatcag 1050  
gatgggagaa tagttgaaac cgatgaatcg caaggatatt ttgttgaaaa 1100  
gaacatgatt cacaactgct ccttgattgc aagtgcccta accattttcta 1150  
atattcaggc tggatctact ggaaattggg gctgtcatgt ccagaccaa 1200  
cgtgggaata atacaggac tgtggatatt gtggtattag agagtctctgc 1250  
acagtactgt cctccagaga ggggtggtaaa caacaaaggc gacttcagat 1300  
ggcccagaac attggcaggc attactgcat atctgcagtg tacgcggaac 1350  
acccatggca gtgggatata tcccggaac ccacaggatg agagaaaagc 1400  
ttggcgcaga tgtgatagag gtggcttttg ggcagatgat gattattctc 1450  
gctgtcagta tgcaaatgat gtcactagag ttctttatat gtttaatcag 1500  
atgccctca atcttaccaa tgccgtggca acagctcgac agttactggc 1550  
ttacactgtg gaagcagcca acttttctga caaaatggat gttatatttg 1600  
tggcagaaat gattgaaaaa tttggaagat ttaccaagga ggaaaaatca 1650  
aaagagctag gtgacgtgat ggttgacatt gcaagtaaca tcatgttggc 1700  
tgatgaacgt gtctgtggc tggcgcagag ggaagctaaa gcctgcagta 1750  
ggattgtgca gtgtcttcag cgcattgcta cctaccggct agccggtgga 1800  
gtcacggtt attcaacata ttcaccaat attgctctgg aagcttatgt 1850

catcaagtct actggcttca cggggatgac ctgtaccgtg ttccagaaag 1900  
tggcagcctc tgatcgtaca ggactttcgg attatgggag gcgggatcca 1950  
gagggaaacc tggataagca gctgagcttt aagtgcaatg tttcaaatac 2000  
attttcgagt ctggcactaa aggtatgtta cattctgcaa tcatttaaga 2050  
ctatttacag ttaaattaga atgctccaaa tgttctgctt cgcaaaataa 2100  
ccttattaaa agattttttt ttgcaggaag ataggtatta ttgcttttgc 2150  
tactgtttta aagaaaacta accaggaaga actgcattac gactttcaag 2200  
ggccctaggc atttttgcct ttgattccct ttcttcacat aaaaatatca 2250  
gaaattacat tttataactg cagtgggtata aatgcaaata tactattggt 2300  
acatgtgaaa aaattttatt tgacttaaaa gtttatttat ttgttttttt 2350  
gctcctgatt ttaagacaat aagatgtttt catgggcccc taaaagtatc 2400  
atgagccttt ggcaactgcg ctgccaaagg tagtggagaa gtcaaccctg 2450  
agaccaggtg tttaatcaag caagctgtat atcaaaattt ttggcagaaa 2500  
acacaaatat gtcatatatc tttttttaaa aaaagtattt cattgaagca 2550  
agcaaatga aagcattttt actgattttt aaaattgggtg ctttagatat 2600  
atttgactac actgtattga agcaaataga ggaggcacia ctccagcacc 2650  
ctaattggaac cacatttttt tcaattagct ttctgtgggc atgtgtaatt 2700  
gtattctctg cggtttttta totcacagta ctttatttct gtcttgtccc 2750  
tcaataatat cacaacaat attccagtca ttttaatggc tgcataataa 2800  
ctgatccaac aggtgttagg tgttctgggt tagtgtgagc actcaataaa 2850  
tattgaatga atgaacgaaa aaaaaaaaaa aaa 2883

<210> 24

<211> 616

<212> PRT

<213> Homo sapiens

<220>

<221> sig\_peptide

<222> 1-33

<223> Signal peptide.

<220>

<221> TRANSMEM

<222> 13-40

<223> Transmembrane domain (type II).

<400> 24

Met	Glu	Pro	Pro	Gly	Arg	Arg	Arg	Gly	Arg	Ala	Gln	Pro	Pro	Leu
1				5					10					15
Leu	Leu	Pro	Leu	Ser	Leu	Leu	Ala	Leu	Leu	Ala	Leu	Leu	Gly	Gly
				20					25					30
Gly	Gly	Gly	Gly	Gly	Ala	Ala	Ala	Leu	Pro	Ala	Gly	Cys	Lys	His
				35					40					45
Asp	Gly	Arg	Pro	Arg	Gly	Ala	Gly	Arg	Ala	Ala	Gly	Ala	Ala	Glu
				50					55					60
Gly	Lys	Val	Val	Cys	Ser	Ser	Leu	Glu	Leu	Ala	Gln	Val	Leu	Pro
				65					70					75
Pro	Asp	Thr	Leu	Pro	Asn	Arg	Thr	Val	Thr	Leu	Ile	Leu	Ser	Asn
				80					85					90
Asn	Lys	Ile	Ser	Glu	Leu	Lys	Asn	Gly	Ser	Phe	Ser	Gly	Leu	Ser
				95					100					105
Leu	Leu	Glu	Arg	Leu	Asp	Leu	Arg	Asn	Asn	Leu	Ile	Ser	Ser	Ile
				110					115					120
Asp	Pro	Gly	Ala	Phe	Trp	Gly	Leu	Ser	Ser	Leu	Lys	Arg	Leu	Asp
				125					130					135
Leu	Thr	Asn	Asn	Arg	Ile	Gly	Cys	Leu	Asn	Ala	Asp	Ile	Phe	Arg
				140					145					150
Gly	Leu	Thr	Asn	Leu	Val	Arg	Leu	Asn	Leu	Ser	Gly	Asn	Leu	Phe
				155					160					165
Ser	Ser	Leu	Ser	Gln	Gly	Thr	Phe	Asp	Tyr	Leu	Ala	Ser	Leu	Arg
				170					175					180
Ser	Leu	Glu	Phe	Gln	Thr	Glu	Tyr	Leu	Leu	Cys	Asp	Cys	Asn	Ile
				185					190					195
Leu	Trp	Met	His	Arg	Trp	Val	Lys	Glu	Lys	Asn	Ile	Thr	Val	Arg
				200					205					210
Asp	Thr	Arg	Cys	Val	Tyr	Pro	Lys	Ser	Leu	Gln	Ala	Gln	Pro	Val
				215					220					225
Thr	Gly	Val	Lys	Gln	Glu	Leu	Leu	Thr	Cys	Asp	Pro	Pro	Leu	Glu
				230					235					240
Leu	Pro	Ser	Phe	Tyr	Met	Thr	Pro	Ser	His	Arg	Gln	Val	Val	Phe
				245					250					255
Glu	Gly	Asp	Ser	Leu	Pro	Phe	Gln	Cys	Met	Ala	Ser	Tyr	Ile	Asp
				260					265					270
Gln	Asp	Met	Gln	Val	Leu	Trp	Tyr	Gln	Asp	Gly	Arg	Ile	Val	Glu
				275					280					285

Thr Asp Glu Ser	Gln Gly Ile Phe Val	Glu Lys Asn Met Ile His	290	295	300
Asn Cys Ser Leu	Ile Ala Ser Ala Leu	Thr Ile Ser Asn Ile Gln	305	310	315
Ala Gly Ser Thr	Gly Asn Trp Gly Cys	His Val Gln Thr Lys Arg	320	325	330
Gly Asn Asn Thr	Arg Thr Val Asp Ile	Val Val Leu Glu Ser Ser	335	340	345
Ala Gln Tyr Cys	Pro Pro Glu Arg Val	Val Asn Asn Lys Gly Asp	350	355	360
Phe Arg Trp Pro	Arg Thr Leu Ala Gly	Ile Thr Ala Tyr Leu Gln	365	370	375
Cys Thr Arg Asn	Thr His Gly Ser Gly	Ile Tyr Pro Gly Asn Pro	380	385	390
Gln Asp Glu Arg	Lys Ala Trp Arg Arg	Cys Asp Arg Gly Gly Phe	395	400	405
Trp Ala Asp Asp	Asp Tyr Ser Arg Cys	Gln Tyr Ala Asn Asp Val	410	415	420
Thr Arg Val Leu	Tyr Met Phe Asn Gln	Met Pro Leu Asn Leu Thr	425	430	435
Asn Ala Val Ala	Thr Ala Arg Gln Leu	Leu Ala Tyr Thr Val Glu	440	445	450
Ala Ala Asn Phe	Ser Asp Lys Met Asp	Val Ile Phe Val Ala Glu	455	460	465
Met Ile Glu Lys	Phe Gly Arg Phe Thr	Lys Glu Glu Lys Ser Lys	470	475	480
Glu Leu Gly Asp	Val Met Val Asp Ile	Ala Ser Asn Ile Met Leu	485	490	495
Ala Asp Glu Arg	Val Leu Trp Leu Ala	Gln Arg Glu Ala Lys Ala	500	505	510
Cys Ser Arg Ile	Val Gln Cys Leu Gln	Arg Ile Ala Thr Tyr Arg	515	520	525
Leu Ala Gly Gly	Ala His Val Tyr Ser	Thr Tyr Ser Pro Asn Ile	530	535	540
Ala Leu Glu Ala	Tyr Val Ile Lys Ser	Thr Gly Phe Thr Gly Met	545	550	555
Thr Cys Thr Val	Phe Gln Lys Val Ala	Ala Ser Asp Arg Thr Gly	560	565	570

Leu Ser Asp Tyr Gly Arg Arg Asp Pro Glu Gly Asn Leu Asp Lys  
575 580 585

Gln Leu Ser Phe Lys Cys Asn Val Ser Asn Thr Phe Ser Ser Leu  
590 595 600

Ala Leu Lys Val Cys Tyr Ile Leu Gln Ser Phe Lys Thr Ile Tyr  
605 610 615

Ser

<210> 25  
<211> 24  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 25  
gaggactcac caatctgggt cggc 24

<210> 26  
<211> 24  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 26  
aactggaaag gaaggctgtc tccc 24

<210> 27  
<211> 50  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 27  
gtaaaggaga agaacatcac ggtacgggat accaggtgtg tttatcctaa 50

<210> 28  
<211> 683  
<212> DNA  
<213> Homo sapiens

<400> 28  
gcgtggggat gtctaggagc tcgaagggtg tgctgggcct ctcggtgctg 50  
ctgacggcgg ccacagtggc cggcgtacat gtgaagcagc agtgggacca 100  
gcagaggctt cgtgaaggag ttatcagaga cattgagagg caaattcgga 150



aaaaagaaaa cattcgtctt ttgggagAAC agattatTTT gactgagcaa 200  
 cttgaagcag aaagagagaa gatgttattg gcaaaaggat ctcaaaaatc 250  
 atgacttgaa tgtgaaatat ctgttggaCa gacaacacga gtttgtgtgt 300  
 gtgtgttgat ggagagtagc ttagtagtat cttcatcttt ttttttggtc 350  
 actgtccttt taaacttgat caaataaagg acagtgggtc atataagtta 400  
 ctgctttcag ggtcccttat atctgaataa aggagtgtgg gcagacactt 450  
 tttggaagag tctgtctggg tgatcctggt agaagcccca ttagggtcac 500  
 tgtccagtgc ttagggttgt tactgagaag cactgccgag cttgtgagaa 550  
 ggaagggatg gatagtagca tccacctgag tagtctgac agtcggcatg 600  
 atgacgaagc cagagaaca tcgacctcag aaggactgga ggaaggtgaa 650  
 gtggagggag agacgctcct gatcgtcgaa tcc 683

<210> 29  
 <211> 81  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> sig\_peptide  
 <222> 1-21  
 <223> Signal peptide.

<400> 29  
 Met Ser Arg Ser Ser Lys Val Val Leu Gly Leu Ser Val Leu Leu  
 1 5 10 15  
 Thr Ala Ala Thr Val Ala Gly Val His Val Lys Gln Gln Trp Asp  
 20 25 30  
 Gln Gln Arg Leu Arg Asp Gly Val Ile Arg Asp Ile Glu Arg Gln  
 35 40 45  
 Ile Arg Lys Lys Glu Asn Ile Arg Leu Leu Gly Glu Gln Ile Ile  
 50 55 60  
 Leu Thr Glu Gln Leu Glu Ala Glu Arg Glu Lys Met Leu Leu Ala  
 65 70 75  
 Lys Gly Ser Gln Lys Ser  
 80

<210> 30  
 <211> 2128  
 <212> DNA  
 <213> Homo sapiens

<400> 30

ctgtcgtctt tgcttcagcc gcagtcgcca ctggctgcct gaggtgctct 50  
tacagcctgt tccaagtgtg gcttaatccg tctccaccac cagatctttc 100  
tccgtggatt cctctgctaa gaccgctgcc atgccagtga cggttaaccg 150  
caccaccatc acaaccacca cgacgtcatc ttcgggcctg gggcccccca 200  
tgatcgtggg gtccccctcg gccctgacac agccccctggg tctccttcgc 250  
ctgctgcagc tgggtgtctac ctgctgggcc ttctcgtctg tggttagcgt 300  
gggcgcctgg acgggggtcca tgggcaactg gtccatgttc acctggtgct 350  
tctgcttctc cgtgaccctg atcatcctca tcgtggagct gtgcgggctc 400  
caggccccgt tccccctgtc ttggcgcaac ttcccatca ccttcgcctg 450  
ctatgcggcc ctctttctgcc tctcgccctc catcatctac cccaccacct 500  
atgtccagtt cctgtcccaac ggccgttcgc gggaccacgc catcgccgcc 550  
accttcttct cctgcatcgc gtgtgtggct tacgccaccg aagtggcctg 600  
gaccggggcc cggccccggc agatcactgg ctatatggcc accgtaccg 650  
ggctgctgaa ggtgctggag accttcgttg cctgcatcat cttcgcgttc 700  
atcagcgacc ccaacctgta ccagcaccag ccggccctgg agtgggtcgt 750  
ggcgggtgtac gccatctgct tcctcctagc ggccatcgcc atcctgctga 800  
acctggggga gtgcaccaac gtgctacca tccccctccc cagcttcctg 850  
tcggggctgg ccttgctgtc tgtcctctc tatgccaccg cccttgttct 900  
ctggcccctc taccagttcg atgagaagta tggcgccag cctcggcgct 950  
cgagagatgt aagctgcagc cgcagccatg cctactacgt gtgtgcctgg 1000  
gaccgccgac tggtgtggc catcctgacg gccatcaacc tactggcgta 1050  
tgtggctgac ctggtgcaact ctgccacct ggtttttgtc aaggtctaag 1100  
actctcccaa gaggtcccg ttcctctcc aacctcttg ttcttcttg 1150  
ccgagttttc tttatggagt acttctttcc tcgcctttc ctctgttttc 1200  
ctcttctgt ctccccctcc tcccacctt ttctttcctt cccaattcct 1250  
tgcaactctaa ccagttcttg gatgcatctt ctctctccc ttctctcttg 1300  
ctgtttcctt cctgtgttgt tttgttgccc acatcctgtt ttcacccctg 1350  
agctgtttct ctttttcttt tctttctttt ttttttttt ttttaagacg 1400

gattctcact ctgtggccca ggctggagtg cagtgggtgcg atctcagctc 1450  
actgcaaccc ccgcctcctg gggtcaagcg attctcctcc cccagcctcc 1500  
caagtagctg ggaggacagg tgtgagctgc cgcaccacgc ctgtttctct 1550  
ttttccactc ttcttttttc tcatctcttt tctgggttgc ctgtcggctt 1600  
tcttatctgc ctgttttgca agcaccttct cctgtgtcct tgggagccct 1650  
gagacttctt tctctccttg cctccaccca cctccaaagg tgctgagctc 1700  
acatccacac cccttgacgc cgtccatgcc acagccccc aaggggcccc 1750  
attgccaaag catgcctgcc caccctcgct gtgccttagt cagtgtgtac 1800  
gtgtgtgtgt gtgtgtgttt ggggggtggg ggggtggtag ctggggattg 1850  
ggccctcttt ctcccagtg aggaaggtgt gcagtgtact tcccctttaa 1900  
attaaaaaac atatatatat atatatttgg aggtcagtaa tttccaatgg 1950  
gcgggaggca ttaagcaccg accctgggtc cctaggcccc gcctggcact 2000  
cagccttgcc agagattggc tccagaattt ttgccaggct tacagaacac 2050  
ccactgccta gaggccatct taaaggaagc aggggctgga tgcctttcat 2100  
cccaactatt ctctgtggta tgaaaaag 2128

<210> 31  
<211> 322  
<212> PRT  
<213> Homo sapiens

<400> 31  
Met Pro Val Thr Val Thr Arg Thr Thr Ile Thr Thr Thr Thr Thr  
1 5 10 15  
Ser Ser Ser Gly Leu Gly Ser Pro Met Ile Val Gly Ser Pro Arg  
20 25 30  
Ala Leu Thr Gln Pro Leu Gly Leu Leu Arg Leu Leu Gln Leu Val  
35 40 45  
Ser Thr Cys Val Ala Phe Ser Leu Val Ala Ser Val Gly Ala Trp  
50 55 60  
Thr Gly Ser Met Gly Asn Trp Ser Met Phe Thr Trp Cys Phe Cys  
65 70 75  
Phe Ser Val Thr Leu Ile Ile Leu Ile Val Glu Leu Cys Gly Leu  
80 85 90  
Gln Ala Arg Phe Pro Leu Ser Trp Arg Asn Phe Pro Ile Thr Phe  
95 100 105

Ala Cys Tyr Ala	Ala Leu Phe Cys Leu Ser Ala Ser Ile Ile Tyr	
	110	115 120
Pro Thr Thr Tyr	Val Gln Phe Leu Ser His Gly Arg Ser Arg Asp	
	125	130 135
His Ala Ile Ala	Ala Thr Phe Phe Ser Cys Ile Ala Cys Val Ala	
	140	145 150
Tyr Ala Thr Glu	Val Ala Trp Thr Arg Ala Arg Pro Gly Glu Ile	
	155	160 165
Thr Gly Tyr Met	Ala Thr Val Pro Gly Leu Leu Lys Val Leu Glu	
	170	175 180
Thr Phe Val Ala	Cys Ile Ile Phe Ala Phe Ile Ser Asp Pro Asn	
	185	190 195
Leu Tyr Gln His	Gln Pro Ala Leu Glu Trp Cys Val Ala Val Tyr	
	200	205 210
Ala Ile Cys Phe	Ile Leu Ala Ala Ile Ala Ile Leu Leu Asn Leu	
	215	220 225
Gly Glu Cys Thr	Asn Val Leu Pro Ile Pro Phe Pro Ser Phe Leu	
	230	235 240
Ser Gly Leu Ala	Leu Leu Ser Val Leu Leu Tyr Ala Thr Ala Leu	
	245	250 255
Val Leu Trp Pro	Leu Tyr Gln Phe Asp Glu Lys Tyr Gly Gly Gln	
	260	265 270
Pro Arg Arg Ser	Arg Asp Val Ser Cys Ser Arg Ser His Ala Tyr	
	275	280 285
Tyr Val Cys Ala	Trp Asp Arg Arg Leu Ala Val Ala Ile Leu Thr	
	290	295 300
Ala Ile Asn Leu	Leu Ala Tyr Val Ala Asp Leu Val His Ser Ala	
	305	310 315
His Leu Val Phe	Val Lys Val	
	320	

<210> 32

<211> 3680

<212> DNA

<213> Homo sapiens

<400> 32

gaacgtgccca ccatgcccag ctaatttttg tatttttagt agagacgggg 50

tttcaccatg ttggccaggc tggctcttgaa ctcgtgacct catgatccgc 100

tcacctcggc ctcccaaagt gctgggatta caggcatgag ccactgacgc 150

ctggccagcc tatgcatttt taagaaatta ttctgtatta ggtgctgtgc 200  
taaacattgg gcactacagt gaccaaaca gactgaattc cccaagagcc 250  
aaagaccagt gagggagacc aacaagaaac aggaaatgca aaagagacca 300  
ttattactca ctatgactaa gggtcacaaa tggggtacgt tgatggagag 350  
tgatttggtta agagactaca gagggaggac agactaccaa gaggggggccc 400  
aggaaagctc ctctgacgag gtggtatttc agcccaaact ggaagaatga 450  
gaaagagcta gccagccatc agaatagtcc agaagagatg gggagcacta 500  
cactcactac actttggcct gagaaaatag catgggattg gaggaggctg 550  
ggggaacacc acttctgccg acctgggcag gaggcattga gggcttgaga 600  
aagggaatg gcagtagcag tagaaaggac agggtaggag cagggacttt 650  
gcaggtggaa tcattaggtc ttatcaacag atatgggcaa gcaaagccag 700  
gggagaattg atggtaatgc tgaggtttgg agccaggcta gatgggacag 750  
tggtgggtga tgcaaaggaa agaggtcagg aagcagggcc agacgtgggg 800  
agaaggtgtg ggggttttgt ttccatcttg ccgagtctgc cggaatgtgg 850  
atgggaagac caagaggagg agcaaggggc agagggaag ggaatcttaa 900  
agaagtcctg gatgccacac tcttcttctt tctcctctt cctctctctc 950  
agaggtctca ctcggtggtc ttcatcttct gccctgcctc catctcctct 1000  
gggtgctggg aaagtggagg attagctgaa gttttgcttc tcggggcctg 1050  
tctgaatctc cattgctttc tgggaggaca taattcacct gtcttagctt 1100  
cttatcatct tacatttccc tgtagccact gggacatatg tgggtgttct 1150  
tcctagctcc tgtctcctcc tcatgccttt gctgggtatg ggcattgttag 1200  
ggggaaggtc attgctgtca gaggggcact gactttctaa tgggtgttacc 1250  
caaggtgaat gttggagaca cagtcgcgat gctgcccaag tcccgcgag 1300  
ccctaactat ccaggagatc gctgcgctgg ccaggtcctc cctgcatggt 1350  
atgcagcccc tcccatgttt ctggccactt tgcctttct cctcccgttt 1400  
gcacatccct ttggaactgt ttctgtgag tacatgctgg ggtctcccct 1450  
ttcttccctt gctcagggtga atctcagccc cttctccac ccaaagggtc 1500  
acatggatcc taactactgc cacccttcca cctccctgca cctgtgctcc 1550  
ctggcctggt cctttaccag gcttctccac cctcccctat ctccaggat 1600

ttcccaggtg gtgaaggacc acgtgaccaa gcctaccgcc atggcccagg 1650  
gccgagtggc tcacctcatt gagtgaagg gctggagcaa gccgagtga 1700  
tcacctgctg ccctggaatc agccttttcc tcctattcag acctcagcga 1750  
gggcgaacaa gaggctcgct ttgcagcagg agtggctgag cagtttgcca 1800  
tcgcggaagc caagctccga gcatgggtctt cgggtggatgg cgaggactcc 1850  
actgatgact cctatgatga ggactttgct gggggaatgg acacagacat 1900  
ggctgggcag ctgcccctgg ggccgcacct ccaggacctg ttcaccggcc 1950  
accggttctc ccggcctgtg cgccagggct ccgtggagcc tgagagcgac 2000  
tgctcacaga ccgtgtcccc agacaccctg tgctctagtc tgtgcagcct 2050  
ggaggatggg ttgttgggct ccccgccccg gctggcctcc cagctgctgg 2100  
gcgatgagct gcttctcgcc aaactgcccc ccagccggga aagtgccttc 2150  
cgcagcctgg gccactgga ggcccaggac tcactctaca actcgcccct 2200  
cacagagtcc tgcccttccc ccgcggagga ggagccagcc ccctgcaagg 2250  
actgccagcc actctgcccc ccaactaacgg gcagctggga acggcagcgg 2300  
caagcctctg acctggcctc ttctggggtg gtgtccttag atgaggatga 2350  
ggcagagcca gaggaacagt gacccacatc atgcctggca gtggcatgca 2400  
tccccggct gctgccaggg gcagagcctc tgtgcccaag tgtgggctca 2450  
aggctcccag cagagctcca cagcctagag ggctcctggg agcgctcgct 2500  
tctccgttgt gtgttttgca tgaaagtgtt tggagaggag gcaggggctg 2550  
ggctgggggc gcatgtcctg cccccactcc cggggcttgc cgggggttgc 2600  
ccggggcctc tggggcatgg ctacagctgt ggcagacagt gatgttcatg 2650  
ttcttaaaat gccacacaca catttccctc tcggataatg tgaaccacta 2700  
aggggggtgt gactgggctg tgtgagggtg ggggtggagg gggcccagca 2750  
acccccacc ctccccatgc ctctctcttc tctgcttttc ttctcacttc 2800  
cgagtccatg tgcagtgctt gatagaatca cccccacctg gaggggctgg 2850  
ctctgcct cccggagcct atgggttgag ccgtccctca agggcccctg 2900  
cccagctggg ctctgtctgt gcttcattca cctctccatc gtctctaaat 2950  
cttctcttt tttcctaaag acagaagggt tttggtctgt tttttcagtc 3000

ggatcttctc ttctctggga ggctttggaa tgatgaaagc atgtaccctc 3050  
 cacccttttc ctggccccct aatggggcct gggccctttc ccaaccctc 3100  
 ctaggatgtg cgggcagtgt gctggcgcct cacagccagc cgggctgccc 3150  
 attcacgcag agctctctga gcgggaggtg gaagaaagga tggctctggt 3200  
 tgccacagag ctgggacttc atgttcttct agagagggcc acaagagggc 3250  
 cacaggggtg gccgggagtt gtcagctgat gcctgctgag aggcaggaat 3300  
 tgtgccagtg agtgacagtc atgagggagt gtctcttctt ggggaggaaa 3350  
 gaaggtagag ctttctgtc tgaatgaaag gccaaggcta cagtacaggg 3400  
 ccccgcccca gccaggggtg taatgccac gtagtggagg cctctggcag 3450  
 atcctgcatt ccaaggtcac tggactgtac gtttttatgg ttgtgggaag 3500  
 ggtgggtggc tttagaatta agggccttgt aggccttggc aggtaagagg 3550  
 gcccaaggta agaacgagag ccaacgggca caagcattct atatataagt 3600  
 ggctcattag gtgtttattt tgttctattt aagaatttgt tttattaaat 3650  
 taatataaaa atctttgtaa atctctaaaa 3680

<210> 33

<211> 335

<212> PRT

<213> Homo sapiens

<400> 33

Met	Phe	Leu	Ala	Thr	Leu	Ser	Phe	Leu	Leu	Pro	Phe	Ala	His	Pro
1					5					10				15
Phe	Gly	Thr	Val	Ser	Cys	Glu	Tyr	Met	Leu	Gly	Ser	Pro	Leu	Ser
				20					25					30
Ser	Leu	Ala	Gln	Val	Asn	Leu	Ser	Pro	Phe	Ser	His	Pro	Lys	Val
				35					40					45
His	Met	Asp	Pro	Asn	Tyr	Cys	His	Pro	Ser	Thr	Ser	Leu	His	Leu
				50					55					60
Cys	Ser	Leu	Ala	Trp	Ser	Phe	Thr	Arg	Leu	Leu	His	Pro	Pro	Leu
				65					70					75
Ser	Pro	Gly	Ile	Ser	Gln	Val	Val	Lys	Asp	His	Val	Thr	Lys	Pro
				80					85					90
Thr	Ala	Met	Ala	Gln	Gly	Arg	Val	Ala	His	Leu	Ile	Glu	Trp	Lys
				95					100					105
Gly	Trp	Ser	Lys	Pro	Ser	Asp	Ser	Pro	Ala	Ala	Leu	Glu	Ser	Ala
				110					115					120

Phe Ser Ser Tyr Ser Asp Leu Ser Glu Gly Glu Gln Glu Ala Arg	125	130	135
Phe Ala Ala Gly Val Ala Glu Gln Phe Ala Ile Ala Glu Ala Lys	140	145	150
Leu Arg Ala Trp Ser Ser Val Asp Gly Glu Asp Ser Thr Asp Asp	155	160	165
Ser Tyr Asp Glu Asp Phe Ala Gly Gly Met Asp Thr Asp Met Ala	170	175	180
Gly Gln Leu Pro Leu Gly Pro His Leu Gln Asp Leu Phe Thr Gly	185	190	195
His Arg Phe Ser Arg Pro Val Arg Gln Gly Ser Val Glu Pro Glu	200	205	210
Ser Asp Cys Ser Gln Thr Val Ser Pro Asp Thr Leu Cys Ser Ser	215	220	225
Leu Cys Ser Leu Glu Asp Gly Leu Leu Gly Ser Pro Ala Arg Leu	230	235	240
Ala Ser Gln Leu Leu Gly Asp Glu Leu Leu Leu Ala Lys Leu Pro	245	250	255
Pro Ser Arg Glu Ser Ala Phe Arg Ser Leu Gly Pro Leu Glu Ala	260	265	270
Gln Asp Ser Leu Tyr Asn Ser Pro Leu Thr Glu Ser Cys Leu Ser	275	280	285
Pro Ala Glu Glu Glu Pro Ala Pro Cys Lys Asp Cys Gln Pro Leu	290	295	300
Cys Pro Pro Leu Thr Gly Ser Trp Glu Arg Gln Arg Gln Ala Ser	305	310	315
Asp Leu Ala Ser Ser Gly Val Val Ser Leu Asp Glu Asp Glu Ala	320	325	330
Glu Pro Glu Glu Gln	335		

<210> 34

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 34

tgtcctttgt cccagacttc tgtcc 25



<210> 35  
<211> 50  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 35  
ctggatgcta atgtgtccag taaatgatcc cttatcccg tcgcatgct 50

<210> 36  
<211> 25  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 36  
ttccactcaa tgaggtgagc cactc 25

<210> 37  
<211> 23  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 37  
ggcgagccct aactatccag gag 23

<210> 38  
<211> 39  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 38  
ggagatcgct gcgctggcca ggtcctccct gcatggat 39

<210> 39  
<211> 22  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 39  
ctgctgcaaa gcgagcctct tg 22

<210> 40  
<211> 2084

<212> DNA

<213> Homo sapiens

<400> 40

ggttcctggg cgctctgtta cacaagcaag atacagccag cccaccta 50  
ttttgtttcc ctggcaccct cctgctcagt gcgacattgt cacacttaac 100  
ccatctgttt tctctaattgc acgacagatt cctttcagac aggacaactg 150  
tgatatattca gttcctgatt gtaaatacct cctaagcctg aagcttctgt 200  
tactagccat tgtgagcttc agtttcttca tctgcaaaat gggcataata 250  
caatctattc ttgccacatc aagggattgt tattccttta aaaaaaacc 300  
aataccaaaag aagcctacaa tgttggcctt agccaaaatt ctgttgattt 350  
caacgttggt ttattcactt ctatcgggga gccatggaaa agaaaatcaa 400  
gacataaaca caacacagaa cattgcagaa gtttttaaaa caatggaaaa 450  
taaacctatt tctttggaaa gtgaagcaaa cttaaactca gataaagaaa 500  
atataaccac ctcaaattc aaggcgagtc attccctcc tttgaatcta 550  
cccaacaaca gccacggaat aacagatttc tccagtaact catcagcaga 600  
gcattctttg ggcagtctaa aaccacatc taccatttc acaagccctc 650  
ccttgatcca tagctttgtt tctaaagtgc cttggaatgc acctatagca 700  
gatgaagatc ttttgcccat ctacgacat cccaatgcta cacctgctct 750  
gtcttcagaa aacttcactt ggtctttggt caatgacacc gtgaaaactc 800  
ctgataacag ttccattaca gttagcatcc tctcttcaga accaacttct 850  
ccatctgtga ccccttgat agtggaaacca agtggatggc ttaccacaaa 900  
cagtgatagc ttactgggt ttaccctta tcaagaaaaa acaactctac 950  
agcctacctt aaaattcacc aataattcaa aactctttcc aaatacgtca 1000  
gatcccaaaa aagaaaatag aaatacagga atagtattcg gggccatttt 1050  
aggtgctatt ctgggtgtct cattgcttac tcttggtggc tacttggtgt 1100  
gtggaaaaag gaaaacggat tcattttccc atcggcgact ttatgacgac 1150  
agaaatgaac cagttctgcg attagacaat gcaccggaac cttatgatgt 1200  
gagttttggg aattctagct actacaatcc aactttgaat gattcagcca 1250  
tgccagaaaag tgaagaaaat gcacgtgatg gcattcctat ggatgacata 1300  
cctccacttc gtacttctgt atagaactaa cagcaaaaag gcgttaaaca 1350

gcaagtgtca tctacatcct agccttttga caaattcatc tttcaaaagg 1400  
ttacacaaaa ttactgtcac gtggattttg tcaaggagaa tcataaaagc 1450  
aggagaccag tagcagaaat gtagacagga tgtatcatcc aaaggttttc 1500  
tttcttacia tttttggcca tcctgaggca ttactaagt agccttaatt 1550  
tgtattttag tagtattttc ttagtagaaa atatttgtgg aatcagataa 1600  
aactaaaaga tttcaccatt acagccctgc ctcataacta aataataaaa 1650  
attattccac caaaaaattc taaaacaatg aagatgactc tttactgctc 1700  
tgctgaagc cctagtagca taattcaaga ttgcattttc ttaaatgaaa 1750  
attgaaaggg tgctttttta agaaaatttg acttaaagct aaaaagagga 1800  
catagcccag agtttctggt attgggaaat tgaggcaata gaaatgacag 1850  
acctgtattc tagtagctta taattttcta gatcagcaca cacatgatca 1900  
gcccactgag ttatgaagct gacaatgact gcattcaacg gggccatggc 1950  
aggaaagctg accctacca ggaaagtaat agcttcttta aaagtcttca 2000  
aaggttttgg gaattttaac ttgtcttaat atatcttagg cttcaattat 2050  
ttgggtgcct taaaaactca atgagaatca tgggt 2084

<210> 41  
<211> 334  
<212> PRT  
<213> Homo sapiens

<400> 41  
Met Leu Ala Leu Ala Lys Ile Leu Leu Ile Ser Thr Leu Phe Tyr  
1 5 10 15  
Ser Leu Leu Ser Gly Ser His Gly Lys Glu Asn Gln Asp Ile Asn  
20 25 30  
Thr Thr Gln Asn Ile Ala Glu Val Phe Lys Thr Met Glu Asn Lys  
35 40 45  
Pro Ile Ser Leu Glu Ser Glu Ala Asn Leu Asn Ser Asp Lys Glu  
50 55 60  
Asn Ile Thr Thr Ser Asn Leu Lys Ala Ser His Ser Pro Pro Leu  
65 70 75  
Asn Leu Pro Asn Asn Ser His Gly Ile Thr Asp Phe Ser Ser Asn  
80 85 90  
Ser Ser Ala Glu His Ser Leu Gly Ser Leu Lys Pro Thr Ser Thr  
95 100 105

Ile Ser Thr Ser	Pro Pro Leu Ile His	Ser Phe Val Ser Lys Val	
	110	115	120
Pro Trp Asn Ala	Pro Ile Ala Asp Glu Asp	Leu Leu Pro Ile Ser	
	125	130	135
Ala His Pro Asn	Ala Thr Pro Ala Leu Ser	Ser Glu Asn Phe Thr	
	140	145	150
Trp Ser Leu Val	Asn Asp Thr Val Lys Thr	Pro Asp Asn Ser Ser	
	155	160	165
Ile Thr Val Ser	Ile Leu Ser Ser Glu Pro	Thr Ser Pro Ser Val	
	170	175	180
Thr Pro Leu Ile	Val Glu Pro Ser Gly Trp	Leu Thr Thr Asn Ser	
	185	190	195
Asp Ser Phe Thr	Gly Phe Thr Pro Tyr Gln	Glu Lys Thr Thr Leu	
	200	205	210
Gln Pro Thr Leu	Lys Phe Thr Asn Asn Ser	Lys Leu Phe Pro Asn	
	215	220	225
Thr Ser Asp Pro	Gln Lys Glu Asn Arg Asn	Thr Gly Ile Val Phe	
	230	235	240
Gly Ala Ile Leu	Gly Ala Ile Leu Gly Val	Ser Leu Leu Thr Leu	
	245	250	255
Val Gly Tyr Leu	Leu Cys Gly Lys Arg Lys	Thr Asp Ser Phe Ser	
	260	265	270
His Arg Arg Leu	Tyr Asp Asp Arg Asn Glu	Pro Val Leu Arg Leu	
	275	280	285
Asp Asn Ala Pro	Glu Pro Tyr Asp Val Ser	Phe Gly Asn Ser Ser	
	290	295	300
Tyr Tyr Asn Pro	Thr Leu Asn Asp Ser Ala	Met Pro Glu Ser Glu	
	305	310	315
Glu Asn Ala Arg	Asp Gly Ile Pro Met Asp	Asp Ile Pro Pro Leu	
	320	325	330
Arg Thr Ser Val			

<210> 42

<211> 1594

<212> DNA

<213> Homo sapiens

<400> 42

aacaggatct cctcttgcag tctgcagccc aggacgctga ttccagcagc 50

gccttaccgc gcagcccgaa gattcactat ggtgaaaatc gccttcaata 100  
cccctaccgc cgtgcaaaag gaggaggcgc ggcaagacgt ggaggccctc 150  
ctgagccgca cggtcagaac tcagatactg accggcaagg agctccgagt 200  
tgccaccag gaaaaagagg gctcctctgg gagatgtatg cttactctct 250  
taggcctttc attcatcttg gcaggactta ttgttggtgg agcctgcatt 300  
tacaagtact tcatgcccaa gagcaccatt taccgtggag agatgtgctt 350  
ttttgattct gaggatcctg caaattccct tcgtggagga gaggcctaact 400  
tcctgcctgt gactgaggag gctgacattc gtgaggatga caacattgca 450  
atcattgatg tgccgtgcc cagtttctct gatagtgacc ctgcagcaat 500  
tattcatgac ttgaaaagg gaatgactgc ttacctggac ttgttgctgg 550  
ggaactgcta tctgatgcc ctcaatactt ctattgttat gcctccaaaa 600  
aatctggtag agctctttgg caaactggcg agtggcagat atctgcctca 650  
aacttatgtg gttcgagaag acctagtgtc tgtggaggaa attcgtgatg 700  
ttagtaacct tggcatcttt atttaccac tttgcaataa cagaaagtcc 750  
ttccgccttc gtcgcagaga cctcttgctg gggttcaaca aacgtgccat 800  
tgataaatgc tggaagatta gacacttccc caacgaattt attgttgaga 850  
ccaagatctg tcaagagtaa gaggcaacag atagagtgtc cttggtaata 900  
agaagtcaga gatttacaat atgactttaa cattaagggt tatgggatac 950  
tcaagatatt tactcatgca ttactctat tgcttatgct ttaaaaaaag 1000  
gaaaaaaaaa aaaactacta accactgcaa gctcttgtca aatttttagtt 1050  
taattggcat tgcttgTTTT ttgaaactga aattacatga gtttcatttt 1100  
ttctttgcat ttatagggtt tagatttctg aaagcagcat gaatatatca 1150  
cctaacatcc tgacaataaa ttccatccgt tgtttttttt gtttgtttgt 1200  
tttttctttt cctttaagta agctctttat tcatcttatg gtggagcaat 1250  
tttaaaattt gaaatatatt aaattgtttt tgaacttttt gtgtaaaata 1300  
tatcagatct caacattggt ggtttctttt gtttttcatt ttgtacaact 1350  
ttcttgaatt tagaaattac atctttgcag ttctgttagg tgctctgtaa 1400  
ttaacctgac ttatatgtga acaattttca tgagacagtc atttttaact 1450  
aatgcagtga ttcttttctca ctactatctg tattgtggaa tgcacaaaat 1500

tgtgtaggtg ctgaatgctg taaggagttt aggttgatg aattctacaa 1550

ccctataata aattttactc tatacaaaaa aaaaaaaaaa aaaa 1594

<210> 43

<211> 263

<212> PRT

<213> Homo sapiens

<400> 43

Met	Val	Lys	Ile	Ala	Phe	Asn	Thr	Pro	Thr	Ala	Val	Gln	Lys	Glu
1				5					10					15

Glu	Ala	Arg	Gln	Asp	Val	Glu	Ala	Leu	Leu	Ser	Arg	Thr	Val	Arg
			20						25					30

Thr	Gln	Ile	Leu	Thr	Gly	Lys	Glu	Leu	Arg	Val	Ala	Thr	Gln	Glu
			35						40					45

Lys	Glu	Gly	Ser	Ser	Gly	Arg	Cys	Met	Leu	Thr	Leu	Leu	Gly	Leu
			50						55					60

Ser	Phe	Ile	Leu	Ala	Gly	Leu	Ile	Val	Gly	Gly	Ala	Cys	Ile	Tyr
			65						70					75

Lys	Tyr	Phe	Met	Pro	Lys	Ser	Thr	Ile	Tyr	Arg	Gly	Glu	Met	Cys
			80						85					90

Phe	Phe	Asp	Ser	Glu	Asp	Pro	Ala	Asn	Ser	Leu	Arg	Gly	Gly	Glu
			95						100					105

Pro	Asn	Phe	Leu	Pro	Val	Thr	Glu	Glu	Ala	Asp	Ile	Arg	Glu	Asp
			110						115					120

Asp	Asn	Ile	Ala	Ile	Ile	Asp	Val	Pro	Val	Pro	Ser	Phe	Ser	Asp
			125						130					135

Ser	Asp	Pro	Ala	Ala	Ile	Ile	His	Asp	Phe	Glu	Lys	Gly	Met	Thr
			140						145					150

Ala	Tyr	Leu	Asp	Leu	Leu	Leu	Gly	Asn	Cys	Tyr	Leu	Met	Pro	Leu
			155						160					165

Asn	Thr	Ser	Ile	Val	Met	Pro	Pro	Lys	Asn	Leu	Val	Glu	Leu	Phe
			170						175					180

Gly	Lys	Leu	Ala	Ser	Gly	Arg	Tyr	Leu	Pro	Gln	Thr	Tyr	Val	Val
			185						190					195

Arg	Glu	Asp	Leu	Val	Ala	Val	Glu	Glu	Ile	Arg	Asp	Val	Ser	Asn
			200						205					210

Leu	Gly	Ile	Phe	Ile	Tyr	Gln	Leu	Cys	Asn	Asn	Arg	Lys	Ser	Phe
			215						220					225

Arg Leu Arg Arg Arg Asp Leu Leu Leu Gly Phe Asn Lys Arg Ala

230	235	240
Ile Asp Lys Cys Trp Lys Ile Arg His	Phe Pro Asn Glu Phe Ile	
245	250	255

Val Glu Thr Lys Ile Cys Gln Glu  
260

<210> 44  
 <211> 24  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 44  
 gaaagacacg acacagcagc ttgc 24

<210> 45  
 <211> 20  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 45  
 gggaactgct atctgatgcc 20

<210> 46  
 <211> 26  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 46  
 caggatctcc tcttgacgac tgcagc 26

<210> 47  
 <211> 28  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 47  
 cttctcgaac cacataagtt tgaggcag 28

<210> 48  
 <211> 25  
 <212> DNA  
 <213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 48

cacgattccc tccacagcaa ctggg 25

<210> 49

<211> 1969

<212> DNA

<213> Homo sapiens

<400> 49

ggaggaggga gggcgggcag ggcagagccc agagcagccc cgggcaccag 50  
cacggactct ctcttcacag ccagggtgccc cccactctcg ctccattcgg 100  
cgggagcacc cagtcctgta cgccaaggaa ctgggtcctgg gggcaccatg 150  
gtttcggcgg cagccccag cctcctcatc cttctgttgc tgctgctggg 200  
gtctgtgcct gctaccgacg cccgctctgt gcccctgaag gccacgttcc 250  
tggaggatgt ggcgggtagt ggggaggccg agggctcgtc ggcctcctcc 300  
ccgagcctcc cgccaccctg gaccccgccc ctacagccca catcgatggg 350  
gccccagccc acaaccctgg ggggcccac accccacc aacttcctgg 400  
atgggatagt ggaacttctc cgccagtacg tgatgctgat tgctgtggtg 450  
ggctccctgg cttttctgct gatgttcac gtctgtgccg cggcatcac 500  
ccggcagaag cagaaggcct cggcctatta cccatcgtcc ttccccaaga 550  
agaagtacgt ggaccagagt gaccgggccc ggggcccccg ggccttcagt 600  
gagggtcccc acagagcccc cgacagcagg cccgaggaag ccctggattc 650  
ctcccggcag ctccaggccg acatcttggc cgccaccag aacctcaagt 700  
ccccaccag ggctgcactg ggcggtgggg acggagccag gatgggtggag 750  
ggcaggggag cagaggaaga ggagaagggc agccaggagg gggaccagga 800  
agtccaggga catggggctc cagtggagac accagaggcg caggaggagc 850  
cgtgctcagg ggtccttgag ggggtgtgg tggccgtga gggccaaggg 900  
gagctggaag ggtctctctt gttagcccag gaagcccagg gaccagtggg 950  
tcccccgaa agcccctgtg cttgcagcag tgtccacccc agtgtctaac 1000  
agtctcccc ggctgccagc cctgactgtc gggccccaa gtggtcacct 1050  
ccccgtgtat gaaaaggcct tcagccctga ctgcttcctg aactccctc 1100  
cttggcctcc ctgtgggtgcc aatccagca tgtgctgatt ctacagcagg 1150



cagaaatgct ggtccccggt gccccggagg aatcttacca agtgccatca 1200  
 tccttcacct cagcagcccc aaagggctac atcctacagc acagctcccc 1250  
 tgacaaagtg agggagggca cgtgtccctg tgacagccag gataaaacat 1300  
 cccccaaagt gctgggatta caggcgtgag ccaccgtgcc cggcccaaac 1350  
 tactttttaa aacagctaca gggtaaaatc ctgcagcacc cactctggaa 1400  
 aatactgctc ttaattttcc tgaaggtggc cccctgtttc tagttgggtcc 1450  
 aggattaggg atgtggggta tagggcattt aaatcctctc aagcgtctc 1500  
 caagcacccc cggcctgggg gtgagtttct catcccgcta ctgctgctgg 1550  
 gatcaggttg aatgaatgga actcttcctg tctggcctcc aaagcagcct 1600  
 agaagctgag gggctgtgtt tgaggggacc tccaccctgg ggaagtccga 1650  
 ggggctgggg aagggtttct gacgcccagc ctggagcagg ggggccctgg 1700  
 ccaccccctg ttgctcacac attgtctggc agcctgtgtc cacaatattc 1750  
 gtcagtcctc gacagggagc ctgggctccg tctgtcttta gggaggctct 1800  
 ggcaggaggt cctctcccc atccctccat ctggggctcc cccaacctct 1850  
 gcacagctct ccaggtgctg agatataatg caccagcaca ataaaccttt 1900  
 attccggcct gaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 1950  
 aaaaaaaaaa aaaaaaaga 1969

<210> 50

<211> 283

<212> PRT

<213> Homo sapiens

<400> 50

Met	Val	Ser	Ala	Ala	Ala	Pro	Ser	Leu	Leu	Ile	Leu	Leu	Leu	Leu
1				5					10					15
Leu	Leu	Gly	Ser	Val	Pro	Ala	Thr	Asp	Ala	Arg	Ser	Val	Pro	Leu
				20					25					30
Lys	Ala	Thr	Phe	Leu	Glu	Asp	Val	Ala	Gly	Ser	Gly	Glu	Ala	Glu
				35					40					45
Gly	Ser	Ser	Ala	Ser	Ser	Pro	Ser	Leu	Pro	Pro	Pro	Trp	Thr	Pro
				50					55					60
Ala	Leu	Ser	Pro	Thr	Ser	Met	Gly	Pro	Gln	Pro	Thr	Thr	Leu	Gly
				65					70					75
Gly	Pro	Ser	Pro	Pro	Thr	Asn	Phe	Leu	Asp	Gly	Ile	Val	Asp	Phe

	80	85	90
Phe Arg Gln Tyr Val Met Leu Ile Ala Val Val Gly Ser Leu Ala	95	100	105
Phe Leu Leu Met Phe Ile Val Cys Ala Ala Val Ile Thr Arg Gln	110	115	120
Lys Gln Lys Ala Ser Ala Tyr Tyr Pro Ser Ser Phe Pro Lys Lys	125	130	135
Lys Tyr Val Asp Gln Ser Asp Arg Ala Gly Gly Pro Arg Ala Phe	140	145	150
Ser Glu Val Pro Asp Arg Ala Pro Asp Ser Arg Pro Glu Glu Ala	155	160	165
Leu Asp Ser Ser Arg Gln Leu Gln Ala Asp Ile Leu Ala Ala Thr	170	175	180
Gln Asn Leu Lys Ser Pro Thr Arg Ala Ala Leu Gly Gly Gly Asp	185	190	195
Gly Ala Arg Met Val Glu Gly Arg Gly Ala Glu Glu Glu Glu Lys	200	205	210
Gly Ser Gln Glu Gly Asp Gln Glu Val Gln Gly His Gly Val Pro	215	220	225
Val Glu Thr Pro Glu Ala Gln Glu Glu Pro Cys Ser Gly Val Leu	230	235	240
Glu Gly Ala Val Val Ala Gly Glu Gly Gln Gly Glu Leu Glu Gly	245	250	255
Ser Leu Leu Leu Ala Gln Glu Ala Gln Gly Pro Val Gly Pro Pro	260	265	270
Glu Ser Pro Cys Ala Cys Ser Ser Val His Pro Ser Val	275	280	

<210> 51  
 <211> 1734  
 <212> DNA  
 <213> Homo sapiens

<400> 51  
 gtggactctg agaagcccag gcagttgagg acaggagaga gaaggctgca 50  
 gaccagagg gagggaggac agggagtcgg aaggaggagg acagaggagg 100  
 gcacagagac gcagagcaag ggcggcaagg aggagaccct ggtgggagga 150  
 agacactctg gagagagagg gggctgggca gagatgaagt tccaggggcc 200  
 cctggcctgc ctctgctgg ccctctgcct gggcagtggg gaggctggcc 250

ccctgcagag cggagaggaa agcactggga caaatattgg ggaggccctt 300  
ggacatggcc tgggagacgc cctgagcgaa ggggtgggaa aggccattgg 350  
caaagaggcc ggaggggag ctggctctaa agtcagttag gcccttggcc 400  
aagggaccag agaagcagtt ggcaactggag tcaggcaggt tccaggcttt 450  
ggcgagcag atgctttggg caacagggtc ggggaagcag cccatgctct 500  
gggaaacact gggcacgaga ttggcagaca ggcagaagat gtcattcgac 550  
acggagcaga tgctgtccgc ggctcctggc aggggggtgcc tggccacagt 600  
ggtgcttggg aaacttcttg aggccatggc atctttggct ctcaagggtg 650  
ccttgagggc cagggccagg gcaatcctgg aggtctgggg actccgtggg 700  
tccacggata ccccgaaac tcagcaggca gctttggaat gaatcctcag 750  
ggagctccct ggggtcaagg aggcaatgga gggccaccaa actttgggac 800  
caacactcag ggagctgttg cccagcctgg ctatggttca gtgagagcca 850  
gcaaccagaa tgaagggtgc acgaatcccc caccatctgg ctgaggtgga 900  
ggctccagca actctggggg aggcagcggc tcacagtcgg gcagcagtgg 950  
cagtggcagc aatggtgaca acaacaatgg cagcagcagt ggtggcagca 1000  
gcagtggcag cagcagtggc agcagcagtg gcggcagcag tggcggcagc 1050  
agtgggtggc gcagtggcaa cagtgggtggc agcagaggtg acagcggcag 1100  
tgagtcctcc tggggatcca gcaccggctc ctctccggc aaccacggtg 1150  
ggagcggcgg aggaaatgga cataaaccg ggtgtgaaaa gccagggaat 1200  
gaagcccgcg ggagcgggga atctgggatt cagggttca gaggacaggg 1250  
agtttcagc aacatgaggg aaataagcaa agagggcaat cgctccttg 1300  
gaggctctgg agacaattat cgggggcaag ggtcgagctg gggcagtgga 1350  
ggaggtgacg ctgttggttg agtcaatact gtgaactctg agacgtctcc 1400  
tgggatgttt aactttgaca ctttctggaa gaattttaaa tccaagctgg 1450  
gtttcatcaa ctgggatgcc ataaacaagg accagagaag ctctcgcatc 1500  
ccgtgacctc cagacaagga gccaccagat tggatgggag cccccacact 1550  
ccctccttaa aacaccaccc tctcatcact aatctcagcc cttgcccttg 1600  
aaataaacct tagctgcccc acaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 1650  
aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 1700

aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaa 1734

<210> 52

<211> 440

<212> PRT

<213> Homo sapiens

<400> 52

Met	Lys	Phe	Gln	Gly	Pro	Leu	Ala	Cys	Leu	Leu	Leu	Ala	Leu	Cys
1				5					10					15

Leu	Gly	Ser	Gly	Glu	Ala	Gly	Pro	Leu	Gln	Ser	Gly	Glu	Glu	Ser
				20					25					30

Thr	Gly	Thr	Asn	Ile	Gly	Glu	Ala	Leu	Gly	His	Gly	Leu	Gly	Asp
				35					40					45

Ala	Leu	Ser	Glu	Gly	Val	Gly	Lys	Ala	Ile	Gly	Lys	Glu	Ala	Gly
				50					55					60

Gly	Ala	Ala	Gly	Ser	Lys	Val	Ser	Glu	Ala	Leu	Gly	Gln	Gly	Thr
				65					70					75

Arg	Glu	Ala	Val	Gly	Thr	Gly	Val	Arg	Gln	Val	Pro	Gly	Phe	Gly
				80					85					90

Ala	Ala	Asp	Ala	Leu	Gly	Asn	Arg	Val	Gly	Glu	Ala	Ala	His	Ala
				95					100					105

Leu	Gly	Asn	Thr	Gly	His	Glu	Ile	Gly	Arg	Gln	Ala	Glu	Asp	Val
				110					115					120

Ile	Arg	His	Gly	Ala	Asp	Ala	Val	Arg	Gly	Ser	Trp	Gln	Gly	Val
				125					130					135

Pro	Gly	His	Ser	Gly	Ala	Trp	Glu	Thr	Ser	Gly	Gly	His	Gly	Ile
				140					145					150

Phe	Gly	Ser	Gln	Gly	Gly	Leu	Gly	Gly	Gln	Gly	Gln	Gly	Asn	Pro
				155					160					165

Gly	Gly	Leu	Gly	Thr	Pro	Trp	Val	His	Gly	Tyr	Pro	Gly	Asn	Ser
				170					175					180

Ala	Gly	Ser	Phe	Gly	Met	Asn	Pro	Gln	Gly	Ala	Pro	Trp	Gly	Gln
				185					190					195

Gly	Gly	Asn	Gly	Gly	Pro	Pro	Asn	Phe	Gly	Thr	Asn	Thr	Gln	Gly
				200					205					210

Ala	Val	Ala	Gln	Pro	Gly	Tyr	Gly	Ser	Val	Arg	Ala	Ser	Asn	Gln
				215					220					225

Asn	Glu	Gly	Cys	Thr	Asn	Pro	Pro	Pro	Ser	Gly	Ser	Gly	Gly	Gly
				230					235					240

Ser Ser Asn Ser	Gly Gly Gly Ser Gly Ser Gln Ser Gly Ser Ser	245	250	255
Gly Ser Gly Ser	Asn Gly Asp Asn Asn Asn Gly Ser Ser Ser Gly	260	265	270
Gly Ser Ser Ser	Gly Ser Ser Ser Gly Ser Ser Ser Gly Gly Ser	275	280	285
Ser Gly Gly Ser	Ser Gly Gly Ser Ser Gly Asn Ser Gly Gly Ser	290	295	300
Arg Gly Asp Ser	Gly Ser Glu Ser Ser Trp Gly Ser Ser Thr Gly	305	310	315
Ser Ser Ser Gly	Asn His Gly Gly Ser Gly Gly Gly Asn Gly His	320	325	330
Lys Pro Gly Cys	Glu Lys Pro Gly Asn Glu Ala Arg Gly Ser Gly	335	340	345
Glu Ser Gly Ile	Gln Gly Phe Arg Gly Gln Gly Val Ser Ser Asn	350	355	360
Met Arg Glu Ile	Ser Lys Glu Gly Asn Arg Leu Leu Gly Gly Ser	365	370	375
Gly Asp Asn Tyr	Arg Gly Gln Gly Ser Ser Trp Gly Ser Gly Gly	380	385	390
Gly Asp Ala Val	Gly Gly Val Asn Thr Val Asn Ser Glu Thr Ser	395	400	405
Pro Gly Met Phe	Asn Phe Asp Thr Phe Trp Lys Asn Phe Lys Ser	410	415	420
Lys Leu Gly Phe	Ile Asn Trp Asp Ala Ile Asn Lys Asp Gln Arg	425	430	435
Ser Ser Arg Ile	Pro	440		

<210> 53

<211> 3580

<212> DNA

<213> Homo sapiens

<400> 53

```

gaccggtccc tccggtcctg gatgtgcgga ctctgctgca gcgagggctg 50
caggcccgcc gggcggtgct caccgtgccc tggtggtgg agtttctctc 100
ctttgctgac catgttggtc ccttgctgga atattaccgg gacatcttca 150
ctctcctgct gcgcctgcac cggagcttgg tgttgctgca ggagagtgag 200
gggaagatgt gtttcctgaa caagctgctg ctacttgctg tcctgggctg 250

```

gcttttccag attcccacag tccctgagga cttgttcttt ctggaagagg 300  
gtccctcata tgcctttgag gtggacacag tagccccaga gcatggcttg 350  
gacaatgcgc ctgtggtgga ccagcagctg ctctacacct gctgccccta 400  
catcggagag ctccggaaac tgctcgcttc gtgggtgtca ggcagtagtg 450  
gacggagtgg gggcttcatg aggaaaatca cccccaccac taccaccagc 500  
ctgggagccc agccttccca gaccagccag gggctgcagg cacagctcgc 550  
ccaggccttt ttccacaacc agccgccctc cttgcgccgg accgtagagt 600  
tcgtggcaga aagaattgga tcaaactgtg taaacatat caaggctaca 650  
ctggtggcag atctggtgcg ccaggcagag tcacttctcc aagagcagct 700  
ggtgacacag ggagaggaag ggggagacc agccagctg ttggagatct 750  
tgtgttccca gctgtgccct cacggggccc aggcattggc cctggggcgg 800  
gagttctgtc aaaggaagag cctggggct gtgcgggcgc tgcttcaga 850  
ggagaccccg gcagccgttc tgagcagtgc agagaacatt gctgtggggc 900  
ttgcaacaga gaaagcctgt gcttggctgt cagccaacat cacagcactg 950  
atcaggaggg aggtgaaagc agcagtgagt cgcacacttc gagcccagg 1000  
tcctgaacct gctgcccggg gggagcggag gggctgctcc cgcgcctgac 1050  
gtgctctcct tggccgtggg gccacgggac cctgacgagg gagtctcccc 1100  
agagcatctg gaacagctcc taggccagct gggccagacg ctgcggtgcc 1150  
gccagttcct gtgcccacct gctgagcagc atctggcaaa gtgctctgtg 1200  
gagttagctt ccctcctcgt tgcagatcaa attcctatcc tagggcccc 1250  
ggcacagtac aggctggaga gagggcaggc tcgaaggctt ctgcacatgc 1300  
tgctttcctt gtggaaggaa gactttcagg ggccggttcc gctgcagctg 1350  
ctgctgagcc caagaaatgt ggggcttctg gcagacacaa ggccaaggga 1400  
gtgggacttg ctgctattct tgctacggga gctggtggag aagggtctga 1450  
tgggacggat ggagatagag gcctgcctgg gcagcctcca ccaggcccag 1500  
tggccagggg actttgctga agaattagca aactgtcta atctgtttct 1550  
agccgagccc cacctgccag aacccagct aagagcctgt gagggtgtgc 1600  
agccaaaccg gggcactgtg ctggcccaga gctagggctg agaagtggcc 1650

ctgccttggg cattgcacca gaaccctgga ccccgccctc acgaggaggc 1700  
ccaagtgcc aatgcagacc ctactgggtt ggggtgtagc tgggtctaca 1750  
gtcagacttc ctgctctaag ggtgtcactg cctggcatcc caccacgca 1800  
atcctagagg aaggagagtt ggcctgattt gggattatgg cagaaaagtc 1850  
cagagatgcc agtcctggag tagaagaggt ggtgtttgtt tatctcttgg 1900  
atactaaatg aaatgaggtg tgtgggcttg tcaacacaga attcaagcct 1950  
catttgctat ccagcatct cttaaaactt tgtagtcttg gaattcatga 2000  
cagaggcaaa tgactcctgc ttaacttatg aagaaagtta aaacatgaat 2050  
cttgggagtc tacatcttct tatcaccagg agctggactg ccatctcctt 2100  
ataaatgcct aacacaggcc gggctcgtg gctcatgcct gtaatcccag 2150  
cactttgaga ggcctgaggt cggcggactg cctgaggtca ggaattcaag 2200  
accagcctgg ccaacatggc aaaaccccat ctctactaaa aataaaaaaa 2250  
ttattagctg ggcctgggtg tgtgtgcctg taatcccagc tactcaggag 2300  
gatgaggcag gagacctgct tgaacctgga ggtggagggt gcagtgagcc 2350  
gaggtcgcac cactgcactc cagtctgggt aacagagcga gactttctag 2400  
aaaaagccta acaaacagat aaggtaggac tcaaccaact gaaacctgac 2450  
tttccccctg taccttcagc ccctgtgcag gtagtaacct cttgagacct 2500  
ctccctgacc agggaccaag cacagggcat ttagagcttt ttagaataaa 2550  
ctggttttct ttaaaaaaaaa aaaaaaaaaa agggcgccg cccttttttt 2600  
tttttttttt tttttttttt tttttttttt tttttttttt taaaaagggc 2650  
ttttattaaa attctcccca cacgatggct cctgcaatct gccacagctc 2700  
tggggcgtgt cctgtaggga aaggccctgt tttccctgag gcggggctgg 2750  
gcttgccat ggggtccgcg agctggccgt gcttgccgcc ctggcgtgtg 2800  
tctagctgct tcttgccggg cacagagctg cggggtctgg gggcaccggg 2850  
agctaagagc aggtctggt gcaggggtgg aggcctgtct cttaacgac 2900  
accctgaggt gctcctgaga tgctgggtcc accctgagtg gcacggggag 2950  
cagctgtggc cgggtgctct tcytaggcca gtctgggga aactaagctc 3000  
gggcccttct ttgcaaagac cgaggatggg gtgggtgtgg gggactcatg 3050  
gggaatggcc tgaggagcta cgtgtgaaga gggcgccggt ttgttggtg 3100

cagcggcctg gagcgctct ctcctgagcc tcagtttccc tttccgtcta 3150  
 atgaagaaca tgccgtctcg gtgtctcagg gctattagga cttgccctca 3200  
 ggaagtggcc ttggacgagc gtcattgttat tttcacaact gtccctgcgac 3250  
 gttggcctgg gcacgtcatg gaatggccca tgtccctctg ctgcgtggac 3300  
 gtcgcggctg ggagtgcgca gccagaggcg gggccagacg tgcgcctggg 3350  
 ggtgagggga ggcgccccgg gagggcctca caggaagttg ggctcccga 3400  
 ccaccaggca gggcgggctc ccgccgccgc cgccgccacc accgtccagg 3450  
 ggccggtaga caaagtggaa gtcgcgcttg ggctcgctgc gcagcaggta 3500  
 gcccttgatg cagtgcggca gcgcgtcgtc cgccagctgg aagcagcgcc 3550  
 cgtccaccag cacgaacagc cggtgcgcct 3580

<210> 54

<211> 280

<212> PRT

<213> Homo sapiens

<400> 54

Met	Cys	Phe	Leu	Asn	Lys	Leu	Leu	Leu	Leu	Ala	Val	Leu	Gly	Trp
1				5						10				15
Leu	Phe	Gln	Ile	Pro	Thr	Val	Pro	Glu	Asp	Leu	Phe	Phe	Leu	Glu
				20					25					30
Glu	Gly	Pro	Ser	Tyr	Ala	Phe	Glu	Val	Asp	Thr	Val	Ala	Pro	Glu
				35					40					45
His	Gly	Leu	Asp	Asn	Ala	Pro	Val	Val	Asp	Gln	Gln	Leu	Leu	Tyr
				50					55					60
Thr	Cys	Cys	Pro	Tyr	Ile	Gly	Glu	Leu	Arg	Lys	Leu	Leu	Ala	Ser
				65					70					75
Trp	Val	Ser	Gly	Ser	Ser	Gly	Arg	Ser	Gly	Gly	Phe	Met	Arg	Lys
				80					85					90
Ile	Thr	Pro	Thr	Thr	Thr	Thr	Ser	Leu	Gly	Ala	Gln	Pro	Ser	Gln
				95					100					105
Thr	Ser	Gln	Gly	Leu	Gln	Ala	Gln	Leu	Ala	Gln	Ala	Phe	Phe	His
				110					115					120
Asn	Gln	Pro	Pro	Ser	Leu	Arg	Arg	Thr	Val	Glu	Phe	Val	Ala	Glu
				125					130					135
Arg	Ile	Gly	Ser	Asn	Cys	Val	Lys	His	Ile	Lys	Ala	Thr	Leu	Val
				140					145					150



Ala Asp Leu Val	Arg Gln Ala Glu Ser	Leu Leu Gln Glu Gln Leu
155	160	165
Val Thr Gln Gly	Glu Glu Gly Gly Asp	Pro Ala Gln Leu Leu Glu
170	175	180
Ile Leu Cys Ser	Gln Leu Cys Pro His	Gly Ala Gln Ala Leu Ala
185	190	195
Leu Gly Arg Glu	Phe Cys Gln Arg Lys	Ser Pro Gly Ala Val Arg
200	205	210
Ala Leu Leu Pro	Glu Glu Thr Pro Ala	Ala Val Leu Ser Ser Ala
215	220	225
Glu Asn Ile Ala	Val Gly Leu Ala Thr	Glu Lys Ala Cys Ala Trp
230	235	240
Leu Ser Ala Asn	Ile Thr Ala Leu Ile	Arg Arg Glu Val Lys Ala
245	250	255
Ala Val Ser Arg	Thr Leu Arg Ala Gln	Gly Pro Glu Pro Ala Ala
260	265	270
Arg Gly Glu Arg	Arg Gly Cys Ser Arg	Ala
275	280	

<210> 55

<211> 2401

<212> DNA

<213> Homo sapiens

<400> 55

```

tcccttgaca ggtctggtgg ctggttcggg gtctactgaa ggctgtcttg 50
atcaggaaac tgaagactct ctgcttttgc cacagcagtt cctgcagctt 100
ccttgaggtg tgaaccacaca tccctgcccc cagggccacc tgcaggacgc 150
cgacacctac ccctcagcag acgccggaga gaaatgagta gcaacaaaga 200
gcagcgggtca gcagtgttcg tgatcctctt tgccctcatc accatcctca 250
tcctctacag ctccaacagt gccaatgagg tcttcatta cggtccctg 300
cggggccgta gccgccgacc tgtcaacctc aagaagtga gcatcactga 350
cggctatgtc ccattctctg gcaacaagac actgccctct cggtgccacc 400
agtgtgtgat tgtcagcagc tccagccacc tgctgggcac caagctgggc 450
cctgagatcg agcgggctga gtgtacaatc cgcataatg atgcacccac 500
cactggctac tcagctgatg tgggcaacaa gaccacctac cgcgtcgtgg 550
ccattccag tgtgttcgc gtgctgagga ggccccagga gtttgtcaac 600

```

cggaccctg aaaccgtgtt catcttctgg gggccccga gcaagatgca 650  
gaagccccag ggcagcctcg tgcgtgtgat ccagcgagcg ggcctggtgt 700  
tccccaacat ggaagcatat gccgtctctc ccggccgcat gcggaattt 750  
gacgacctct tccggggtga gacgggcaag gacagggaga agtctcattc 800  
gtgggtgagc acaggctggt ttaccatggt gatcgcggtg gagttgtgtg 850  
accacgtgca tgtctatggc atgggtcccc ccaactactg cagccagcgg 900  
ccccgcctcc agcgcatgcc ctaccactac tacgagccca aggggccgga 950  
cgaatgtgtc acctacatcc agaatgagca cagtcgcaag ggcaaccacc 1000  
accgcttcat caccgagaaa agggctcttct catcgtgggc ccagctgtat 1050  
ggcatcacct tctcccaccc ctcttgacc taggccaccc agcctgtggg 1100  
acctcaggag ggtcagagga gaagcagcct ccgccagcc gctaggccag 1150  
ggaccatctt ctggccaatc aaggcttgct ggagtgtctc ccagccaatc 1200  
agggccttga ggaggatgta tctccagcc aatcagggcc tggggaatct 1250  
gttggcgaat cagggaattg ggagtctatg tggttaatca ggggtgtctt 1300  
tcttgtgcag tcagggtctg cgcacagtca atcagggtag aggggtatt 1350  
tctgagtcaa tctgaggcta aggacatgtc ctttcccatg aggccttgg 1400  
tcagagcccc aggaatggac cccccaatca ctcccactc tgctgggata 1450  
atggggtcct gtccaagga gctgggaact tgggtgtgcc ccctcaattt 1500  
ccagcaccag aaagagagat tgtgtggggg tagaagctgt ctggaggccc 1550  
ggccagagaa tttgtggggt tgtggagggt gtgggggcgg tggggaggtc 1600  
ccagaggtgg gaggctggca tccaggctct ggctctgcc tgagaccttg 1650  
gacaaaccct tccccctctc tgggcacct tctgccaca ccagtttcca 1700  
gtgcggagtc tgagacctt tccacctccc ctacaagtgc cctcgggtct 1750  
gtctccccg tctggacct cccagccact atcccttgct ggaaggctca 1800  
gctctttggg gggctctggg tgacctcccc acctcctgga aaactttagg 1850  
gtatttttgc gcaaactcct tcagggttgg gggactctga aggaaacggg 1900  
acaaaacctt aagctgtttt cttagccct cagccagctg ccattagctt 1950  
ggctcttaaa gggccaggcc tcttttctg ccctctagca gggaggtttt 2000  
ccaactgttg gaggcgcctt tggggctgcc ccttgtctg gagtcactgg 2050

gggcttccga gggctccct cgacctctg tcgtcctggg atggctgtcg 2100  
 ggagctgtat cacctgggtt ctgtccctg gctctgtatc aggcacttta 2150  
 ttaaagctgg gcctcagtgg ggtgtgtttg tctcctgctc ttctggagcc 2200  
 tggaaggaaa gggcttcagg aggaggctgt gaggctggag ggaccagatg 2250  
 gaggaggcca gcagctagcc attgcacact ggggtgatgg gtgggggcgg 2300  
 tgactgcccc agacttggtt ttgtaatgat ttgtacagga ataaacacac 2350  
 ctacgtccg gaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 2400

a 2401

<210> 56

<211> 299

<212> PRT

<213> Homo sapiens

<400> 56

Met	Ser	Ser	Asn	Lys	Glu	Gln	Arg	Ser	Ala	Val	Phe	Val	Ile	Leu
1				5					10					15

Phe	Ala	Leu	Ile	Thr	Ile	Leu	Ile	Leu	Tyr	Ser	Ser	Asn	Ser	Ala
				20					25					30

Asn	Glu	Val	Phe	His	Tyr	Gly	Ser	Leu	Arg	Gly	Arg	Ser	Arg	Arg
				35					40					45

Pro	Val	Asn	Leu	Lys	Lys	Trp	Ser	Ile	Thr	Asp	Gly	Tyr	Val	Pro
				50					55					60

Ile	Leu	Gly	Asn	Lys	Thr	Leu	Pro	Ser	Arg	Cys	His	Gln	Cys	Val
				65					70					75

Ile	Val	Ser	Ser	Ser	Ser	His	Leu	Leu	Gly	Thr	Lys	Leu	Gly	Pro
				80					85					90

Glu	Ile	Glu	Arg	Ala	Glu	Cys	Thr	Ile	Arg	Met	Asn	Asp	Ala	Pro
				95					100					105

Thr	Thr	Gly	Tyr	Ser	Ala	Asp	Val	Gly	Asn	Lys	Thr	Thr	Tyr	Arg
				110					115					120

Val	Val	Ala	His	Ser	Ser	Val	Phe	Arg	Val	Leu	Arg	Arg	Pro	Gln
				125					130					135

Glu	Phe	Val	Asn	Arg	Thr	Pro	Glu	Thr	Val	Phe	Ile	Phe	Trp	Gly
				140					145					150

Pro	Pro	Ser	Lys	Met	Gln	Lys	Pro	Gln	Gly	Ser	Leu	Val	Arg	Val
				155					160					165

Ile	Gln	Arg	Ala	Gly	Leu	Val	Phe	Pro	Asn	Met	Glu	Ala	Tyr	Ala
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

170	175	180
Val Ser Pro Gly Arg Met Arg Gln Phe Asp Asp Leu Phe Arg Gly		
185	190	195
Glu Thr Gly Lys Asp Arg Glu Lys Ser His Ser Trp Leu Ser Thr		
200	205	210
Gly Trp Phe Thr Met Val Ile Ala Val Glu Leu Cys Asp His Val		
215	220	225
His Val Tyr Gly Met Val Pro Pro Asn Tyr Cys Ser Gln Arg Pro		
230	235	240
Arg Leu Gln Arg Met Pro Tyr His Tyr Tyr Glu Pro Lys Gly Pro		
245	250	255
Asp Glu Cys Val Thr Tyr Ile Gln Asn Glu His Ser Arg Lys Gly		
260	265	270
Asn His His Arg Phe Ile Thr Glu Lys Arg Val Phe Ser Ser Trp		
275	280	285
Ala Gln Leu Tyr Gly Ile Thr Phe Ser His Pro Ser Trp Thr		
290	295	

<210> 57  
 <211> 4277  
 <212> DNA  
 <213> Homo sapiens

<400> 57  
 gtttctcata gttggcgtct tctaaaggaa aaacactaaa atgaggaact 50  
 cagcggaccg ggagcgacgc agcttgaggg aagcatccct agctgttggc 100  
 gcagaggggc gaggtgaag ccgagtggcc cgaggtgtct gaggggctgg 150  
 ggcaaagggtg aaagagtttc agaacaagct tcctggaacc catgacccat 200  
 gaagtcttgt cgacatttat accgtctgag ggtagcagct cgaaactaga 250  
 agaagtggag tgttgccagg gacggcagta tctctttgtg tgaccctggc 300  
 ggcctatggg acgttggtt cagacctttg tgataacca tgctgcgtgg 350  
 gacgatgacg gcgtggagag gaatgaggcc tgaggtcaca ctggcttgcc 400  
 tcctcctagc cacagcaggc tgctttgctg acttgaacga ggtccctcag 450  
 gtcaccgtcc agcctgcgtc caccgtccag aagcccggag gcactgtgat 500  
 cttgggctgc gtgggtgaac ctccaaggat gaatgtaacc tggcgctga 550  
 atggaaagga gctgaatggc tcggatgatg ctctgggtgt cctcatcacc 600  
 cacgggaccc tcgtcatcac tgcccttaac aaccacactg tgggacgta 650

ccagtgtgtg gcccgatgc ctgcgggggc tgtggccagc gtgccagcca 700  
ctgtgacact agccaatctc caggacttca agttagatgt gcagcacgtg 750  
attgaagtgg atgagggaaa cacagcagtc attgcctgcc acctgcctga 800  
gagccacccc aaagcccagg tccggtacag cgtcaaacia gagtggctgg 850  
aggcctccag aggtaactac ctgatcatgc cctcaggga cctccagatt 900  
gtgaatgcca gccaggagga cgagggcagc tacaagtgtg cagcctacia 950  
cccagtgacc caggaagtga aaacctccgg ctccagcagc aggctacgtg 1000  
tgcgccgctc caccgctgag gctgcccgca tcactatccc cccagaggcc 1050  
caaaccatca tcgtcaccaa aggccagagt ctattctgg agtgtgtggc 1100  
cagtggaatc ccacccccac gggtcacctg ggccaaggat gggtcagtg 1150  
tcaccggcta caacaagacg cgcttctctg tgagcaacct cctcatcgac 1200  
accaccagcg aggaggactc aggcaacctc cgctgcatgg ccgacaatgg 1250  
ggttgggcag cccggggcag cggtcatcct ctacaatgtc caggtgtttg 1300  
aaccacctga ggtcacctg gagctatccc agctggctat cccctggggc 1350  
cagagtgcca agcttacctg tgagggtcgt gggaaccccc cgccctccgt 1400  
gctgtggctg aggaatgctg tgccctcat ctccagccag cgctccggc 1450  
tctccgcag gccctgcgc gtgctcagca tggggcctga ggacgaaggc 1500  
gtctaccagt gcatggccga gaacgaggtt gggagcgccc atgccgtagt 1550  
ccagctgcgg acctccaggc caagcataac cccaaggcta tggcaggatg 1600  
ctgagctggc tactggcaca cctcctgtat caccctcaa actcggcaac 1650  
cctgagcaga tgctgagggg gcaaccggcg ctccccagac ccccaacgtc 1700  
agtggggcct gcttccccga agtgtccagg agagaagggg cagggggctc 1750  
ccgccaggc tcccatcatc ctgagctcgc ccgcacctc caagacagac 1800  
tcatatgaac tgggtgtggc gcctcggcat gagggcagtg gccgggcgcc 1850  
aatcctctac tatgtggtga aacaccgcaa gcaggtcaca aattcctctg 1900  
acgattggac catctctggc attccagcca accagcaccg cctgaccctc 1950  
accagacttg accccgggag cttgtatgaa gtggagatgg cagcttacia 2000  
ctgtgcggga gagggccaga cagccatggt caccttccga actggacggc 2050

ggcccaaacc cgagatcatg gccagcaaag agcagcagat ccagagagac 2100  
gaccttgag ccagtcccca gagcagcagc cagccagacc acggccgcct 2150  
ctcccccca gaagctcccg acaggccac catctccacg gcctccgaga 2200  
cctcagtgt cgtgacctg attccccgtg ggaatggtg gttcccaatc 2250  
cagtccttcc gtgtggagta caagaagcta aagaaagtgg gagactggat 2300  
tctggccacc agcgccatcc ccccatcgcg gctgtccgtg gagatcacgg 2350  
gcctagagaa aggcacctcc tacaagtttc gagtccgggc tctgaacatg 2400  
ctgggggaga gcgagcccag cgccccctct cggccctacg tgggtgcggg 2450  
ctacagcgt cgcggtacg agaggccgt ggcaggtcct tatatcacct 2500  
tcacggatgc ggtcaatgag accaccatca tgctcaagtg gatgtacatc 2550  
ccagcaagta acaacaacac cccaatccat ggcttttata tctattatcg 2600  
accacagac agtgacaatg atagtacta caagaaggat atggtggaag 2650  
gggacaagta ctggcactcc atcagccacc tgcagccaga gacctcctac 2700  
gacattaaga tgcagtgtt caatgaagga ggggagagcg agttcagcaa 2750  
cgtgatgatc tgtgagacca aagctcgaa gtcttctggc cagcctggtc 2800  
gactgccacc cccaactctg gccccaccac agcgcgccct tcctgaaacc 2850  
atagagcggc cgggtggcac tggggccatg gtggctcgct ccagcgacct 2900  
gccctatctg attgtcgggg tcgtcctggg ctccatcggt ctcacatcg 2950  
tcacctcat ccccttctgc ttgtggaggg cctggtctaa gcaaaaacat 3000  
acaacagacc tgggttttcc tcgaagtgc cttccaccct cctgcccgt 3050  
tactatggtg ccattgggag gactcccagg ccaccaggcc agtggacagc 3100  
cctacctcag tggcatcagt ggacgggcct gtgctaattg gatccacatg 3150  
aataggggct gcccctcggc tgcagtgggc taccgggca tgaagcccca 3200  
gcagcactgc ccaggcgagc ttcagcagca gagtgacacc agcagcctgc 3250  
tgaggcagac ccatcttggc aatggatatg acccccaaag tcaccagatc 3300  
acgaggggtc ccaagtctag cccggacgag ggctctttct tatacacact 3350  
gcccgacgac tccactcacc agctgctgca gcccacac gactgctgcc 3400  
aacgccagga gcagcctgct gctgtgggac agtcaggggt gaggagagcc 3450  
cccgacgtc ctgtcctgga agcagtgtgg gacctccat ttcactcagg 3500

gcccccatgc tgettgggcc ttgtgccagt tgaagaggtg gacagtcttg 3550  
 actcctgcc aagttagtga ggagactggt gtccccagca ccccgtaggg 3600  
 gcctacgtag gacaggaacc tggaatgcag ctctccccgg ggccactggt 3650  
 gcgtgtgtct tttgaaacac cacctctcac aatttaggca gaagctgata 3700  
 tcccagaaag actatatatt gttttttttt taaaaaaaaa agaagaaaaa 3750  
 agagacagag aaaattggtt tttatttttc tattatagcc atatttatat 3800  
 atttatgcac ttgtaaataa atgtatatgt ttataattc tggagagaca 3850  
 taaggagtcc taccggttga ggttgagag ggaaaataaa gaagctgcc 3900  
 cctaacagga gtcaccagg aaagcaccgc acaggctggc gcgggacaga 3950  
 ctctaacct ggggcctctg cagtggcagg cgaggctgca ggaggccac 4000  
 agataagctg gcaagaggaa ggatcccagg cacatggttc atcacgagca 4050  
 tgagggaaca gcaaggggca cggtatcaca gcctggagac acccacacag 4100  
 atggctggat ccggtgctac gggaaacatt ttctaagat gcccattgaga 4150  
 acagaccaag atgtgtacag cactatgagc attaaaaaac cttccagaat 4200  
 caataatccg tggcaacata tctctgtaaa aacaaacact gtaacttcta 4250  
 aataaatggt tagtcttccc tgtaaaa 4277

<210> 58

<211> 1115

<212> PRT

<213> Homo sapiens

<400> 58

Met	Leu	Arg	Gly	Thr	Met	Thr	Ala	Trp	Arg	Gly	Met	Arg	Pro	Glu
1				5					10					15

Val	Thr	Leu	Ala	Cys	Leu	Leu	Leu	Ala	Thr	Ala	Gly	Cys	Phe	Ala
				20					25					30

Asp	Leu	Asn	Glu	Val	Pro	Gln	Val	Thr	Val	Gln	Pro	Ala	Ser	Thr
				35					40					45

Val	Gln	Lys	Pro	Gly	Gly	Thr	Val	Ile	Leu	Gly	Cys	Val	Val	Glu
				50					55					60

Pro	Pro	Arg	Met	Asn	Val	Thr	Trp	Arg	Leu	Asn	Gly	Lys	Glu	Leu
				65					70					75

Asn	Gly	Ser	Asp	Asp	Ala	Leu	Gly	Val	Leu	Ile	Thr	His	Gly	Thr
				80					85					90

Leu Val Ile Thr	Ala Leu Asn Asn His	Thr Val Gly Arg Tyr	Gln
	95	100	105
Cys Val Ala Arg	Met Pro Ala Gly Ala	Val Ala Ser Val Pro	Ala
	110	115	120
Thr Val Thr Leu	Ala Asn Leu Gln Asp	Phe Lys Leu Asp Val	Gln
	125	130	135
His Val Ile Glu	Val Asp Glu Gly Asn	Thr Ala Val Ile Ala	Cys
	140	145	150
His Leu Pro Glu	Ser His Pro Lys Ala	Gln Val Arg Tyr Ser	Val
	155	160	165
Lys Gln Glu Trp	Leu Glu Ala Ser Arg	Gly Asn Tyr Leu Ile	Met
	170	175	180
Pro Ser Gly Asn	Leu Gln Ile Val Asn	Ala Ser Gln Glu Asp	Glu
	185	190	195
Gly Met Tyr Lys	Cys Ala Ala Tyr Asn	Pro Val Thr Gln Glu	Val
	200	205	210
Lys Thr Ser Gly	Ser Ser Asp Arg Leu	Arg Val Arg Arg Ser	Thr
	215	220	225
Ala Glu Ala Ala	Arg Ile Ile Tyr Pro	Pro Glu Ala Gln Thr	Ile
	230	235	240
Ile Val Thr Lys	Gly Gln Ser Leu Ile	Leu Glu Cys Val Ala	Ser
	245	250	255
Gly Ile Pro Pro	Pro Arg Val Thr Trp	Ala Lys Asp Gly Ser	Ser
	260	265	270
Val Thr Gly Tyr	Asn Lys Thr Arg Phe	Leu Leu Ser Asn Leu	Leu
	275	280	285
Ile Asp Thr Thr	Ser Glu Glu Asp Ser	Gly Thr Tyr Arg Cys	Met
	290	295	300
Ala Asp Asn Gly	Val Gly Gln Pro Gly	Ala Ala Val Ile Leu	Tyr
	305	310	315
Asn Val Gln Val	Phe Glu Pro Pro Glu	Val Thr Met Glu Leu	Ser
	320	325	330
Gln Leu Val Ile	Pro Trp Gly Gln Ser	Ala Lys Leu Thr Cys	Glu
	335	340	345
Val Arg Gly Asn	Pro Pro Pro Ser Val	Leu Trp Leu Arg Asn	Ala
	350	355	360
Val Pro Leu Ile	Ser Ser Gln Arg Leu	Arg Leu Ser Arg Arg	Ala
	365	370	375



Leu	Arg	Val	Leu	Ser	Met	Gly	Pro	Glu	Asp	Glu	Gly	Val	Tyr	Gln	
				380					385					390	
Cys	Met	Ala	Glu	Asn	Glu	Val	Gly	Ser	Ala	His	Ala	Val	Val	Gln	
				395					400					405	
Leu	Arg	Thr	Ser	Arg	Pro	Ser	Ile	Thr	Pro	Arg	Leu	Trp	Gln	Asp	
				410					415					420	
Ala	Glu	Leu	Ala	Thr	Gly	Thr	Pro	Pro	Val	Ser	Pro	Ser	Lys	Leu	
				425					430					435	
Gly	Asn	Pro	Glu	Gln	Met	Leu	Arg	Gly	Gln	Pro	Ala	Leu	Pro	Arg	
				440					445					450	
Pro	Pro	Thr	Ser	Val	Gly	Pro	Ala	Ser	Pro	Lys	Cys	Pro	Gly	Glu	
				455					460					465	
Lys	Gly	Gln	Gly	Ala	Pro	Ala	Glu	Ala	Pro	Ile	Ile	Leu	Ser	Ser	
				470					475					480	
Pro	Arg	Thr	Ser	Lys	Thr	Asp	Ser	Tyr	Glu	Leu	Val	Trp	Arg	Pro	
				485					490					495	
Arg	His	Glu	Gly	Ser	Gly	Arg	Ala	Pro	Ile	Leu	Tyr	Tyr	Val	Val	
				500					505					510	
Lys	His	Arg	Lys	Gln	Val	Thr	Asn	Ser	Ser	Asp	Asp	Trp	Thr	Ile	
				515					520					525	
Ser	Gly	Ile	Pro	Ala	Asn	Gln	His	Arg	Leu	Thr	Leu	Thr	Arg	Leu	
				530					535					540	
Asp	Pro	Gly	Ser	Leu	Tyr	Glu	Val	Glu	Met	Ala	Ala	Tyr	Asn	Cys	
				545					550					555	
Ala	Gly	Glu	Gly	Gln	Thr	Ala	Met	Val	Thr	Phe	Arg	Thr	Gly	Arg	
				560					565					570	
Arg	Pro	Lys	Pro	Glu	Ile	Met	Ala	Ser	Lys	Glu	Gln	Gln	Ile	Gln	
				575					580					585	
Arg	Asp	Asp	Pro	Gly	Ala	Ser	Pro	Gln	Ser	Ser	Ser	Gln	Pro	Asp	
				590					595					600	
His	Gly	Arg	Leu	Ser	Pro	Pro	Glu	Ala	Pro	Asp	Arg	Pro	Thr	Ile	
				605					610					615	
Ser	Thr	Ala	Ser	Glu	Thr	Ser	Val	Tyr	Val	Thr	Trp	Ile	Pro	Arg	
				620					625					630	
Gly	Asn	Gly	Gly	Phe	Pro	Ile	Gln	Ser	Phe	Arg	Val	Glu	Tyr	Lys	
				635					640					645	
Lys	Leu	Lys	Lys	Val	Gly	Asp	Trp	Ile	Leu	Ala	Thr	Ser	Ala	Ile	
				650					655					660	

Pro	Pro	Ser	Arg	Leu	Ser	Val	Glu	Ile	Thr	Gly	Leu	Glu	Lys	Gly		665	670	675
Thr	Ser	Tyr	Lys	Phe	Arg	Val	Arg	Ala	Leu	Asn	Met	Leu	Gly	Glu		680	685	690
Ser	Glu	Pro	Ser	Ala	Pro	Ser	Arg	Pro	Tyr	Val	Val	Ser	Gly	Tyr		695	700	705
Ser	Gly	Arg	Val	Tyr	Glu	Arg	Pro	Val	Ala	Gly	Pro	Tyr	Ile	Thr		710	715	720
Phe	Thr	Asp	Ala	Val	Asn	Glu	Thr	Thr	Ile	Met	Leu	Lys	Trp	Met		725	730	735
Tyr	Ile	Pro	Ala	Ser	Asn	Asn	Asn	Thr	Pro	Ile	His	Gly	Phe	Tyr		740	745	750
Ile	Tyr	Tyr	Arg	Pro	Thr	Asp	Ser	Asp	Asn	Asp	Ser	Asp	Tyr	Lys		755	760	765
Lys	Asp	Met	Val	Glu	Gly	Asp	Lys	Tyr	Trp	His	Ser	Ile	Ser	His		770	775	780
Leu	Gln	Pro	Glu	Thr	Ser	Tyr	Asp	Ile	Lys	Met	Gln	Cys	Phe	Asn		785	790	795
Glu	Gly	Gly	Glu	Ser	Glu	Phe	Ser	Asn	Val	Met	Ile	Cys	Glu	Thr		800	805	810
Lys	Ala	Arg	Lys	Ser	Ser	Gly	Gln	Pro	Gly	Arg	Leu	Pro	Pro	Pro		815	820	825
Thr	Leu	Ala	Pro	Pro	Gln	Pro	Pro	Leu	Pro	Glu	Thr	Ile	Glu	Arg		830	835	840
Pro	Val	Gly	Thr	Gly	Ala	Met	Val	Ala	Arg	Ser	Ser	Asp	Leu	Pro		845	850	855
Tyr	Leu	Ile	Val	Gly	Val	Val	Leu	Gly	Ser	Ile	Val	Leu	Ile	Ile		860	865	870
Val	Thr	Phe	Ile	Pro	Phe	Cys	Leu	Trp	Arg	Ala	Trp	Ser	Lys	Gln		875	880	885
Lys	His	Thr	Thr	Asp	Leu	Gly	Phe	Pro	Arg	Ser	Ala	Leu	Pro	Pro		890	895	900
Ser	Cys	Pro	Tyr	Thr	Met	Val	Pro	Leu	Gly	Gly	Leu	Pro	Gly	His		905	910	915
Gln	Ala	Ser	Gly	Gln	Pro	Tyr	Leu	Ser	Gly	Ile	Ser	Gly	Arg	Ala		920	925	930
Cys	Ala	Asn	Gly	Ile	His	Met	Asn	Arg	Gly	Cys	Pro	Ser	Ala	Ala		935	940	945

Val Gly Tyr Pro Gly Met Lys Pro Gln Gln His Cys Pro Gly Glu	950	955	960
Leu Gln Gln Gln Ser Asp Thr Ser Ser Leu Leu Arg Gln Thr His	965	970	975
Leu Gly Asn Gly Tyr Asp Pro Gln Ser His Gln Ile Thr Arg Gly	980	985	990
Pro Lys Ser Ser Pro Asp Glu Gly Ser Phe Leu Tyr Thr Leu Pro	995	1000	1005
Asp Asp Ser Thr His Gln Leu Leu Gln Pro His His Asp Cys Cys	1010	1015	1020
Gln Arg Gln Glu Gln Pro Ala Ala Val Gly Gln Ser Gly Val Arg	1025	1030	1035
Arg Ala Pro Asp Ser Pro Val Leu Glu Ala Val Trp Asp Pro Pro	1040	1045	1050
Phe His Ser Gly Pro Pro Cys Cys Leu Gly Leu Val Pro Val Glu	1055	1060	1065
Glu Val Asp Ser Pro Asp Ser Cys Gln Val Ser Gly Gly Asp Trp	1070	1075	1080
Cys Pro Gln His Pro Val Gly Ala Tyr Val Gly Gln Glu Pro Gly	1085	1090	1095
Met Gln Leu Ser Pro Gly Pro Leu Val Arg Val Ser Phe Glu Thr	1100	1105	1110
Pro Pro Leu Thr Ile	1115		

<210> 59

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 59

gggaaacaca gcagtcattg cctgc 25

<210> 60

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 60

gcacacgtag cctgtcgctg gagc 24

<210> 61  
<211> 42  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 61  
caccccaaag cccaggtccg gtacagcgtc aaacaagagt gg 42

<210> 62  
<211> 1661  
<212> DNA  
<213> Homo sapiens

<220>  
<221> unsure  
<222> 678  
<223> unknown base

<400> 62  
cgggaggctg ggtcgatcatg atccggaccc cattgtcggc ctctgcccatt 50  
cgctgtctcc tcccaggctc ccgcggccga ccccgcgca acatgcagcc 100  
cacgggcccgc gaggggtccc gcgcgctcag ccggcggtat ctgcggcgtc 150  
tgctgtctcct gctactgctg ctgctgctgc ggcagcccgt aaccgcgcgcg 200  
gagaccacgc cgggcgcccc cagagccctc tccacgctgg gctccccag 250  
cctcttcacc acgcgggtg tcccagcgc cctcactacc ccaggcctca 300  
ctacgccagg caccccc aaa accctggacc ttcggggctc gcgcagggcc 350  
ctgatgcgga gtttcccact cgtggacggc cacaatgacc tgccccaggt 400  
cctgagacag cgttacaaga atgtgcttca ggatgttaac ctgcgaaatt 450  
tcagccatgg tcagaccagc ctggacaggc ttagagacgg cctcgtgggt 500  
gcccagttct ggtcagcctc cgtctcatgc cagtcccagg accagactgc 550  
cgtgcgcctc gccctggagc agattgacct cattcaccgc atgtgtgcct 600  
cctactctga actcgagctt gtgacctcag ctgaaggtct gaacagctct 650  
caaaagctgg cctgcctcat tggcgtgnag ggtggtcact cactggacag 700  
cagcctctct gtgctgcgca gtttctatgt gctgggggtg cgctacctga 750  
cacttacctt cacctgcagt acaccatggg cagagagttc caccaagttc 800  
agacaccaca tgtacaccaa cgtcagcgga ttgacaagct ttggtgagaa 850

agtagtagag gagttgaacc gcctgggcat gatgatagat ttgtcctatg 900  
 catcggacac cttgataaga agggtcctgg aagtgtctca ggctcctgtg 950  
 atcttctccc actcagctgc cagagctgtg tgtgacaatt tgttgaatgt 1000  
 tcccgatgat atcctgcagc ttctgaagaa cgggtggcatc gtgatgggtga 1050  
 cactgtccat ggggggtgctg cagtgaacc tgcttgctaa cgtgtccact 1100  
 gtggcagatc actttgacca catcagggca gtcattggat ctgagttcat 1150  
 cgggattggg ggaaattatg acgggactgg ccggttccct caggggctgg 1200  
 aggatgtgtc cacataccca gtcctgatag aggagttgct gagtcgtasc 1250  
 tggagcagagg aagagcttca aggtgtcctt cgtggaaacc tgctgcgggt 1300  
 cttcagacaa gtggaaaagg tgagagagga gagcagggcg cagagccccg 1350  
 tggaggctga gtttccatat gggcaactga gcacatcctg ccactcccac 1400  
 ctcgtgcctc agaatggaca ccaggctact catctggagg tgaccaagca 1450  
 gccaaccaat cgggtcccct ggaggtcctc aaatgcctcc ccataccttg 1500  
 ttccaggcct tgtggctgct gccaccatcc caaccttcac ccagtggctc 1550  
 tgctgacaca gtcgggtcccc gcagaggtca ctgtggcaaa gcctcacaaa 1600  
 gccccctctc ctagttcatt cacaagcata tgctgagaat aaacatgtta 1650  
 cacatggaaa a 1661

<210> 63  
 <211> 487  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> unsure  
 <222> 196, 386  
 <223> unknown amino acid

<400> 63  
 Met Gln Pro Thr Gly Arg Glu Gly Ser Arg Ala Leu Ser Arg Arg  
 1 5 10 15  
 Tyr Leu Arg Arg Leu Leu Leu Leu Leu Leu Leu Leu Leu Arg  
 20 25 30  
 Gln Pro Val Thr Arg Ala Glu Thr Thr Pro Gly Ala Pro Arg Ala  
 35 40 45  
 Leu Ser Thr Leu Gly Ser Pro Ser Leu Phe Thr Thr Pro Gly Val  
 50 55 60

Pro	Ser	Ala	Leu	Thr	Thr	Pro	Gly	Leu	Thr	Thr	Pro	Gly	Thr	Pro				65	70	75
Lys	Thr	Leu	Asp	Leu	Arg	Gly	Arg	Ala	Gln	Ala	Leu	Met	Arg	Ser				80	85	90
Phe	Pro	Leu	Val	Asp	Gly	His	Asn	Asp	Leu	Pro	Gln	Val	Leu	Arg				95	100	105
Gln	Arg	Tyr	Lys	Asn	Val	Leu	Gln	Asp	Val	Asn	Leu	Arg	Asn	Phe				110	115	120
Ser	His	Gly	Gln	Thr	Ser	Leu	Asp	Arg	Leu	Arg	Asp	Gly	Leu	Val				125	130	135
Gly	Ala	Gln	Phe	Trp	Ser	Ala	Ser	Val	Ser	Cys	Gln	Ser	Gln	Asp				140	145	150
Gln	Thr	Ala	Val	Arg	Leu	Ala	Leu	Glu	Gln	Ile	Asp	Leu	Ile	His				155	160	165
Arg	Met	Cys	Ala	Ser	Tyr	Ser	Glu	Leu	Glu	Leu	Val	Thr	Ser	Ala				170	175	180
Glu	Gly	Leu	Asn	Ser	Ser	Gln	Lys	Leu	Ala	Cys	Leu	Ile	Gly	Val				185	190	195
Xaa	Gly	Gly	His	Ser	Leu	Asp	Ser	Ser	Leu	Ser	Val	Leu	Arg	Ser				200	205	210
Phe	Tyr	Val	Leu	Gly	Val	Arg	Tyr	Leu	Thr	Leu	Thr	Phe	Thr	Cys				215	220	225
Ser	Thr	Pro	Trp	Ala	Glu	Ser	Ser	Thr	Lys	Phe	Arg	His	His	Met				230	235	240
Tyr	Thr	Asn	Val	Ser	Gly	Leu	Thr	Ser	Phe	Gly	Glu	Lys	Val	Val				245	250	255
Glu	Glu	Leu	Asn	Arg	Leu	Gly	Met	Met	Ile	Asp	Leu	Ser	Tyr	Ala				260	265	270
Ser	Asp	Thr	Leu	Ile	Arg	Arg	Val	Leu	Glu	Val	Ser	Gln	Ala	Pro				275	280	285
Val	Ile	Phe	Ser	His	Ser	Ala	Ala	Arg	Ala	Val	Cys	Asp	Asn	Leu				290	295	300
Leu	Asn	Val	Pro	Asp	Asp	Ile	Leu	Gln	Leu	Leu	Lys	Asn	Gly	Gly				305	310	315
Ile	Val	Met	Val	Thr	Leu	Ser	Met	Gly	Val	Leu	Gln	Cys	Asn	Leu				320	325	330
Leu	Ala	Asn	Val	Ser	Thr	Val	Ala	Asp	His	Phe	Asp	His	Ile	Arg				335	340	345

Ala Val Ile Gly	Ser Glu Phe Ile Gly	Ile Gly Gly Asn Tyr Asp
350	355	360
Gly Thr Gly Arg	Phe Pro Gln Gly Leu	Glu Asp Val Ser Thr Tyr
365	370	375
Pro Val Leu Ile	Glu Glu Leu Leu Ser	Arg Xaa Trp Ser Glu Glu
380	385	390
Glu Leu Gln Gly	Val Leu Arg Gly Asn	Leu Leu Arg Val Phe Arg
395	400	405
Gln Val Glu Lys	Val Arg Glu Glu Ser	Arg Ala Gln Ser Pro Val
410	415	420
Glu Ala Glu Phe	Pro Tyr Gly Gln Leu	Ser Thr Ser Cys His Ser
425	430	435
His Leu Val Pro	Gln Asn Gly His Gln	Ala Thr His Leu Glu Val
440	445	450
Thr Lys Gln Pro	Thr Asn Arg Val Pro	Trp Arg Ser Ser Asn Ala
455	460	465
Ser Pro Tyr Leu	Val Pro Gly Leu Val	Ala Ala Ala Thr Ile Pro
470	475	480
Thr Phe Thr Gln	Trp Leu Cys	
485		

<210> 64  
 <211> 25  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 64  
 ccttcacctg cagtacacca tgggc 25

<210> 65  
 <211> 25  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 65  
 gtcacacaca gctctggcag ctgag 25

<210> 66  
 <211> 47  
 <212> DNA  
 <213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 66

ccaagttcag acaccacatg tacaccaacg tcagcggatt gacaagc 47

<210> 67

<211> 1564

<212> DNA

<213> Homo sapiens

<400> 67

tgctaggctc tgtcccacaa tgcacccgag agcaggagct gaaagcctct 50  
aacaccccaca gatccctcta tgactgcaat gtgaggtgtc cggctttgct 100  
ggcccagcaa gcctgataag catgaagctc ttatcttttg tggctgtggt 150  
cgggtgtttg ctggtgcccc cagctgaagc caacaagagt tctgaagata 200  
tccggtgcaa atgcatctgt ccaccttata gaaacatcag tgggcacatt 250  
tacaaccaga atgtatccca gaaggactgc aactgcctgc acgtggtgga 300  
gcccattgca gtgcctggcc atgacgtgga ggcctactgc ctgctgtgcg 350  
agtgcaggta cgaggagcgc agcaccacca ccatcaaggt catcattgtc 400  
atctacctgt ccgtggtggg tgccctgttg ctctacatgg ccttcctgat 450  
gctggtggac cctctgatcc gaaagccgga tgcatacact gagcaactgc 500  
acaatgagga ggagaatgag gatgctcgct ctatggcagc agctgctgca 550  
tccctcgggg gaccccgagc aaacacagtc ctggagcgtg tggaaggtgc 600  
ccagcagcgg tggaagctgc aggtgcagga gcagcgggaag acagtcttcg 650  
atcggcacia gatgctcagc tagatgggct ggtgtggttg ggtcaaggcc 700  
ccaacaccat ggctgccagc ttccaggctg gacaaagcag ggggctactt 750  
ctcccttccc tcggttccag tcttcccttt aaaagcctgt ggcatttttc 800  
ctccttctcc ctaactttag aaatgttgta cttggctatt ttgattaggg 850  
aagagggatg tggctctctga tctctgttgt cttcttgggt ctttgggggt 900  
gaagggaggg ggaaggcagg ccagaaggga atggagacat tcgaggcggc 950  
ctcaggagtg gatgcgatct gtctctcctg gctccactct tgccgccttc 1000  
cagctctgag tcttgggaat gttgttacct ttggaagata aagctgggtc 1050  
ttcaggaact cagtgtctgg gaggaaagca tggcccagca ttcagcatgt 1100  
gttcctttct gcagtgggtc ttatcaccac ctccctccca gccccggcgc 1150



ctcagcccca gccccagctc cagccctgag gacagctctg atgggagagc 1200  
 tgggccccct gagcccactg ggtcttcagg gtgcactgga agctgggtgtt 1250  
 cgctgtcccc tgtgcacttc tcgcactggg gcatggagtg cccatgcata 1300  
 ctctgctgcc ggtccccctca cctgcacttg aggggtcttg gcagtcacctc 1350  
 ctctccccag tgtccacagt cactgagcca gacggtcggt tggaacatga 1400  
 gactcgaggc tgagcgtgga tctgaacacc acagcccctg tacttggggtt 1450  
 gcctcttgtc cctgaacttc gttgtaccag tgcattggaga gaaaattttg 1500  
 tcctcttgtc ttagagttgt gtgtaaatca aggaagccat cattaaattg 1550  
 ttttatttct ctca 1564

<210> 68  
 <211> 183  
 <212> PRT  
 <213> Homo sapiens

<400> 68  
 Met Lys Leu Leu Ser Leu Val Ala Val Val Gly Cys Leu Leu Val  
     1                    5                    10                    15  
 Pro Pro Ala Glu Ala Asn Lys Ser Ser Glu Asp Ile Arg Cys Lys  
                     20                    25                    30  
 Cys Ile Cys Pro Pro Tyr Arg Asn Ile Ser Gly His Ile Tyr Asn  
                     35                    40                    45  
 Gln Asn Val Ser Gln Lys Asp Cys Asn Cys Leu His Val Val Glu  
                     50                    55                    60  
 Pro Met Pro Val Pro Gly His Asp Val Glu Ala Tyr Cys Leu Leu  
                     65                    70                    75  
 Cys Glu Cys Arg Tyr Glu Glu Arg Ser Thr Thr Thr Ile Lys Val  
                     80                    85                    90  
 Ile Ile Val Ile Tyr Leu Ser Val Val Gly Ala Leu Leu Leu Tyr  
                     95                    100                    105  
 Met Ala Phe Leu Met Leu Val Asp Pro Leu Ile Arg Lys Pro Asp  
                     110                    115                    120  
 Ala Tyr Thr Glu Gln Leu His Asn Glu Glu Glu Asn Glu Asp Ala  
                     125                    130                    135  
 Arg Ser Met Ala Ala Ala Ala Ser Leu Gly Gly Pro Arg Ala  
                     140                    145                    150  
 Asn Thr Val Leu Glu Arg Val Glu Gly Ala Gln Gln Arg Trp Lys  
                     155                    160                    165

Leu Gln Val Gln Glu Gln Arg Lys Thr Val Phe Asp Arg His Lys  
170 175 180

Met Leu Ser

<210> 69  
<211> 3170  
<212> DNA  
<213> Homo sapiens

<400> 69  
agcgggtctc gcttgggttc cgctaatttc tgtcctgagg cgtgagactg 50  
agtcatagg gtctgggttc cccgaaccag gaagggttga gggaacacaa 100  
tctgcaagcc cccgcgaccc aagtgagggg ccccggtgtg gggcctccc 150  
tccctttgca tccccacccc tccgggcttt gcgtcttcct ggggaccccc 200  
tcgccgggag atggccgcgt tgatgcggag caaggattcg tcctgctgcc 250  
tgctcctact ggccgcggtg ctgatggtgg agagctcaca gatcggcagt 300  
tcgcggggcca aactcaactc catcaagtcc tctctgggcg gggagacgcc 350  
tggtcaggcc gccaatcgat ctgcgggcat gtaccaagga ctggcattcg 400  
gcggcagtaa gaagggcaaa aacctggggc aggcctaccc ttgtagcagt 450  
gataaggagt gtgaagttgg gaggtattgc cacagtcccc accaaggatc 500  
atcggcctgc atggtgtgtc ggagaaaaaa gaagcgctgc caccgagatg 550  
gcatgtgctg ccccagtacc cgctgcaata atggcatctg tatcccagtt 600  
actgaaagca tcttaacccc tcacatcccg gctctggatg gtactcggca 650  
cagagatcga aaccacggtc attactcaaa ccatgacttg ggatggcaga 700  
atctaggaag accacacact aagatgtcac atataaaagg gcatgaagga 750  
gacccctgcc tacgatcatc agactgcatt gaagggtttt gctgtgctcg 800  
tcatttctgg accaaaatct gcaaaccagt gctccatcag ggggaagtct 850  
gtaccaaaca acgcaagaag ggttctcatg ggctggaaat tttccagcgt 900  
tgcgactgtg cgaagggcct gtcttgcaaa gtatggaaag atgccaccta 950  
ctctccaaa gccagactcc atgtgtgtca gaaaatttga tcaccattga 1000  
ggaacatcat caattgcaga ctgtgaagtt gtgtatttaa tgcattatag 1050  
catggtggaa aataagggtc agatgcagaa gaatggctaa aataagaaac 1100

gtgataagaa tatagatgat cacaaaaagg gagaaagaaa acatgaactg 1150  
aatagattag aatgggtgac aaatgcagtg cagccagtgt ttccattatg 1200  
caacttgtct atgtaaataa tgtacacatt tgtggaaaat gctattatta 1250  
agagaacaag cacacagtgg aaattactga tgagtagcat gtgactttcc 1300  
aagagtttag gttgtgctgg aggagagggtt tccttcagat tgctgattgc 1350  
ttatacaaat aacctacatg ccagatttct attcaacggt agagtttaac 1400  
aaaatactcc tagaataact tggtatacaa taggttctaa aaataaaaatt 1450  
gctaaacaag aaatgaaaac atggagcatt gttaatttac aacagaaaat 1500  
taccttttga tttgtaacac tacttctgct gttcaatcaa gagtcttggt 1550  
agataagaaa aaaatcagtc aatatttcca aataattgca aaataatggc 1600  
cagttgttta ggaaggcctt taggaagaca aataaataac aaacaaacag 1650  
ccacaaatac ttttttttca aaattttagt tttaacctgta attaataaga 1700  
actgatacaa gacaaaaaca gttccttcag attctacgga atgacagtat 1750  
atctctcttt atcctatgtg attcctgctc tgaatgcatt atattttcca 1800  
aactataccc ataaattgtg actagtaaaa tacttacaca gagcagaatt 1850  
ttcacagatg gcaaaaaaat tttaagatgt ccaatatatg tgggaaaaga 1900  
gctaacagag agatcattat ttcttaaaga ttggccataa cctatatttt 1950  
gatagaatta gattggtaaa tacatgtatt catacatact ctgtggtaat 2000  
agagacttaa gctggatctg tactgcactg gagtaagcaa gaaaattggg 2050  
aaaacttttt cgtttgttca ggttttggca acacatagat catatgtctg 2100  
aggcacaagt tggctgttca tctttgaaac caggggatgc acagtctaaa 2150  
tgaatatctg catgggattt gctatcataa tatttactat gcagatgaat 2200  
tcagtgtgag gtcctgtgtc cgtactatcc tcaaattatt tattttatag 2250  
tgctgagatc ctcaaataat ctcaatttca ggaggtttca caaaatgtac 2300  
tcctgaagta gacagagtag tgaggtttca ttgccctcta taagcttctg 2350  
actagccaat ggcatcatcc aattttcttc ccaaacctct gcagcatctg 2400  
ctttattgcc aaagggttag tttcggtttt ctgcagccat tgcggttaaa 2450  
aaatataagt aggataactt gtaaaacctg catattgcta atctatagac 2500  
accacagttt ctaaattctt tgaaaccact ttactacttt ttttaaactt 2550

aactcagttc taaatacttt gtctggagca caaaacaata aaaggttatc 2600  
ttatagtcgt gactttaaac tttttagtac cacaattcac tttttagttt 2650  
tcttttactt aaatcccatc tgcagttctca aatttaagtt ctcccagtag 2700  
agattgagtt tgagcctgta tatctattaa aaatttcaac ttcccacata 2750  
tatttactaa gatgattaag acttacattt tctgcacagg tctgcaaaaa 2800  
caaaaattat aaactagtcc atccaagaac caaagtttgt ataaacaggt 2850  
tgctataagc ttgtgaaatg aaaatggaac atttcaatca aacatttcct 2900  
atataacaat tattatatattt acaatttggt ttctgcaata tttttcttat 2950  
gtccaccctt ttaaaaatta ttatttgaag taatttattt acaggaaatg 3000  
ttaatgagat gtattttctt atagagatat ttcttacaga aagctttgta 3050  
gcagaatata tttgcagcta ttgactttgt aatttaggaa aaatgtataa 3100  
taagataaaa tctattaaat ttttctcctc taaaaactga aaaaaaaaaa 3150  
aaaaaaaaaa aaaaaaaaaa 3170

<210> 70  
<211> 259  
<212> PRT  
<213> Homo sapiens

<400> 70  
Met Ala Ala Leu Met Arg Ser Lys Asp Ser Ser Cys Cys Leu Leu  
1 5 10 15  
Leu Leu Ala Ala Val Leu Met Val Glu Ser Ser Gln Ile Gly Ser  
20 25 30  
Ser Arg Ala Lys Leu Asn Ser Ile Lys Ser Ser Leu Gly Gly Glu  
35 40 45  
Thr Pro Gly Gln Ala Ala Asn Arg Ser Ala Gly Met Tyr Gln Gly  
50 55 60  
Leu Ala Phe Gly Gly Ser Lys Lys Gly Lys Asn Leu Gly Gln Ala  
65 70 75  
Tyr Pro Cys Ser Ser Asp Lys Glu Cys Glu Val Gly Arg Tyr Cys  
80 85 90  
His Ser Pro His Gln Gly Ser Ser Ala Cys Met Val Cys Arg Arg  
95 100 105  
Lys Lys Lys Arg Cys His Arg Asp Gly Met Cys Cys Pro Ser Thr  
110 115 120

Arg	Cys	Asn	Asn	Gly	Ile	Cys	Ile	Pro	Val	Thr	Glu	Ser	Ile	Leu
				125					130					135
Thr	Pro	His	Ile	Pro	Ala	Leu	Asp	Gly	Thr	Arg	His	Arg	Asp	Arg
				140					145					150
Asn	His	Gly	His	Tyr	Ser	Asn	His	Asp	Leu	Gly	Trp	Gln	Asn	Leu
				155					160					165
Gly	Arg	Pro	His	Thr	Lys	Met	Ser	His	Ile	Lys	Gly	His	Glu	Gly
				170					175					180
Asp	Pro	Cys	Leu	Arg	Ser	Ser	Asp	Cys	Ile	Glu	Gly	Phe	Cys	Cys
				185					190					195
Ala	Arg	His	Phe	Trp	Thr	Lys	Ile	Cys	Lys	Pro	Val	Leu	His	Gln
				200					205					210
Gly	Glu	Val	Cys	Thr	Lys	Gln	Arg	Lys	Lys	Gly	Ser	His	Gly	Leu
				215					220					225
Glu	Ile	Phe	Gln	Arg	Cys	Asp	Cys	Ala	Lys	Gly	Leu	Ser	Cys	Lys
				230					235					240
Val	Trp	Lys	Asp	Ala	Thr	Tyr	Ser	Ser	Lys	Ala	Arg	Leu	His	Val
				245					250					255

Cys Gln Lys Ile

<210> 71

<211> 1809

<212> DNA

<213> Homo sapiens

<400> 71

```

tctcaatctg ctgacctcgt gatccgcctg accttgtaat ccacctacct 50
tggcctccca aagtgttggg attacaggcg tgagccaccg cgcccggcca 100
acatcacgtt tttaaaaatt gatttcttca aattcatggc aaatatttcc 150
cttcccttta acttcttatg tcagaatgag gaaggatagc tgcatttatt 200
tagtcagttt tcattgcata gtaatatattt catgtagtat tttctaagtt 250
atattttagt aattcatatg ttttagatta taggttttaa catacttggtg 300
aaaatacttg atgtgtttta aagccttggg cagaaattct gtattgttga 350
ggatttgttc ttttatcccc cttttaaaagt catccgtcct tggctcagga 400
tttggagagc ttgcaccacc aaaaatggca aacatcacca gctcccagat 450
tttggaccag ttgaaagctc cgagtttggg ccagtttacc accaccccaa 500
gtacacagca gaatagtaca agtcacccta caactactac ttcttgggac 550

```

ctcaagcccc caacatccca gtcctcagtc ctcaagtcac ttgacttcaa 600  
 atctcaacct gagccatccc cagttcttag ccagttgagc cagcgacaac 650  
 agcaccagag ccaggcagtc actgttcctc ctcttggttt ggagtccttt 700  
 ccttcccagg caaaacttcg agaatcaaca cctggagaca gtccctccac 750  
 tgtgaacaag cttttgcagc ttcccagcac gaccattgaa aatatctctg 800  
 tgtctgtcca ccagccacag cccaaacaca tcaaacttgc taagcggcgg 850  
 atacccccag cttctaagat ccagcttct gcagtggaaa tgcttggttc 900  
 agcagatgtc acaggattaa atgtgcagtt tggggctctg gaatttggtt 950  
 cagaaccttc tctctctgaa tttgatcag ctccaagcag tgaaaatagt 1000  
 aatcagattc ccatcagctt gtattcgaag tctttaagtg agcctttgaa 1050  
 tacatcttta tcaatgacca gtgcagtaca gaactccaca tatacaactt 1100  
 ccgtcattac ctctgcagtc ctgacaagct catcactgaa ttctgctagt 1150  
 ccagtagcaa tgtcttcctc ttatgaccag agttctgtgc ataacaggat 1200  
 cccataccaa agccctgtga gttcatcaga gtcagctcca ggaaccatca 1250  
 tgaatggaca tgggtgggtg cgaagtcagc agacactaga cagtaagtat 1300  
 agcagcaagc tactcttgtc atggctgggtg ccaaccaaac agaggaagag 1350  
 gatagctcac gtgatgtgga aaacaccagt tggccaatgg ctcatcgtt 1400  
 aaaaagcagc ctttttgctt ttttggtttt ggaccagggtg ttggctgtgg 1450  
 tggtattaga aatgtcttaa ccacagcaag aaggagggtg tggtctcata 1500  
 ttcttctgcc ctaatcagac tgcaccacaa gtgcagcata cagtatgcat 1550  
 tttaaagatg cttgggccag gcgggggtggc tgatgcccat aatcccagtg 1600  
 ctttgggggg ccaaggcagg cagattgccc aagctcagga gtttgagacc 1650  
 accctgggca acatggtgaa actctgtctc tactaaaata cgaaaaacta 1700  
 gccgggtgtg gtggcggcgc gtgcctgtaa tcccagctac ttgggaggct 1750  
 gaggcacaag aatcgcttga gccagcttgg gctacaaagt gagactccgt 1800  
 ctgaaaaga 1809

<210> 72

<211> 363

<212> PRT

<213> Homo sapiens

<400> 72

Met	Cys	Phe	Lys	Ala	Leu	Gly	Arg	Asn	Ser	Val	Leu	Leu	Arg	Ile
1				5					10					15
Cys	Ser	Phe	Ile	Pro	Leu	Leu	Lys	Ser	Ser	Val	Leu	Gly	Ser	Gly
				20					25					30
Phe	Gly	Glu	Leu	Ala	Pro	Pro	Lys	Met	Ala	Asn	Ile	Thr	Ser	Ser
				35					40					45
Gln	Ile	Leu	Asp	Gln	Leu	Lys	Ala	Pro	Ser	Leu	Gly	Gln	Phe	Thr
				50					55					60
Thr	Thr	Pro	Ser	Thr	Gln	Gln	Asn	Ser	Thr	Ser	His	Pro	Thr	Thr
				65					70					75
Thr	Thr	Ser	Trp	Asp	Leu	Lys	Pro	Pro	Thr	Ser	Gln	Ser	Ser	Val
				80					85					90
Leu	Ser	His	Leu	Asp	Phe	Lys	Ser	Gln	Pro	Glu	Pro	Ser	Pro	Val
				95					100					105
Leu	Ser	Gln	Leu	Ser	Gln	Arg	Gln	Gln	His	Gln	Ser	Gln	Ala	Val
				110					115					120
Thr	Val	Pro	Pro	Pro	Gly	Leu	Glu	Ser	Phe	Pro	Ser	Gln	Ala	Lys
				125					130					135
Leu	Arg	Glu	Ser	Thr	Pro	Gly	Asp	Ser	Pro	Ser	Thr	Val	Asn	Lys
				140					145					150
Leu	Leu	Gln	Leu	Pro	Ser	Thr	Thr	Ile	Glu	Asn	Ile	Ser	Val	Ser
				155					160					165
Val	His	Gln	Pro	Gln	Pro	Lys	His	Ile	Lys	Leu	Ala	Lys	Arg	Arg
				170					175					180
Ile	Pro	Pro	Ala	Ser	Lys	Ile	Pro	Ala	Ser	Ala	Val	Glu	Met	Pro
				185					190					195
Gly	Ser	Ala	Asp	Val	Thr	Gly	Leu	Asn	Val	Gln	Phe	Gly	Ala	Leu
				200					205					210
Glu	Phe	Gly	Ser	Glu	Pro	Ser	Leu	Ser	Glu	Phe	Gly	Ser	Ala	Pro
				215					220					225
Ser	Ser	Glu	Asn	Ser	Asn	Gln	Ile	Pro	Ile	Ser	Leu	Tyr	Ser	Lys
				230					235					240
Ser	Leu	Ser	Glu	Pro	Leu	Asn	Thr	Ser	Leu	Ser	Met	Thr	Ser	Ala
				245					250					255
Val	Gln	Asn	Ser	Thr	Tyr	Thr	Thr	Ser	Val	Ile	Thr	Ser	Cys	Ser
				260					265					270
Leu	Thr	Ser	Ser	Ser	Leu	Asn	Ser	Ala	Ser	Pro	Val	Ala	Met	Ser

	275	280	285
Ser Ser Tyr Asp Gln Ser Ser Val His Asn Arg Ile Pro Tyr Gln			
	290	295	300
Ser Pro Val Ser Ser Ser Glu Ser Ala Pro Gly Thr Ile Met Asn			
	305	310	315
Gly His Gly Gly Gly Arg Ser Gln Gln Thr Leu Asp Ser Lys Tyr			
	320	325	330
Ser Ser Lys Leu Leu Leu Ser Trp Leu Val Pro Thr Lys Gln Arg			
	335	340	345
Lys Arg Ile Ala His Val Met Trp Lys Thr Pro Val Gly Gln Trp			
	350	355	360

Leu Ile Arg

<210> 73  
 <211> 26  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 73  
 aattcatggc aaatatttcc cttccc 26

<210> 74  
 <211> 22  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 74  
 tggtaaactg gcccaaactc gg 22

<210> 75  
 <211> 50  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 75  
 ttaaagtcac ccgtccttgg ctcaggattt ggagagcttg caccaccaa 50

<210> 76  
 <211> 1989  
 <212> DNA  
 <213> Homo sapiens



<400> 76

gccgagtggg acaaagcctg gggctgggcg ggggccatgg cgctgccatc 50  
ccgaatcctg ctttggaac ttgtgcttct gcagagctct gctgttctcc 100  
tgcaactcagc ggtggaggag acggacgcgg ggctgtacac ctgcaacctg 150  
caccatcact actgccacct ctacgagagc ctggccgtcc gcctggaggt 200  
caccgacggc cccccggcca cccccgcta ctgggacggc gagaaggagg 250  
tgctggcggt ggcgcgcggc gcacccgcgc ttctgacctg cgtgaaccgc 300  
gggcacgtgt ggaccgaccg gcacgtggag gaggctcaac aggtggtgca 350  
ctgggaccgg cagccgcccg ggggtccgca cgaccgcgcg gaccgcctgc 400  
tggacctcta cgcgtcgggc gagcgccgcg cctacgggcc cctttttctg 450  
cgcgaccgcg tggctgtggg cgcggatgcc tttgagcgcg gtgacttctc 500  
actgcgtatc gagccgctgg aggtcgccga cgagggcacc tactcctgcc 550  
acctgcacca ccattactgt ggcctgcacg aacgcgcgt cttccacctg 600  
acggtcgccg aacccccacgc ggagccgccc ccccggggct ctccgggcaa 650  
cggctccagc cacagcggcg cccagggccc agacccaca ctggcgcgcg 700  
gccacaacgt catcaatgtc atcgtccccg agagccgagc ccacttcttc 750  
cagcagctgg gctacgtgct ggccacgctg ctgctcttca tctgctact 800  
ggtcactgtc ctctggccg cccgcaggcg ccgcggaggc tacgaatact 850  
cggaccagaa gtcgggaaag tcaaagggga aggatgttaa cttggcggag 900  
ttcgctgtgg ctgcagggga ccagatgctt tacaggagtg aggacatcca 950  
gctagattac aaaaacaaca tctgaagga gaggcgag ctggcccaca 1000  
gccccctgcc tgccaagtac atcgacctag acaaagggtt ccggaaggag 1050  
aactgcaaat agggaggccc tgggtcctg gctgggccag cagctgcacc 1100  
tctctgtct gtgctcctcg gggcatctcc tgatgtccg gggctcacc 1150  
ccctccagc ggctggtccc gctttcctgg aatttggcct gggcgtatgc 1200  
agaggccgcc tccacacccc tccccaggg gcttgggtggc agcatagccc 1250  
ccaccctgc ggcctttgct cacgggtggc cctgccacc cctggcacia 1300  
ccaaaatccc actgatgcc atcatgcct cagaccctt tgggtctctgc 1350  
ccgctggggg cctgaagaca ttctggagg aactcccat cagaacctgg 1400

cagccccaaa actggggtca gcctcagggc aggagtccca ctctccagg 1450  
gctctgctcg tccggggctg ggagatgttc ctggaggagg acactcccat 1500  
cagaacttgg cagccttgaa gttggggtca gcctcggcag gactccact 1550  
ctctctgggg tgctgcctgc caccaagagc tccccacct gtaccacat 1600  
gtgggactcc aggcaccatc tgttctcccc agggacctgc tgacttgaat 1650  
gccagccctt gctcctctgt gttgctttgg gccacctggg gctgcacccc 1700  
ctgccctttc tctgccccat ccctacccta gccttgctct cagccacctt 1750  
gatagtcaact gggctccctg tgacttctga ccctgacacc cctcccttgg 1800  
actctgcctg ggctggagtc tagggctggg gctacatttg gcttctgtac 1850  
tggctgagga caggggaggg agtgaagttg gtttggggtg gcctgtgttg 1900  
ccactctcag caccacat ttgcatctgc tgggtggacct gccaccatca 1950  
caataaagtc cccatctgat ttttaaaaaa aaaaaaaaaa 1989

<210> 77  
<211> 341  
<212> PRT  
<213> Homo sapiens

<400> 77  
Met Ala Leu Pro Ser Arg Ile Leu Leu Trp Lys Leu Val Leu Leu  
1 5 10 15  
Gln Ser Ser Ala Val Leu Leu His Ser Ala Val Glu Glu Thr Asp  
20 25 30  
Ala Gly Leu Tyr Thr Cys Asn Leu His His His Tyr Cys His Leu  
35 40 45  
Tyr Glu Ser Leu Ala Val Arg Leu Glu Val Thr Asp Gly Pro Pro  
50 55 60  
Ala Thr Pro Ala Tyr Trp Asp Gly Glu Lys Glu Val Leu Ala Val  
65 70 75  
Ala Arg Gly Ala Pro Ala Leu Leu Thr Cys Val Asn Arg Gly His  
80 85 90  
Val Trp Thr Asp Arg His Val Glu Glu Ala Gln Gln Val Val His  
95 100 105  
Trp Asp Arg Gln Pro Pro Gly Val Pro His Asp Arg Ala Asp Arg  
110 115 120  
Leu Leu Asp Leu Tyr Ala Ser Gly Glu Arg Arg Ala Tyr Gly Pro  
125 130 135

Leu Phe Leu Arg Asp Arg Val Ala Val Gly Ala Asp Ala Phe Glu	140	145	150
Arg Gly Asp Phe Ser Leu Arg Ile Glu Pro Leu Glu Val Ala Asp	155	160	165
Glu Gly Thr Tyr Ser Cys His Leu His His His Tyr Cys Gly Leu	170	175	180
His Glu Arg Arg Val Phe His Leu Thr Val Ala Glu Pro His Ala	185	190	195
Glu Pro Pro Pro Arg Gly Ser Pro Gly Asn Gly Ser Ser His Ser	200	205	210
Gly Ala Pro Gly Pro Asp Pro Thr Leu Ala Arg Gly His Asn Val	215	220	225
Ile Asn Val Ile Val Pro Glu Ser Arg Ala His Phe Phe Gln Gln	230	235	240
Leu Gly Tyr Val Leu Ala Thr Leu Leu Leu Phe Ile Leu Leu Leu	245	250	255
Val Thr Val Leu Leu Ala Ala Arg Arg Arg Arg Gly Gly Tyr Glu	260	265	270
Tyr Ser Asp Gln Lys Ser Gly Lys Ser Lys Gly Lys Asp Val Asn	275	280	285
Leu Ala Glu Phe Ala Val Ala Ala Gly Asp Gln Met Leu Tyr Arg	290	295	300
Ser Glu Asp Ile Gln Leu Asp Tyr Lys Asn Asn Ile Leu Lys Glu	305	310	315
Arg Ala Glu Leu Ala His Ser Pro Leu Pro Ala Lys Tyr Ile Asp	320	325	330
Leu Asp Lys Gly Phe Arg Lys Glu Asn Cys Lys	335	340	

<210> 78  
 <211> 2243  
 <212> DNA  
 <213> Homo sapiens

<400> 78  
 cgccggaggc agcggcgggc tggcgcagcg gcgacatggc cgttgtctca 50  
 gaggacgact ttcagcacag ttcaaactcc acctacggaa ccacaagcag 100  
 cagtctccga gctgaccagg aggcactgct tgagaagctg ctggaccgcc 150  
 cgccccctgg cctgcagagg cccgaggacc gcttctgtgg cacatacatc 200

atctttcttca gcctgggcat tggcagtcta ctgccatgga acttctttat 250  
cactgccaaag gactactgga tgttcaaact ccgcaactcc tccagcccag 300  
ccaccgggga ggaccctgag ggctcagaca tcctgaacta ctttgagagc 350  
taccttgccg ttgcctccac cgtgccctcc atgctgtgcc tgggtggcaa 400  
cttcctgctt gtcaacaggg ttgcagtcca catccgtgtc ctggcctcac 450  
tgacggtcac cctggccatc ttcattggtga taactgcaact ggtgaagggtg 500  
gacacttctt cctggaccgg tgggtttttt gcggtcacca ttgtctgcat 550  
ggtgatcttc agcgggtgct ccaactgtctt cagcagcagc atctacggca 600  
tgaccggctc ctttctatg aggaactccc aagcactgat atcaggagga 650  
gccatgggag ggacgggtcag cgcctgggcc tcattggtgg acttggtgc 700  
atccagtgat gtgaggaaca gcgccctggc cttcttcttg acggccacca 750  
tcttctctgt gctctgcatg ggactctacc tgctgctgtc caggctggag 800  
tatgccaggt actacatgag gcctgttctt gcggcccatg tgttttctgg 850  
tgaagaggag cttcccagg actccctcag tgccctctcg gtggcctcca 900  
gattcattga ttccacaca cccctctcc gcccatcct gaagaagacg 950  
gccagcctgg gcttctgtgt cacctacgtc ttcttcatca ccagcctcat 1000  
ctaccccgcc gtctgcacca acatcgagtc cctcaacaag ggctcgggct 1050  
cactgtggac caccaagttt ttcattcccc tcaactacct cctcctgtac 1100  
aactttgctg acctatgtgg ccggcagctc accgctgga tccaggtgcc 1150  
agggcccaac agcaaggcgc tcccagggtt cgtgctctc cggaacctgcc 1200  
tcattccctt cttcgtgtc tgtaactacc agccccgct ccacctgaag 1250  
actgtggtct tccagtcga tgtgtacccc gcaactcctca gctccctgct 1300  
ggggctcagc aacggctacc tcagcaccct ggccctctc tacgggcta 1350  
agattgtgcc caggagctg gctgaggcca cgggagtgg gatgtcctt 1400  
tatgtgtgct tgggcttaac actgggctca gcctgtctc cctcctgg 1450  
gcacctcatc tagaaggag gacacaagga cattggtgct tcagagcctt 1500  
tgaagatgag aagagagtgc aggagggtg ggggcatgg aggaaaggcc 1550  
taaagtttca cttggggaca gagagcagag cacactcggg cctcatcct 1600  
ccaagatgc cagtgaacca cgtccatgcc cattccgtgc aaggcagata 1650

ttccagtcac attaacagaa cactcctgag acagttgaag aagaaatagc 1700  
 acaaatacagg ggtactccct tcacagctga tggtaacat tccaccttct 1750  
 ttctagccct tcaaagatgc tgccagtgtt cgccctagag ttattacaaa 1800  
 gccagtgccaa aaaccagcc atgggctctt tgcaacctcc cagctgcgct 1850  
 cattccagct gacagcgaga tgcaagcaaa tgctcagctc tccttaccct 1900  
 gaaggggtct ccctggaatg gaagtcccct ggcatgggtca gtcctcaggc 1950  
 ccaagactca agtgtgcaca gaccctgtg ttctgcgggt gaacaactgc 2000  
 ccactaacca gactggaaaa ccagaaaga tgggccttcc atgaatgctt 2050  
 cattccagag ggaccagagg gcctccctgt gcaagggatc aagcatgtct 2100  
 ggctggggtt ttcaaaaaaa gagggatcct catgacctgg tggcttatgg 2150  
 cctgggtcaa gatgaggggc tttcagtgtt cctgtttaca acatgtcaaa 2200  
 gccattgggt caagggcgta ataaatactt gcgtattcaa aaa 2243

<210> 79

<211> 475

<212> PRT

<213> Homo sapiens

<400> 79

Met	Ala	Val	Val	Ser	Glu	Asp	Asp	Phe	Gln	His	Ser	Ser	Asn	Ser	1	5	10	15
Thr	Tyr	Gly	Thr	Thr	Ser	Ser	Ser	Leu	Arg	Ala	Asp	Gln	Glu	Ala	20	25	30	
Leu	Leu	Glu	Lys	Leu	Leu	Asp	Arg	Pro	Pro	Pro	Gly	Leu	Gln	Arg	35	40	45	
Pro	Glu	Asp	Arg	Phe	Cys	Gly	Thr	Tyr	Ile	Ile	Phe	Phe	Ser	Leu	50	55	60	
Gly	Ile	Gly	Ser	Leu	Leu	Pro	Trp	Asn	Phe	Phe	Ile	Thr	Ala	Lys	65	70	75	
Glu	Tyr	Trp	Met	Phe	Lys	Leu	Arg	Asn	Ser	Ser	Ser	Pro	Ala	Thr	80	85	90	
Gly	Glu	Asp	Pro	Glu	Gly	Ser	Asp	Ile	Leu	Asn	Tyr	Phe	Glu	Ser	95	100	105	
Tyr	Leu	Ala	Val	Ala	Ser	Thr	Val	Pro	Ser	Met	Leu	Cys	Leu	Val	110	115	120	
Ala	Asn	Phe	Leu	Leu	Val	Asn	Arg	Val	Ala	Val	His	Ile	Arg	Val	125	130	135	

Leu Ala Ser Leu	Thr Val Ile Leu Ala	Ile Phe Met Val Ile Thr	140	145	150
Ala Leu Val Lys	Val Asp Thr Ser Ser	Trp Thr Arg Gly Phe Phe	155	160	165
Ala Val Thr Ile	Val Cys Met Val Ile	Leu Ser Gly Ala Ser Thr	170	175	180
Val Phe Ser Ser	Ser Ile Tyr Gly Met	Thr Gly Ser Phe Pro Met	185	190	195
Arg Asn Ser Gln	Ala Leu Ile Ser Gly	Gly Ala Met Gly Gly Thr	200	205	210
Val Ser Ala Val	Ala Ser Leu Val Asp	Leu Ala Ala Ser Ser Asp	215	220	225
Val Arg Asn Ser	Ala Leu Ala Phe Phe	Leu Thr Ala Thr Ile Phe	230	235	240
Leu Val Leu Cys	Met Gly Leu Tyr Leu	Leu Leu Ser Arg Leu Glu	245	250	255
Tyr Ala Arg Tyr	Tyr Met Arg Pro Val	Leu Ala Ala His Val Phe	260	265	270
Ser Gly Glu Glu	Glu Leu Pro Gln Asp	Ser Leu Ser Ala Pro Ser	275	280	285
Val Ala Ser Arg	Phe Ile Asp Ser His	Thr Pro Pro Leu Arg Pro	290	295	300
Ile Leu Lys Lys	Thr Ala Ser Leu Gly	Phe Cys Val Thr Tyr Val	305	310	315
Phe Phe Ile Thr	Ser Leu Ile Tyr Pro	Ala Val Cys Thr Asn Ile	320	325	330
Glu Ser Leu Asn	Lys Gly Ser Gly Ser	Leu Trp Thr Thr Lys Phe	335	340	345
Phe Ile Pro Leu	Thr Thr Phe Leu Leu	Tyr Asn Phe Ala Asp Leu	350	355	360
Cys Gly Arg Gln	Leu Thr Ala Trp Ile	Gln Val Pro Gly Pro Asn	365	370	375
Ser Lys Ala Leu	Pro Gly Phe Val Leu	Leu Arg Thr Cys Leu Ile	380	385	390
Pro Leu Phe Val	Leu Cys Asn Tyr Gln	Pro Arg Val His Leu Lys	395	400	405
Thr Val Val Phe	Gln Ser Asp Val Tyr	Pro Ala Leu Leu Ser Ser	410	415	420

Leu	Leu	Gly	Leu	Ser	Asn	Gly	Tyr	Leu	Ser	Thr	Leu	Ala	Leu	Leu
				425					430					435
Tyr	Gly	Pro	Lys	Ile	Val	Pro	Arg	Glu	Leu	Ala	Glu	Ala	Thr	Gly
				440					445					450
Val	Val	Met	Ser	Phe	Tyr	Val	Cys	Leu	Gly	Leu	Thr	Leu	Gly	Ser
				455					460					465
Ala	Cys	Ser	Thr	Leu	Leu	Val	His	Leu	Ile					
				470					475					

<210> 80  
 <211> 22  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 80  
 ttttgcggtc accattgtct gc 22

<210> 81  
 <211> 23  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 81  
 cgtaggtgac acagaagccc agg 23

<210> 82  
 <211> 49  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 82  
 tacggcatga ccggctcctt tcctatgagg aactcccagg cactgatat 49

<210> 83  
 <211> 1844  
 <212> DNA  
 <213> Homo sapiens

<400> 83  
 gacagtggag ggcagtggag aggaccgcgc tgcctgctg tcaccaagag 50  
 ctggagacac catctccac cgagagtcac ggccccattg gccctgcacc 100  
 tcctcgctct cgtcccatc ctctcagcc tggtagcctc ccaggactgg 150

aaggctgaac gcagccaaga ccccttcgag aaatgcatgc aggatcctga 200  
ctatgagcag ctgctcaagg tggtagacctg ggggctcaat cggaccctga 250  
agccccagag ggtgattgtg gttggcgctg gtgtggccgg gctggtggcc 300  
gccaaggtgc tcagcgatgc tggacacaag gtcaccatcc tggaggcaga 350  
taacaggatc gggggccgca tcttcaccta ccgggaccag aacacgggct 400  
ggattgggga gctgggagcc atgcgcatgc ccagctctca caggatcctc 450  
cacaagctct gccagggcct ggggctcaac ctgaccaagt tcacccagta 500  
cgacaagaac acgtggacgg aggtgcacga agtgaagctg cgcaactatg 550  
tggtaggagaa ggtgcccgag aagctgggct acgccttgcg tccccaggaa 600  
aagggccact cgcccgaaga catctaccag atggctctca accaggccct 650  
caaagacctc aaggcactgg gctgcagaaa ggcgatgaag aagtttgaaa 700  
ggcacacgct cttggaatat cttctcgggg aggggaacct gagccggccg 750  
gccgtgcagc ttctgggaga cgtgatgtcc gaggatggct tcttctatct 800  
cagcttcgcc gaggccctcc gggcccacag ctgcctcagc gacagactcc 850  
agtacagccg catcgtgggt ggctgggacc tgctgccgcg cgcgctgctg 900  
agctcgctgt ccgggcttgt gctgttgaac gcgccgtgg tggcgatgac 950  
ccagggaccg cacgatgtgc acgtgcagat cgagacctct cccccggcgc 1000  
ggaatctgaa ggtgctgaag gccgacgtgg tgctgctgac ggcgagcgga 1050  
ccggcggtga agcgcacac cttctcgccg ccgctgcccc gccacatgca 1100  
ggaggcgctg cggaggctgc actacgtgcc ggccaccaag gtgttcctaa 1150  
gcttccgcag gcccttctgg cgcgaggagc acattgaagg cggccactca 1200  
aacaccgacg gcccgctcgc catgatcttc taccgcgcgc cgcgcgaggg 1250  
cgcgctgctg ctggcctcgt acacgtggtc ggacgcggcg gcagcgctcg 1300  
ccggcttgag ccgggaagag gcgttgcgct tggcgctcga cgacgtggcg 1350  
gcattgcacg ggcctgtcgt gcgccagctc tgggacggca ccggcgctcg 1400  
caagcgttgg gcggaggacc agcacagcca gggtaggcttt gtggtacagc 1450  
cgccggcgct ctggcaaacc gaaaaggatg actggacggg cccttatggc 1500  
cgcatctact ttgccggcga gcacaccgcc taccgcacg gctgggtgga 1550



gacggcggtc aagtcggcgc tgcgcgccgc catcaagatc aacagccgga 1600  
 aggggcctgc atcggacacg gccagccccg aggggcacgc atctgacatg 1650  
 gaggggcagg ggcattgtca tgggggtggcc agcagcccct cgcattgacct 1700  
 ggcaaaggaa gaaggcagcc accctccagt ccaaggccag ttatctctcc 1750  
 aaaacacgac ccacacgagg acctcgcatt aaagtatttt cggaaaaaaa 1800  
 aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaa 1844

<210> 84  
 <211> 567  
 <212> PRT  
 <213> Homo sapiens

<400> 84  
 Met Ala Pro Leu Ala Leu His Leu Leu Val Leu Val Pro Ile Leu  
 1 5 10 15  
 Leu Ser Leu Val Ala Ser Gln Asp Trp Lys Ala Glu Arg Ser Gln  
 20 25 30  
 Asp Pro Phe Glu Lys Cys Met Gln Asp Pro Asp Tyr Glu Gln Leu  
 35 40 45  
 Leu Lys Val Val Thr Trp Gly Leu Asn Arg Thr Leu Lys Pro Gln  
 50 55 60  
 Arg Val Ile Val Val Gly Ala Gly Val Ala Gly Leu Val Ala Ala  
 65 70 75  
 Lys Val Leu Ser Asp Ala Gly His Lys Val Thr Ile Leu Glu Ala  
 80 85 90  
 Asp Asn Arg Ile Gly Gly Arg Ile Phe Thr Tyr Arg Asp Gln Asn  
 95 100 105  
 Thr Gly Trp Ile Gly Glu Leu Gly Ala Met Arg Met Pro Ser Ser  
 110 115 120  
 His Arg Ile Leu His Lys Leu Cys Gln Gly Leu Gly Leu Asn Leu  
 125 130 135  
 Thr Lys Phe Thr Gln Tyr Asp Lys Asn Thr Trp Thr Glu Val His  
 140 145 150  
 Glu Val Lys Leu Arg Asn Tyr Val Val Glu Lys Val Pro Glu Lys  
 155 160 165  
 Leu Gly Tyr Ala Leu Arg Pro Gln Glu Lys Gly His Ser Pro Glu  
 170 175 180  
 Asp Ile Tyr Gln Met Ala Leu Asn Gln Ala Leu Lys Asp Leu Lys  
 185 190 195

Ala	Leu	Gly	Cys	Arg	Lys	Ala	Met	Lys	Lys	Phe	Glu	Arg	His	Thr			
				200					205					210			
Leu	Leu	Glu	Tyr	Leu	Leu	Gly	Glu	Gly	Asn	Leu	Ser	Arg	Pro	Ala			
				215					220					225			
Val	Gln	Leu	Leu	Gly	Asp	Val	Met	Ser	Glu	Asp	Gly	Phe	Phe	Tyr			
				230					235					240			
Leu	Ser	Phe	Ala	Glu	Ala	Leu	Arg	Ala	His	Ser	Cys	Leu	Ser	Asp			
				245					250					255			
Arg	Leu	Gln	Tyr	Ser	Arg	Ile	Val	Gly	Gly	Trp	Asp	Leu	Leu	Pro			
				260					265					270			
Arg	Ala	Leu	Leu	Ser	Ser	Leu	Ser	Gly	Leu	Val	Leu	Leu	Asn	Ala			
				275					280					285			
Pro	Val	Val	Ala	Met	Thr	Gln	Gly	Pro	His	Asp	Val	His	Val	Gln			
				290					295					300			
Ile	Glu	Thr	Ser	Pro	Pro	Ala	Arg	Asn	Leu	Lys	Val	Leu	Lys	Ala			
				305					310					315			
Asp	Val	Val	Leu	Leu	Thr	Ala	Ser	Gly	Pro	Ala	Val	Lys	Arg	Ile			
				320					325					330			
Thr	Phe	Ser	Pro	Pro	Leu	Pro	Arg	His	Met	Gln	Glu	Ala	Leu	Arg			
				335					340					345			
Arg	Leu	His	Tyr	Val	Pro	Ala	Thr	Lys	Val	Phe	Leu	Ser	Phe	Arg			
				350					355					360			
Arg	Pro	Phe	Trp	Arg	Glu	Glu	His	Ile	Glu	Gly	Gly	His	Ser	Asn			
				365					370					375			
Thr	Asp	Arg	Pro	Ser	Arg	Met	Ile	Phe	Tyr	Pro	Pro	Pro	Arg	Glu			
				380					385					390			
Gly	Ala	Leu	Leu	Leu	Ala	Ser	Tyr	Thr	Trp	Ser	Asp	Ala	Ala	Ala			
				395					400					405			
Ala	Phe	Ala	Gly	Leu	Ser	Arg	Glu	Glu	Ala	Leu	Arg	Leu	Ala	Leu			
				410					415					420			
Asp	Asp	Val	Ala	Ala	Leu	His	Gly	Pro	Val	Val	Arg	Gln	Leu	Trp			
				425					430					435			
Asp	Gly	Thr	Gly	Val	Val	Lys	Arg	Trp	Ala	Glu	Asp	Gln	His	Ser			
				440					445					450			
Gln	Gly	Gly	Phe	Val	Val	Gln	Pro	Pro	Ala	Leu	Trp	Gln	Thr	Glu			
				455					460					465			
Lys	Asp	Asp	Trp	Thr	Val	Pro	Tyr	Gly	Arg	Ile	Tyr	Phe	Ala	Gly			
				470					475					480			

Glu	His	Thr	Ala	Tyr	Pro	His	Gly	Trp	Val	Glu	Thr	Ala	Val	Lys
				485					490					495
Ser	Ala	Leu	Arg	Ala	Ala	Ile	Lys	Ile	Asn	Ser	Arg	Lys	Gly	Pro
				500					505					510
Ala	Ser	Asp	Thr	Ala	Ser	Pro	Glu	Gly	His	Ala	Ser	Asp	Met	Glu
				515					520					525
Gly	Gln	Gly	His	Val	His	Gly	Val	Ala	Ser	Ser	Pro	Ser	His	Asp
				530					535					540
Leu	Ala	Lys	Glu	Glu	Gly	Ser	His	Pro	Pro	Val	Gln	Gly	Gln	Leu
				545					550					555
Ser	Leu	Gln	Asn	Thr	Thr	His	Thr	Arg	Thr	Ser	His			
				560					565					

<210> 85

<211> 3316

<212> DNA

<213> Homo sapiens

<400> 85

```

ctgacatggc ctgactcggg acagctcaga gcagggcaga actggggaca 50
ctctgggccg gccttctgcc tgcattggac ctctgaagcc accctgtctc 100
tggaggaacc acgagcgagg gaagaaggac agggactcgt gtggcaggaa 150
gaactcagag ccgggaagcc cccattcact agaagcactg agagatgcgg 200
ccccctcgca ggggtctgaat ttcttctgctc tgttcacaaa gatgcttttt 250
atctttaact ttttgttttc ccacttccg accccggcgt tgatctgcat 300
cctgacattt ggagctgcca tcttcttgctg gctgatcacc agacctcaac 350
ccgtcttacc tcttcttgac ctgaacaatc agtctgtggg aattgaggga 400
ggagcacgga aggggggttc ccagaagaac aatgacctaa caagttgctg 450
cttctcagat gccaaagacta tgtatgaggt tttccaaaga ggactcgctg 500
tgtctgacaa tgggccctgc ttgggatata gaaaaccaa ccagccctac 550
agatggctat cttacaaaca ggtgtctgat agagcagagt acctgggttc 600
ctgtctcttg cataaagggt ataatcatc accagaccag tttgtcggca 650
tctttgctca gaataggcca gagtgatca tctccgaatt ggcttggtac 700
acgtactcta tggtagctgt acctctgtat gacaccttg gaccagaagc 750
catcgtagat attgtcaaca aggctgatat cgccatggtg atctgtgaca 800
caccacaaaa ggcattggtg ctgataggga atgtagagaa aggcttcacc 850

```

ccgagcctga aggtgatcat ccttatggac ccctttgatg atgacctgaa 900  
gcaaagaggg gagaagagtg gaattgagat cttatcccta tatgatgctg 950  
agaacctagg caaagagcac ttcagaaaac ctgtgcctcc tagcccagaa 1000  
gacctgagcg tcatctgctt caccagtggg accacaggtg accccaaagg 1050  
agccatgata acccatcaaa atattgtttc aaatgctgct gcctttctca 1100  
aatgtgtgga gcatgcttat gagccactc ctgatgatgt ggccatatcc 1150  
tacctccctc tggctcatat gtttgagagg attgtacagg ctgttggtga 1200  
cagctgtgga gccagagttg gattcttcca aggggatatt cggttgctgg 1250  
ctgacgacat gaagactttg aagcccacat tgtttccgc ggtgcctcga 1300  
ctccttaaca ggatctacga taaggtaaa aatgaggcca agacaccctt 1350  
gaagaagttc ttgttgaagc tggctgtttc cagtaaattc aaagagcttc 1400  
aaaagggtat catcaggcat gatagtttct gggacaagct catctttgca 1450  
aagatccagg acagcctggg cggaagggtt cgtgtaattg tcaactggagc 1500  
tgccccatg tccacttcag tcatgacatt cttccgggca gcaatgggat 1550  
gtcaggtgta tgaagcttat ggtcaaacag aatgcaacagg tggctgtaca 1600  
tttacattac ctggggactg gacatcaggt cacgttgggg tgcccctggc 1650  
ttgcaattac gtgaagctgg aagatgtggc tgacatgaac tactttacag 1700  
tgaataatga aggagaggtc tgcacaaagg gtacaaacgt gttcaaagga 1750  
tacctgaagg accctgagaa gacacaggaa gccctggaca gtgatggctg 1800  
gcttcacaca ggagacattg gtcgctggct cccgaatgga actctgaaga 1850  
tcatcgaccg taaaaagaac attttcaagc tggccaagg agaatacatt 1900  
gcaccagaga agatagaaaa tatctacaac aggagtcaac cagtgttaca 1950  
aatTTTTgta cacggggaga gcttacggtc atccttagta ggagtgggtg 2000  
ttcctgacac agatgtactt ccctcatttg cagccaagct tggggtgaag 2050  
ggctcctttg aggaactgtg ccaaaaccaa gttgtaaggg aagccatttt 2100  
agaagacttg cagaaaattg ggaaagaaag tggccttaaa acttttgaac 2150  
aggtcaaagc catttttctt catccagagc cattttccat tgaaaatggg 2200  
ctcttgacac caacattgaa agcaaagcga ggagagcttt ccaaatactt 2250

tcggacccaa attgacagcc tgtatgagca catccaggat taggataagg 2300  
 tacttaagta cctgccggcc cactgtgcac tgcttgtgag aaaatggatt 2350  
 aaaaactatt cttacatttg ttttgccttt cctcctatct ttttttaacc 2400  
 tgttaaactc taaagccata gcttttgttt tatattgaga catataatgt 2450  
 gtaaacttag ttcccaaata aatcaatcct gtctttccca tcttcgatgt 2500  
 tgctaataatt aaggcttcag ggctactttt atcaacatgc ctgtcttcaa 2550  
 gatcccagtt tatgttctgt gtccttcctc atgatttcca accttaatac 2600  
 tattagtaac cacaagttca aggggtcaaag ggaccctctg tgccttcttc 2650  
 tttgttttgt gataaacata acttgccaac agtctctatg cttatttaca 2700  
 tcttctactg ttcaaactaa gagattttta aattctgaaa aactgcttac 2750  
 aattcatgtt ttctagccac tccacaaacc actaaaattt tagtttttagc 2800  
 ctatcactca tgtcaatcat atctatgaga caaatgtctc cgatgctctt 2850  
 ctgcgtaaatt taaatttgtt actgaaggga aaagtttgat cataccaaac 2900  
 atttcctaaa ctctctagtt agatatctga cttgggagta ttaaaaattg 2950  
 ggtctatgac atactgtcca aaaggaatgc tgttcttaaa gcattattta 3000  
 cagtaggaac tggggagtaa atctgttccc tacagtttgc tgctgagctg 3050  
 gaagctgtgg gggaaggagt tgacagggtg gccagtgaa cttttccagt 3100  
 aaatgaagca agcactgaat aaaaacctcc tgaactggga acaaagatct 3150  
 acaggcaagc aagatgcca cacaacaggc ttattttctg tgaaggaacc 3200  
 aactgatctc cccaccctt ggattagagt tctgtctcta ccttaccac 3250  
 agataacaca tgttgtttct acttgtaaatt gttaaagtctt taaaataaac 3300  
 tattacagat aaaaaa 3316

<210> 86

<211> 739

<212> PRT

<213> Homo sapiens

<400> 86

Met	Asp	Ala	Leu	Lys	Pro	Pro	Cys	Leu	Trp	Arg	Asn	His	Glu	Arg
1				5					10					15

Gly	Lys	Lys	Asp	Arg	Asp	Ser	Cys	Gly	Arg	Lys	Asn	Ser	Glu	Pro
			20						25					30

Gly	Ser	Pro	His	Ser	Leu	Glu	Ala	Leu	Arg	Asp	Ala	Ala	Pro	Ser
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

35										40					45				
Gln	Gly	Leu	Asn	Phe	Leu	Leu	Leu	Phe	Thr	Lys	Met	Leu	Phe	Ile					
				50					55					60					
Phe	Asn	Phe	Leu	Phe	Ser	Pro	Leu	Pro	Thr	Pro	Ala	Leu	Ile	Cys					
				65					70					75					
Ile	Leu	Thr	Phe	Gly	Ala	Ala	Ile	Phe	Leu	Trp	Leu	Ile	Thr	Arg					
				80					85					90					
Pro	Gln	Pro	Val	Leu	Pro	Leu	Leu	Asp	Leu	Asn	Asn	Gln	Ser	Val					
				95					100					105					
Gly	Ile	Glu	Gly	Gly	Ala	Arg	Lys	Gly	Val	Ser	Gln	Lys	Asn	Asn					
				110					115					120					
Asp	Leu	Thr	Ser	Cys	Cys	Phe	Ser	Asp	Ala	Lys	Thr	Met	Tyr	Glu					
				125					130					135					
Val	Phe	Gln	Arg	Gly	Leu	Ala	Val	Ser	Asp	Asn	Gly	Pro	Cys	Leu					
				140					145					150					
Gly	Tyr	Arg	Lys	Pro	Asn	Gln	Pro	Tyr	Arg	Trp	Leu	Ser	Tyr	Lys					
				155					160					165					
Gln	Val	Ser	Asp	Arg	Ala	Glu	Tyr	Leu	Gly	Ser	Cys	Leu	Leu	His					
				170					175					180					
Lys	Gly	Tyr	Lys	Ser	Ser	Pro	Asp	Gln	Phe	Val	Gly	Ile	Phe	Ala					
				185					190					195					
Gln	Asn	Arg	Pro	Glu	Trp	Ile	Ile	Ser	Glu	Leu	Ala	Cys	Tyr	Thr					
				200					205					210					
Tyr	Ser	Met	Val	Ala	Val	Pro	Leu	Tyr	Asp	Thr	Leu	Gly	Pro	Glu					
				215					220					225					
Ala	Ile	Val	His	Ile	Val	Asn	Lys	Ala	Asp	Ile	Ala	Met	Val	Ile					
				230					235					240					
Cys	Asp	Thr	Pro	Gln	Lys	Ala	Leu	Val	Leu	Ile	Gly	Asn	Val	Glu					
				245					250					255					
Lys	Gly	Phe	Thr	Pro	Ser	Leu	Lys	Val	Ile	Ile	Leu	Met	Asp	Pro					
				260					265					270					
Phe	Asp	Asp	Asp	Leu	Lys	Gln	Arg	Gly	Glu	Lys	Ser	Gly	Ile	Glu					
				275					280					285					
Ile	Leu	Ser	Leu	Tyr	Asp	Ala	Glu	Asn	Leu	Gly	Lys	Glu	His	Phe					
				290					295					300					
Arg	Lys	Pro	Val	Pro	Pro	Ser	Pro	Glu	Asp	Leu	Ser	Val	Ile	Cys					
				305					310					315					
Phe	Thr	Ser	Gly	Thr	Thr	Gly	Asp	Pro	Lys	Gly	Ala	Met	Ile	Thr					

320	325	330
His Gln Asn Ile Val Ser Asn Ala Ala	Ala Phe Leu Lys Cys Val	
335	340	345
Glu His Ala Tyr Glu Pro Thr Pro Asp	Asp Val Ala Ile Ser Tyr	
350	355	360
Leu Pro Leu Ala His Met Phe Glu Arg	Ile Val Gln Ala Val Val	
365	370	375
Tyr Ser Cys Gly Ala Arg Val Gly Phe	Phe Gln Gly Asp Ile Arg	
380	385	390
Leu Leu Ala Asp Asp Met Lys Thr Leu	Lys Pro Thr Leu Phe Pro	
395	400	405
Ala Val Pro Arg Leu Leu Asn Arg Ile	Tyr Asp Lys Val Gln Asn	
410	415	420
Glu Ala Lys Thr Pro Leu Lys Lys Phe	Leu Leu Lys Leu Ala Val	
425	430	435
Ser Ser Lys Phe Lys Glu Leu Gln Lys	Gly Ile Ile Arg His Asp	
440	445	450
Ser Phe Trp Asp Lys Leu Ile Phe Ala	Lys Ile Gln Asp Ser Leu	
455	460	465
Gly Gly Arg Val Arg Val Ile Val Thr	Gly Ala Ala Pro Met Ser	
470	475	480
Thr Ser Val Met Thr Phe Phe Arg Ala	Ala Met Gly Cys Gln Val	
485	490	495
Tyr Glu Ala Tyr Gly Gln Thr Glu Cys	Thr Gly Gly Cys Thr Phe	
500	505	510
Thr Leu Pro Gly Asp Trp Thr Ser Gly	His Val Gly Val Pro Leu	
515	520	525
Ala Cys Asn Tyr Val Lys Leu Glu Asp	Val Ala Asp Met Asn Tyr	
530	535	540
Phe Thr Val Asn Asn Glu Gly Glu Val	Cys Ile Lys Gly Thr Asn	
545	550	555
Val Phe Lys Gly Tyr Leu Lys Asp Pro	Glu Lys Thr Gln Glu Ala	
560	565	570
Leu Asp Ser Asp Gly Trp Leu His Thr	Gly Asp Ile Gly Arg Trp	
575	580	585
Leu Pro Asn Gly Thr Leu Lys Ile Ile	Asp Arg Lys Lys Asn Ile	
590	595	600
Phe Lys Leu Ala Gln Gly Glu Tyr Ile	Ala Pro Glu Lys Ile Glu	

	605		610		615
Asn Ile Tyr Asn	Arg Ser Gln Pro Val	Leu Gln Ile Phe Val	His		
	620		625		630
Gly Glu Ser Leu	Arg Ser Ser Leu Val	Gly Val Val Val Pro	Asp		
	635		640		645
Thr Asp Val Leu	Pro Ser Phe Ala Ala	Lys Leu Gly Val Lys	Gly		
	650		655		660
Ser Phe Glu Glu	Leu Cys Gln Asn Gln	Val Val Arg Glu Ala	Ile		
	665		670		675
Leu Glu Asp Leu	Gln Lys Ile Gly Lys	Glu Ser Gly Leu Lys	Thr		
	680		685		690
Phe Glu Gln Val	Lys Ala Ile Phe Leu	His Pro Glu Pro Phe	Ser		
	695		700		705
Ile Glu Asn Gly	Leu Leu Thr Pro Thr	Leu Lys Ala Lys Arg	Gly		
	710		715		720
Glu Leu Ser Lys	Tyr Phe Arg Thr Gln	Ile Asp Ser Leu Tyr	Glu		
	725		730		735
His Ile Gln Asp					

<210> 87

<211> 2725

<212> DNA

<213> Homo sapiens

<400> 87

```

ggaggcggag gccgcggcga gccgggccga gcagtgaggg ccctagcggg 50
gcccagcggg ggcccggggc ccctaagcca ttctgaagt catgggctgg 100
ccaggacatt ggtgaccgc caatccgta tggacgactg gaagcccagc 150
cccctcatca agccctttgg ggctcgaag aagcggagct ggtaccttac 200
ctggaagtat aaactgacaa accagcgggc cctgcggaga ttctgtcaga 250
caggggccgt gcttttctg ctggtgactg tcattgtcaa tatcaagttg 300
atcctggaca ctgcgcgagc catcagtga gccaatgaag acccagagcc 350
agagcaagac tatgatgagg ccctaggccg cctggagccc ccacggcgca 400
gaggcagtgg tccccggcg gtcctggacg tagaggtgta ttcaagtcgc 450
agcaaagtat atgtggcagt ggatggcacc acggtgctgg aggatgaggc 500
ccgggagcag ggccggggca tccatgtcat tgctctcaac caggccacgg 550

```



gccacgtgat ggcaaaacgt gtgtttgaca cgtactcacc tcatgaggat 600  
gaggccatgg tgctattcct caacatggta gcgcccggcc gagtgctcat 650  
ctgcactgtc aaggatgagg gctccttcca cctcaaggac acagccaagg 700  
ctctgctgag gagcctgggc agccaggctg gccctgccct gggctggagg 750  
gacacatggg ccttcgtggg acgaaaagga ggtcctgtct tcggggagaa 800  
acattctaag tcacctgccc tctcttcctg gggggaccca gtcctgctga 850  
agacagatgt gccattgagc tcagcagaag aggcagagtg cacttgggca 900  
gacacagagc tgaaccgtcg ccgcccggcg ttctgcagca aagttgaggg 950  
ctatggaagt gtatgcagct gcaaggaccc cacacccatc gaggtcagcc 1000  
ctgaccact cccagacaac aaggctcctca atgtgcctgt ggctgtcatt 1050  
gcagggaacc gacccaatta cctgtacagg atgtgcgct ctctgctttc 1100  
agcccagggg gtgtctctc agatgataac agttttcatt gacggctact 1150  
atgaggaacc catggatgtg gtggcactgt ttggtctgag gggcatccag 1200  
catactccca tcagcatcaa gaatgccgc gtgtctcagc actacaaggc 1250  
cagcctcact gccactttca acctgtttcc ggaggccaag tttgctgtgg 1300  
ttctggaaga ggacctggac attgctgtgg attttttcag tttcctgagc 1350  
caatccatcc acctactgga ggaggatgac agcctgtact gcattctctgc 1400  
ctggaatgac caggggtatg aacacacggc tgaggaccca gcactactgt 1450  
accgtgtgga gaccatgcct gggctgggct ggggtgctcag gaggtccttg 1500  
tacaaggagg agcttgagcc caagtggcct acaccgaaa agctctggga 1550  
ttgggacatg tggatgcgga tgcctgaaca acgccggggc cgagagtgca 1600  
tcatccctga cgtttcccga tcctaccact ttggcatcgt cggcctcaac 1650  
atgaatggct actttcacga ggcctacttc aagaagcaca agttcaacac 1700  
ggttccaggt gtccagctca ggaatgtgga cagtctgaag aaagaagctt 1750  
atgaagtgga agttcacagg ctgctcagt aggctgaggt tctggaccac 1800  
agcaagaacc cttgtgaaga ctctttcctg ccagacacag agggccacac 1850  
ctacgtggcc tttattcgaa tggagaaaga tgatgacttc accacctgga 1900  
cccagcttgc caagtgcctc catatctggg acctggatgt gcgtggcaac 1950  
catcggggcc tgtggagatt gtttcggaag aagaaccact tcctggtggt 2000

gggggtcccg gcttccccct actcagtga gaagccaccc tcagtcaccc 2050  
 caattttcct ggagccaccc ccaaaggagg agggagcccc aggagcccca 2100  
 gaacagacat gagacctcct ccaggaccct gcggggctgg gtactgtgta 2150  
 cccccaggct ggctagccct tccctccatc ctgtaggatt ttgtagatgc 2200  
 tggtaggggc tggggctacc ttgtttttaa catgagactt aattactaac 2250  
 tccaagggga gggttcccc gctccaacac cccgttcctg agttaaaagt 2300  
 ctatttattt acttccttgt tggagaaggg caggagagta cctgggaatc 2350  
 attacgatcc ctagcagctc atcctgccct ttgaataccc tcactttcca 2400  
 ggcttggtc agaatctaac ctatttattg actgtcctga gggccttgaa 2450  
 aacaggccga acctggaggg cctggatttc tttttgggct ggaatgctgc 2500  
 cctgagggtg gggctggctc ttactcagga aactgctgtg cccaacccat 2550  
 ggacaggccc agctggggcc cacatgctga cacagactca ctcagagacc 2600  
 cttagacact ggaccaggcc tcctctcagc cttctctttg tccagatttc 2650  
 caaagctgga taagttggtc attgattaaa aaaggagaag ccctctggga 2700  
 aaaaaaaaa aaaaaaaaa aaaaa 2725

<210> 88

<211> 660

<212> PRT

<213> Homo sapiens

<400> 88

Met	Asp	Asp	Trp	Lys	Pro	Ser	Pro	Leu	Ile	Lys	Pro	Phe	Gly	Ala
1				5					10					15
Arg	Lys	Lys	Arg	Ser	Trp	Tyr	Leu	Thr	Trp	Lys	Tyr	Lys	Leu	Thr
				20					25					30
Asn	Gln	Arg	Ala	Leu	Arg	Arg	Phe	Cys	Gln	Thr	Gly	Ala	Val	Leu
				35					40					45
Phe	Leu	Leu	Val	Thr	Val	Ile	Val	Asn	Ile	Lys	Leu	Ile	Leu	Asp
				50					55					60
Thr	Arg	Arg	Ala	Ile	Ser	Glu	Ala	Asn	Glu	Asp	Pro	Glu	Pro	Glu
				65					70					75
Gln	Asp	Tyr	Asp	Glu	Ala	Leu	Gly	Arg	Leu	Glu	Pro	Pro	Arg	Arg
				80					85					90
Arg	Gly	Ser	Gly	Pro	Arg	Arg	Val	Leu	Asp	Val	Glu	Val	Tyr	Ser
				95					100					105

Ser Arg Ser Lys Val Tyr Val Ala Val Asp Gly Thr Thr Val Leu	110	115	120
Glu Asp Glu Ala Arg Glu Gln Gly Arg Gly Ile His Val Ile Val	125	130	135
Leu Asn Gln Ala Thr Gly His Val Met Ala Lys Arg Val Phe Asp	140	145	150
Thr Tyr Ser Pro His Glu Asp Glu Ala Met Val Leu Phe Leu Asn	155	160	165
Met Val Ala Pro Gly Arg Val Leu Ile Cys Thr Val Lys Asp Glu	170	175	180
Gly Ser Phe His Leu Lys Asp Thr Ala Lys Ala Leu Leu Arg Ser	185	190	195
Leu Gly Ser Gln Ala Gly Pro Ala Leu Gly Trp Arg Asp Thr Trp	200	205	210
Ala Phe Val Gly Arg Lys Gly Gly Pro Val Phe Gly Glu Lys His	215	220	225
Ser Lys Ser Pro Ala Leu Ser Ser Trp Gly Asp Pro Val Leu Leu	230	235	240
Lys Thr Asp Val Pro Leu Ser Ser Ala Glu Glu Ala Glu Cys His	245	250	255
Trp Ala Asp Thr Glu Leu Asn Arg Arg Arg Arg Arg Phe Cys Ser	260	265	270
Lys Val Glu Gly Tyr Gly Ser Val Cys Ser Cys Lys Asp Pro Thr	275	280	285
Pro Ile Glu Phe Ser Pro Asp Pro Leu Pro Asp Asn Lys Val Leu	290	295	300
Asn Val Pro Val Ala Val Ile Ala Gly Asn Arg Pro Asn Tyr Leu	305	310	315
Tyr Arg Met Leu Arg Ser Leu Leu Ser Ala Gln Gly Val Ser Pro	320	325	330
Gln Met Ile Thr Val Phe Ile Asp Gly Tyr Tyr Glu Glu Pro Met	335	340	345
Asp Val Val Ala Leu Phe Gly Leu Arg Gly Ile Gln His Thr Pro	350	355	360
Ile Ser Ile Lys Asn Ala Arg Val Ser Gln His Tyr Lys Ala Ser	365	370	375
Leu Thr Ala Thr Phe Asn Leu Phe Pro Glu Ala Lys Phe Ala Val	380	385	390

Val	Leu	Glu	Glu	Asp	Leu	Asp	Ile	Ala	Val	Asp	Phe	Phe	Ser	Phe				395	400	405
Leu	Ser	Gln	Ser	Ile	His	Leu	Leu	Glu	Glu	Asp	Asp	Ser	Leu	Tyr				410	415	420
Cys	Ile	Ser	Ala	Trp	Asn	Asp	Gln	Gly	Tyr	Glu	His	Thr	Ala	Glu				425	430	435
Asp	Pro	Ala	Leu	Leu	Tyr	Arg	Val	Glu	Thr	Met	Pro	Gly	Leu	Gly				440	445	450
Trp	Val	Leu	Arg	Arg	Ser	Leu	Tyr	Lys	Glu	Glu	Leu	Glu	Pro	Lys				455	460	465
Trp	Pro	Thr	Pro	Glu	Lys	Leu	Trp	Asp	Trp	Asp	Met	Trp	Met	Arg				470	475	480
Met	Pro	Glu	Gln	Arg	Arg	Gly	Arg	Glu	Cys	Ile	Ile	Pro	Asp	Val				485	490	495
Ser	Arg	Ser	Tyr	His	Phe	Gly	Ile	Val	Gly	Leu	Asn	Met	Asn	Gly				500	505	510
Tyr	Phe	His	Glu	Ala	Tyr	Phe	Lys	Lys	His	Lys	Phe	Asn	Thr	Val				515	520	525
Pro	Gly	Val	Gln	Leu	Arg	Asn	Val	Asp	Ser	Leu	Lys	Lys	Glu	Ala				530	535	540
Tyr	Glu	Val	Glu	Val	His	Arg	Leu	Leu	Ser	Glu	Ala	Glu	Val	Leu				545	550	555
Asp	His	Ser	Lys	Asn	Pro	Cys	Glu	Asp	Ser	Phe	Leu	Pro	Asp	Thr				560	565	570
Glu	Gly	His	Thr	Tyr	Val	Ala	Phe	Ile	Arg	Met	Glu	Lys	Asp	Asp				575	580	585
Asp	Phe	Thr	Thr	Trp	Thr	Gln	Leu	Ala	Lys	Cys	Leu	His	Ile	Trp				590	595	600
Asp	Leu	Asp	Val	Arg	Gly	Asn	His	Arg	Gly	Leu	Trp	Arg	Leu	Phe				605	610	615
Arg	Lys	Lys	Asn	His	Phe	Leu	Val	Val	Gly	Val	Pro	Ala	Ser	Pro				620	625	630
Tyr	Ser	Val	Lys	Lys	Pro	Pro	Ser	Val	Thr	Pro	Ile	Phe	Leu	Glu				635	640	645
Pro	Pro	Pro	Lys	Glu	Glu	Gly	Ala	Pro	Gly	Ala	Pro	Glu	Gln	Thr				650	655	660

<210> 89

<211> 25

<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 89  
gatggcaaaa cgtgtgtttg acacg 25

<210> 90  
<211> 22  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 90  
cctcaaccag gccacgggcc ac 22

<210> 91  
<211> 24  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 91  
cccaggcaga gatgcagtag aggc 24

<210> 92  
<211> 26  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 92  
cctccagtag gtggatggat tggctc 26

<210> 93  
<211> 47  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 93  
ctcacctcat gaggatgagg ccatggtgct attcctcaac atggtag 47

<210> 94  
<211> 3037  
<212> DNA  
<213> Homo sapiens

<400> 94

cggacgcgtg ggctgctggt gggaaggcct aaagaactgg aaagcccact 50  
ctcttggaac caccacacct gtttaaagaa cctaagcacc atttaaagcc 100  
actggaaatt tggtgtctag tggttggtggg tgaataaagg agggcagaat 150  
ggatgatttc atctccatta gcctgctgtc tctggctatg ttggtgggat 200  
gttacgtggc cggaatcatt cccttggtctg ttaatttctc agaggaacga 250  
ctgaagctgg tgactgtttt ggggtgctggc cttctctgtg gaactgctct 300  
ggcagtcatc gtgcctgaag gagtacatgc cctttatgaa gatattcttg 350  
agggaaaaca ccaccaagca agtgaaacac ataatgtgat tgcacagac 400  
aaagcagcag aaaaatcagt tgtccatgaa catgagcaca gccacgacca 450  
cacacagctg catgcctata ttggtgtttc cctcgttctg ggcttcgttt 500  
tcatgttgct ggtggaccag attggtaact cccatgtgca ttctactgac 550  
gatccagaag cagcaaggtc tagcaattcc aaaatcacca ccacgctggg 600  
tctggttgtc catgctgcag ctgatggtgt tgctttggga gcagcagcat 650  
ctacttcaca gaccagtgtc cagttaattg tgtttgtggc aatcatgcta 700  
cataaggcac cagctgcttt tggactggtt tccttcttga tgcagctgg 750  
cttagagcgg aatcgaatca gaaagcactt gctggtcttt gcattggcag 800  
caccagttat gtccatggtg acatacttag gactgagtaa gagcagtaaa 850  
gaagcccttt cagagggtgaa cgccacggga gtggccatgc ttttctctgc 900  
cgggacattt ctttatgttg ccacagtaca tgctctccct gaggtgggag 950  
gaatagggca cagccacaag cccgatgcca cgggaggag aggcctcagc 1000  
cgcttggaa tggcagccct ggttctgggt tgccctcatcc ctctcatcct 1050  
gtcagtagga caccagcatt aaatgttcaa ggtccagcct tgggtccagg 1100  
ccgtttgcc tccagtgaga acagccggca cgtgacagct actcacttcc 1150  
tcagtctctt gtctcacctt gcgcactctt acatgtattc ctagagtcca 1200  
gaggggaggt gaggttaaaa cctgagtaat ggaaaagctt ttagagtaga 1250  
aacacattta cgttgagtt agctatagac atccattgt gttatctttt 1300  
aaaaggccct tgacattttg cgttttaata tttctcttaa ccctattctc 1350  
agggagatg gaatttagtt ttaaggaaaa gaggagaact tcatactcac 1400

aatgaaatag tgattatgaa aatacagtgt tctgtaatta agctatgtct 1450  
ctttcttctt agtttagagg ctctgctact ttatccattg atttttaaca 1500  
tggttcccac catgtaagac tggtgcttta gcatctatgc cacatgcgtt 1550  
gatggaaggt catagcaccc actcacttag atgctaaagg tgattctagt 1600  
taatctggga ttagggtcag gaaaatgata gcaagacaca ttgaaagctc 1650  
tctttatact caaaagagat atccattgaa aagggatgtc tagagggatt 1700  
taaacagctc ctttggcacg tgcctctctg aatccagcct gccattccat 1750  
caaatggagc aggagaggtg ggaggagcct ctaaagaggt gactggtatt 1800  
ttgtagcatt ccttgtcaag ttctcctttg cagaatacct gtctccacat 1850  
tcctagagag gagccaagtt ctagtagttt cagttctagg ctttccttca 1900  
agaacagtca gatcacaaag tgtctttgga aattaaggga tattaaattt 1950  
taagtgattt ttggatggtt attgatatct ttgtagtagc tttttttaa 2000  
agactaccaa aatgtatggt tgcctttttt ttttgttttt tttttttta 2050  
attatttctc ttagcagatc agcaatccct ctagggacct aaatactagg 2100  
tcagctttgg cgacactgtg tcttctcaca taaccacctg tagcaagatg 2150  
gatcataaat gagaagtgtt tgcctattga tttaaagcct attggaatca 2200  
tgtctcttgt ctcttcgtct tttctttgct tttcttctaa cttttccctc 2250  
tagcctctcc tcgccacaat ttgctgctta ctgctggtgt taatatttgt 2300  
gtgggatgaa ttcttatcag gacaaccact tctcgaactg taataatgaa 2350  
gataataata tctttattct ttatcccctt caaagaaatt accttttgt 2400  
caaatgccgc tttgttgagc ccttaaaata ccacctctc atgtgtaaat 2450  
tgacacaatc actaatctgg taatttaaac aattgagata gcaaaagtgt 2500  
ttaacagact aggataattt ttttttcata ttgccaataa tttttgtaaa 2550  
ccctgtcttg tcaaataagt gtataatatt gtattattaa tttattttta 2600  
ctttctatac catttcaaaa cacattacac taagggggaa ccaagactag 2650  
tttcttcagg gcagtggacg tagtagtttg taaaaacgtt ttctatgacg 2700  
cataagctag catgcctatg atttatttcc ttcatgaatt tgtcactgga 2750  
tcagcagctg tggaaataaa gcttgtgagc cctctgctgg ccacagtgag 2800

gaaagtagca caaataggat acagttgtat gtagtcattg gcaacaattg 2850  
 catacaattt tactaccaag agaaggtata gtatggaaag tccaaatgac 2900  
 ttccttgatt ggatggtaac agctgactgg tgtgagactt gaggtttcat 2950  
 ctagtccctc aaaactatat ggttgcctag attctctctg gaaactgact 3000  
 ttgtcaaata aatagcagat tgtagtgtca aaaaaaa 3037

<210> 95  
 <211> 307  
 <212> PRT  
 <213> Homo sapiens

<400> 95

Met	Asp	Asp	Phe	Ile	Ser	Ile	Ser	Leu	Leu	Ser	Leu	Ala	Met	Leu	1	5	10	15
Val	Gly	Cys	Tyr	Val	Ala	Gly	Ile	Ile	Pro	Leu	Ala	Val	Asn	Phe	20	25	30	
Ser	Glu	Glu	Arg	Leu	Lys	Leu	Val	Thr	Val	Leu	Gly	Ala	Gly	Leu	35	40	45	
Leu	Cys	Gly	Thr	Ala	Leu	Ala	Val	Ile	Val	Pro	Glu	Gly	Val	His	50	55	60	
Ala	Leu	Tyr	Glu	Asp	Ile	Leu	Glu	Gly	Lys	His	His	Gln	Ala	Ser	65	70	75	
Glu	Thr	His	Asn	Val	Ile	Ala	Ser	Asp	Lys	Ala	Ala	Glu	Lys	Ser	80	85	90	
Val	Val	His	Glu	His	Glu	His	Ser	His	Asp	His	Thr	Gln	Leu	His	95	100	105	
Ala	Tyr	Ile	Gly	Val	Ser	Leu	Val	Leu	Gly	Phe	Val	Phe	Met	Leu	110	115	120	
Leu	Val	Asp	Gln	Ile	Gly	Asn	Ser	His	Val	His	Ser	Thr	Asp	Asp	125	130	135	
Pro	Glu	Ala	Ala	Arg	Ser	Ser	Asn	Ser	Lys	Ile	Thr	Thr	Thr	Leu	140	145	150	
Gly	Leu	Val	Val	His	Ala	Ala	Ala	Asp	Gly	Val	Ala	Leu	Gly	Ala	155	160	165	
Ala	Ala	Ser	Thr	Ser	Gln	Thr	Ser	Val	Gln	Leu	Ile	Val	Phe	Val	170	175	180	
Ala	Ile	Met	Leu	His	Lys	Ala	Pro	Ala	Ala	Phe	Gly	Leu	Val	Ser	185	190	195	
Phe	Leu	Met	His	Ala	Gly	Leu	Glu	Arg	Asn	Arg	Ile	Arg	Lys	His	200	205	210	



Leu	Leu	Val	Phe	Ala	Leu	Ala	Ala	Pro	Val	Met	Ser	Met	Val	Thr	215	220	225
Tyr	Leu	Gly	Leu	Ser	Lys	Ser	Ser	Lys	Glu	Ala	Leu	Ser	Glu	Val	230	235	240
Asn	Ala	Thr	Gly	Val	Ala	Met	Leu	Phe	Ser	Ala	Gly	Thr	Phe	Leu	245	250	255
Tyr	Val	Ala	Thr	Val	His	Val	Leu	Pro	Glu	Val	Gly	Gly	Ile	Gly	260	265	270
His	Ser	His	Lys	Pro	Asp	Ala	Thr	Gly	Gly	Arg	Gly	Leu	Ser	Arg	275	280	285
Leu	Glu	Val	Ala	Ala	Leu	Val	Leu	Gly	Cys	Leu	Ile	Pro	Leu	Ile	290	295	300
Leu	Ser	Val	Gly	His	Gln	His									305		

<210> 96  
 <211> 25  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 96  
 gttgtgggtg aataaaggag ggcag 25

<210> 97  
 <211> 25  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 97  
 ctgtgctcat gttcatggac aactg 25

<210> 98  
 <211> 50  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 98  
 ggatgatttc atctccatta gcctgctgtc tctggctatg ttggtgggat 50

<210> 99  
 <211> 1429

<212> DNA

<213> Homo sapiens

<400> 99

gctcgaggcc ggcgggcggc ggagagcgac ccgggaggcc tcgtagcggg 50  
gccccggatc cccgagtggc ggccggagcc tcgaaaagag attctcagcg 100  
ctgattttga gatgatgggc ttgggaaacg ggcgtcgcag catgaagtcg 150  
ccgcccctcg tgctggccgc cctggtggcc tgcattcatg tcttgggctt 200  
caactactgg attgagagct cccggagcgt ggacctccag acacggatca 250  
tggagctgga aggcagggtc cgcagggcgg ctgcagagag aggcgccgtg 300  
gagctgaaga agaacgagtt ccagggagag ctggagaagc agcgggagca 350  
gcttgacaaa atccagtcca gccacaactt ccagctggag agcgtcaaca 400  
agctgtacca ggacgaaaag gcggttttgg tgaataacat caccacaggt 450  
gagaggctca tccgagtgtc gcaagaccag ttaaagacct tgcagaggaa 500  
ttacggcagg ctgcagcagg atgtcctcca gtttcagaag aaccagacca 550  
acctggagag gaagttctcc tacgacctga gccagtgcac caatcagatg 600  
aaggaggtga aggaacagtg tgaggagcga atagaagagg tcaccaaaaa 650  
ggggaatgaa gctgtagctt ccagagacct gagtgaatac aacgaccaga 700  
gacagcagct ccaagccctc agtgagcctc agcccaggct gcaggcagca 750  
ggcctgccac acacagaggt gccacaaggg aagggaacg tgcttggtaa 800  
cagcaagtcc cagacaccag cccccagttc cgaagtgggt ttggattcaa 850  
agagacaagt tgagaaagag gaaaccaatg agatccaggt ggtgaatgag 900  
gagcctcaga gggacaggct gccgcaggag ccaggccggg agcaggtggt 950  
ggaagacaga cctgtaggtg gaagaggctt cgggggagcc ggagaactgg 1000  
gccagacccc acaggtgcag gctgccctgt cagtgcagca ggaaaatcca 1050  
gagatggagg gccctgagcg agaccagctt gtcattcccc acggacagga 1100  
ggaggagcag gaagctgccg gggaaggag aaaccagcag aaactgagag 1150  
gagaagatga ctacaacatg gatgaaaatg aagcagaatc tgagacagac 1200  
aagcaagcag ccctggcagg gaatgacaga aacatagatg tttttaatgt 1250  
tgaagatcag aaaagagaca ccataaattt acttgatcag cgtgaaaagc 1300  
ggaatcatac actctgaatt gaactggaat cacatatttc acaacagggc 1350

cgaagagatg actataaaat gttcatgagg gactgaatac tgaaaactgt 1400

gaaatgtact aaataaaatg tacatctga 1429

<210> 100

<211> 401

<212> PRT

<213> Homo sapiens

<400> 100

Met	Met	Gly	Leu	Gly	Asn	Gly	Arg	Arg	Ser	Met	Lys	Ser	Pro	Pro
1				5					10					15

Leu	Val	Leu	Ala	Ala	Leu	Val	Ala	Cys	Ile	Ile	Val	Leu	Gly	Phe
				20					25					30

Asn	Tyr	Trp	Ile	Ala	Ser	Ser	Arg	Ser	Val	Asp	Leu	Gln	Thr	Arg
				35					40					45

Ile	Met	Glu	Leu	Glu	Gly	Arg	Val	Arg	Arg	Ala	Ala	Ala	Glu	Arg
				50					55					60

Gly	Ala	Val	Glu	Leu	Lys	Lys	Asn	Glu	Phe	Gln	Gly	Glu	Leu	Glu
				65					70					75

Lys	Gln	Arg	Glu	Gln	Leu	Asp	Lys	Ile	Gln	Ser	Ser	His	Asn	Phe
				80					85					90

Gln	Leu	Glu	Ser	Val	Asn	Lys	Leu	Tyr	Gln	Asp	Glu	Lys	Ala	Val
				95					100					105

Leu	Val	Asn	Asn	Ile	Thr	Thr	Gly	Glu	Arg	Leu	Ile	Arg	Val	Leu
				110					115					120

Gln	Asp	Gln	Leu	Lys	Thr	Leu	Gln	Arg	Asn	Tyr	Gly	Arg	Leu	Gln
				125					130					135

Gln	Asp	Val	Leu	Gln	Phe	Gln	Lys	Asn	Gln	Thr	Asn	Leu	Glu	Arg
				140					145					150

Lys	Phe	Ser	Tyr	Asp	Leu	Ser	Gln	Cys	Ile	Asn	Gln	Met	Lys	Glu
				155					160					165

Val	Lys	Glu	Gln	Cys	Glu	Glu	Arg	Ile	Glu	Glu	Val	Thr	Lys	Lys
				170					175					180

Gly	Asn	Glu	Ala	Val	Ala	Ser	Arg	Asp	Leu	Ser	Glu	Asn	Asn	Asp
				185					190					195

Gln	Arg	Gln	Gln	Leu	Gln	Ala	Leu	Ser	Glu	Pro	Gln	Pro	Arg	Leu
				200					205					210

Gln	Ala	Ala	Gly	Leu	Pro	His	Thr	Glu	Val	Pro	Gln	Gly	Lys	Gly
				215					220					225

Asn Val Leu Gly Asn Ser Lys Ser Gln Thr Pro Ala Pro Ser Ser

230	235	240
Glu Val Val Leu Asp Ser Lys Arg Gln Val Glu Lys Glu Glu Thr		
245	250	255
Asn Glu Ile Gln Val Val Asn Glu Glu Pro Gln Arg Asp Arg Leu		
260	265	270
Pro Gln Glu Pro Gly Arg Glu Gln Val Val Glu Asp Arg Pro Val		
275	280	285
Gly Gly Arg Gly Phe Gly Gly Ala Gly Glu Leu Gly Gln Thr Pro		
290	295	300
Gln Val Gln Ala Ala Leu Ser Val Ser Gln Glu Asn Pro Glu Met		
305	310	315
Glu Gly Pro Glu Arg Asp Gln Leu Val Ile Pro Asp Gly Gln Glu		
320	325	330
Glu Glu Gln Glu Ala Ala Gly Glu Gly Arg Asn Gln Gln Lys Leu		
335	340	345
Arg Gly Glu Asp Asp Tyr Asn Met Asp Glu Asn Glu Ala Glu Ser		
350	355	360
Glu Thr Asp Lys Gln Ala Ala Leu Ala Gly Asn Asp Arg Asn Ile		
365	370	375
Asp Val Phe Asn Val Glu Asp Gln Lys Arg Asp Thr Ile Asn Leu		
380	385	390
Leu Asp Gln Arg Glu Lys Arg Asn His Thr Leu		
395	400	

<210> 101

<211> 3671

<212> DNA

<213> Homo sapiens

<400> 101

```

ggatgcagaa agcctcagtg ttgctcttcc tggcctgggt ctgcttcctc 50
ttctacgctg gcattgcctt cttcaccagt ggcttctctg tcacccgttt 100
ggagctcacc aaccatagca gctgccaaga gccccaggc cctgggtccc 150
tgccatgggg gagccaaggg aaacctgggg cctgctggat ggcttcccga 200
ttttcgcggg ttgtgttggg gctgatagat gctctgcgat ttgacttgcg 250
ccagccccag cattcacagc tgcctagaga gcctcctgtc tccctaccct 300
tcctgggcaa actaagctcc ttgcagagga tcctggagat tcagccccac 350
catgcccggc tctaccgatc tcagggttgac cctcctacca ccaccatgca 400

```

gcgcctcaag gccctcacca ctggctcact gcctaccttt attgatgctg 450  
gtagtaactt cgccagccac gccatagtgg aagacaatct cattaagcag 500  
ctcaccagtg caggaaggcg tgtagtcttc atgggagatg atacctggaa 550  
agaccttttc cctggtgctt tctccaaagc tttcttcttc ccatccttca 600  
atgtcagaga cctagacaca gtggacaatg gcatcctgga acacctctac 650  
cccaccatgg acagtgggta atgggacgtg ctgattgctc acttcctggg 700  
tgtggaccac tgtggccaca agcatggccc tcaccaccct gaaatggcca 750  
agaaacttag ccagatggac caggtgatcc agggacttgt ggagcgtctg 800  
gagaatgaca cactgctggt agtggctggg gaccatggga tgaccacaaa 850  
tgagagaccat ggaggggaca gtgagctgga ggtctcagct gctctctttc 900  
tgtatagccc cacagcagtc ttccccagca cccaccaga ggagccagag 950  
gtgattcctc aagttagcct tgtgcccacg ctggccctgc tgctgggcct 1000  
gcccattcca tttgggaata tcggggaagt gatggctgag ctattctcag 1050  
ggggtgagga ctcccagccc cactcctctg ctttagccca agcctcagct 1100  
ctccatctca atgctcagca ggtgtccga tttcttcata cctactcagc 1150  
tgctactcag gaccttcaag ctaaggagct tcactcagctg cagaacctct 1200  
tctccaaggc ctctgctgac taccagtggc ttctccagag cccaagggg 1250  
gctgaggcga cactgccgac tgtgattgct gagctgcagc agttcctgcg 1300  
gggagctcgg gccatgtgca tcgagtcttg ggctcgtttc tctctggtcc 1350  
gcatggcggg gggtagctct ctcttggtg cttcctgctt tatctgcctg 1400  
ctggcatctc agtgggcaat atccccaggc tttcattct gccctctact 1450  
cctgacacct gtggcctggg gcctggttgg ggccatagcg tatgctggac 1500  
tcctgggaac tattgagctg aagctagatc tagtgcttct aggggctgtg 1550  
gctgcagtga gctcattcct cccttttctg tggaaagcct gggctggctg 1600  
ggggtccaag agggccctgg caaccctgtt tcccatccct gggcccgctc 1650  
tgttactcct gctgtttcgc ttggctgtgt tcttctctga tagttttgtt 1700  
gtagctgagg ccagggccac ccccttcctt ttgggctcat tcactcctgct 1750  
cctggttgct cagcttcact gggagggcca gctgcttcca cctaagctac 1800  
tcacaatgcc ccgccttggc acttcagcca caacaaacc cccacggcac 1850

aatggtgcat atgccctgag gcttggaatt gggttgcttt tatgtacaag 1900  
gctagctggg ctttttcatac gttgccctga agagacacct gtttgccact 1950  
cctctccctg gctgagtcct ctggcatcca tggtaggtgg tcgagccaag 2000  
aatttatggt atggagcttg tgtggcggcg ctggtggccc tgtagctgc 2050  
cgtgcgcttg tggcttcgcc gctatggtaa tctcaagagc cccgagccac 2100  
ccatgctctt tgtgcgctgg ggactgcccc taatggcatt gggactgct 2150  
gcctactggg cattggcgtc gggggcagat gaggctcccc cccgtctccg 2200  
ggctctggtc tctggggcat ccatggtgct gcctcgggct gtagcagggc 2250  
tggctgcttc agggctcgcg ctgctgctct ggaagcctgt gacagtgtg 2300  
gtgaaggctg gggcaggcgc tccaaggacc aggactgtcc tctctccctt 2350  
ctcaggcccc cccacttctc aagctgactt ggattatgtg gtccctcaaa 2400  
tctaccgaca catgcaggag gaggttccggg gccggttaga gaggacaaa 2450  
tctcagggtc ccctgactgt ggctgcttat cagttgggga gtgtctactc 2500  
agctgctatg gtcacagccc tcacctgtt ggcttccca cttctgctgt 2550  
tgcatgcgga gcgcatacgc cttgtgttcc tgcttctgtt tctgcagagc 2600  
ttccttctcc tacatctgct tgctgctggg ataccctca ccacctctgg 2650  
tccttttact gtgcatggc aggcagtctc ggcttgggccc ctcatggcca 2700  
cacagacctt ctactccaca ggccaccagc ctgtctttcc agccatccat 2750  
tggcatgcag ccttcgtggg attcccagag ggtcatggct cctgtacttg 2800  
gctgcctgct ttgctagtgg gagccaacac ctttgccctc cacctcctct 2850  
ttgcagtagg ttgccactg ctctgctct ggcttttct gtgtgagagt 2900  
caagggctgc ggaagagaca gcagccccc ggaatgaag ctgatgccag 2950  
agtcagaccc gaggaggaag aggagccact gatggagatg cggctccggg 3000  
atgcgcctca gcacttctat gcagcactgc tgcagctggg cctcaagtac 3050  
ctctttatcc ttggtattca gattctggcc tgtgccttg cagcctccat 3100  
ccttcgcagg catctcatgg tctggaaagt gtttgccct aagttcatat 3150  
ttgaggctgt gggcttcatt gtgagcagcg tgggacttct cctgggcata 3200  
gctttggtga tgagagtgga tggtagctgt agctcctggt tcaggcagct 3250

atttctggcc cagcagaggt agcctagtct gtgattactg gcacttggct 3300  
 acagagagtg ctggagaaca gtgtagcctg gcctgtacag gtactggatg 3350  
 atctgcaaga caggctcagc cataactctta ctatcatgca gccagggggc 3400  
 gctgacatct aggacttcat tattctataa ttcaggacca cagtggagta 3450  
 tgatccctaa ctcttgattt ggatgcatct gagggacaag gggggcggtc 3500  
 tccgaagtgg aataaaatag gccgggcgtg gtgacttgca cctataatcc 3550  
 cagcactttg ggaggcagag gtgggaggat tgcttgggtcc caggagttca 3600  
 agaccagcct gtggaacata acaagacccc gtctctacta tttaaaaaaa 3650  
 agtgtaataa aatgataata t 3671

<210> 102

<211> 1089

<212> PRT

<213> Homo sapiens

<400> 102

Met	Gln	Lys	Ala	Ser	Val	Leu	Leu	Phe	Leu	Ala	Trp	Val	Cys	Phe	1	5	10	15
Leu	Phe	Tyr	Ala	Gly	Ile	Ala	Leu	Phe	Thr	Ser	Gly	Phe	Leu	Leu	20	25	30	
Thr	Arg	Leu	Glu	Leu	Thr	Asn	His	Ser	Ser	Cys	Gln	Glu	Pro	Pro	35	40	45	
Gly	Pro	Gly	Ser	Leu	Pro	Trp	Gly	Ser	Gln	Gly	Lys	Pro	Gly	Ala	50	55	60	
Cys	Trp	Met	Ala	Ser	Arg	Phe	Ser	Arg	Val	Val	Leu	Val	Leu	Ile	65	70	75	
Asp	Ala	Leu	Arg	Phe	Asp	Phe	Ala	Gln	Pro	Gln	His	Ser	His	Val	80	85	90	
Pro	Arg	Glu	Pro	Pro	Val	Ser	Leu	Pro	Phe	Leu	Gly	Lys	Leu	Ser	95	100	105	
Ser	Leu	Gln	Arg	Ile	Leu	Glu	Ile	Gln	Pro	His	His	Ala	Arg	Leu	110	115	120	
Tyr	Arg	Ser	Gln	Val	Asp	Pro	Pro	Thr	Thr	Thr	Met	Gln	Arg	Leu	125	130	135	
Lys	Ala	Leu	Thr	Thr	Gly	Ser	Leu	Pro	Thr	Phe	Ile	Asp	Ala	Gly	140	145	150	
Ser	Asn	Phe	Ala	Ser	His	Ala	Ile	Val	Glu	Asp	Asn	Leu	Ile	Lys	155	160	165	

Gln	Leu	Thr	Ser	Ala	Gly	Arg	Arg	Val	Val	Phe	Met	Gly	Asp	Asp			
				170					175					180			
Thr	Trp	Lys	Asp	Leu	Phe	Pro	Gly	Ala	Phe	Ser	Lys	Ala	Phe	Phe			
				185					190					195			
Phe	Pro	Ser	Phe	Asn	Val	Arg	Asp	Leu	Asp	Thr	Val	Asp	Asn	Gly			
				200					205					210			
Ile	Leu	Glu	His	Leu	Tyr	Pro	Thr	Met	Asp	Ser	Gly	Glu	Trp	Asp			
				215					220					225			
Val	Leu	Ile	Ala	His	Phe	Leu	Gly	Val	Asp	His	Cys	Gly	His	Lys			
				230					235					240			
His	Gly	Pro	His	His	Pro	Glu	Met	Ala	Lys	Lys	Leu	Ser	Gln	Met			
				245					250					255			
Asp	Gln	Val	Ile	Gln	Gly	Leu	Val	Glu	Arg	Leu	Glu	Asn	Asp	Thr			
				260					265					270			
Leu	Leu	Val	Val	Ala	Gly	Asp	His	Gly	Met	Thr	Thr	Asn	Gly	Asp			
				275					280					285			
His	Gly	Gly	Asp	Ser	Glu	Leu	Glu	Val	Ser	Ala	Ala	Leu	Phe	Leu			
				290					295					300			
Tyr	Ser	Pro	Thr	Ala	Val	Phe	Pro	Ser	Thr	Pro	Pro	Glu	Glu	Pro			
				305					310					315			
Glu	Val	Ile	Pro	Gln	Val	Ser	Leu	Val	Pro	Thr	Leu	Ala	Leu	Leu			
				320					325					330			
Leu	Gly	Leu	Pro	Ile	Pro	Phe	Gly	Asn	Ile	Gly	Glu	Val	Met	Ala			
				335					340					345			
Glu	Leu	Phe	Ser	Gly	Gly	Glu	Asp	Ser	Gln	Pro	His	Ser	Ser	Ala			
				350					355					360			
Leu	Ala	Gln	Ala	Ser	Ala	Leu	His	Leu	Asn	Ala	Gln	Gln	Val	Ser			
				365					370					375			
Arg	Phe	Leu	His	Thr	Tyr	Ser	Ala	Ala	Thr	Gln	Asp	Leu	Gln	Ala			
				380					385					390			
Lys	Glu	Leu	His	Gln	Leu	Gln	Asn	Leu	Phe	Ser	Lys	Ala	Ser	Ala			
				395					400					405			
Asp	Tyr	Gln	Trp	Leu	Leu	Gln	Ser	Pro	Lys	Gly	Ala	Glu	Ala	Thr			
				410					415					420			
Leu	Pro	Thr	Val	Ile	Ala	Glu	Leu	Gln	Gln	Phe	Leu	Arg	Gly	Ala			
				425					430					435			
Arg	Ala	Met	Cys	Ile	Glu	Ser	Trp	Ala	Arg	Phe	Ser	Leu	Val	Arg			
				440					445					450			



Met	Ala	Gly	Gly	Thr	Ala	Leu	Leu	Ala	Ala	Ser	Cys	Phe	Ile	Cys	
				455					460					465	
Leu	Leu	Ala	Ser	Gln	Trp	Ala	Ile	Ser	Pro	Gly	Phe	Pro	Phe	Cys	
				470					475					480	
Pro	Leu	Leu	Leu	Thr	Pro	Val	Ala	Trp	Gly	Leu	Val	Gly	Ala	Ile	
				485					490					495	
Ala	Tyr	Ala	Gly	Leu	Leu	Gly	Thr	Ile	Glu	Leu	Lys	Leu	Asp	Leu	
				500					505					510	
Val	Leu	Leu	Gly	Ala	Val	Ala	Ala	Val	Ser	Ser	Phe	Leu	Pro	Phe	
				515					520					525	
Leu	Trp	Lys	Ala	Trp	Ala	Gly	Trp	Gly	Ser	Lys	Arg	Pro	Leu	Ala	
				530					535					540	
Thr	Leu	Phe	Pro	Ile	Pro	Gly	Pro	Val	Leu	Leu	Leu	Leu	Leu	Phe	
				545					550					555	
Arg	Leu	Ala	Val	Phe	Phe	Ser	Asp	Ser	Phe	Val	Val	Ala	Glu	Ala	
				560					565					570	
Arg	Ala	Thr	Pro	Phe	Leu	Leu	Gly	Ser	Phe	Ile	Leu	Leu	Leu	Val	
				575					580					585	
Val	Gln	Leu	His	Trp	Glu	Gly	Gln	Leu	Leu	Pro	Pro	Lys	Leu	Leu	
				590					595					600	
Thr	Met	Pro	Arg	Leu	Gly	Thr	Ser	Ala	Thr	Thr	Asn	Pro	Pro	Arg	
				605					610					615	
His	Asn	Gly	Ala	Tyr	Ala	Leu	Arg	Leu	Gly	Ile	Gly	Leu	Leu	Leu	
				620					625					630	
Cys	Thr	Arg	Leu	Ala	Gly	Leu	Phe	His	Arg	Cys	Pro	Glu	Glu	Thr	
				635					640					645	
Pro	Val	Cys	His	Ser	Ser	Pro	Trp	Leu	Ser	Pro	Leu	Ala	Ser	Met	
				650					655					660	
Val	Gly	Gly	Arg	Ala	Lys	Asn	Leu	Trp	Tyr	Gly	Ala	Cys	Val	Ala	
				665					670					675	
Ala	Leu	Val	Ala	Leu	Leu	Ala	Ala	Val	Arg	Leu	Trp	Leu	Arg	Arg	
				680					685					690	
Tyr	Gly	Asn	Leu	Lys	Ser	Pro	Glu	Pro	Pro	Met	Leu	Phe	Val	Arg	
				695					700					705	
Trp	Gly	Leu	Pro	Leu	Met	Ala	Leu	Gly	Thr	Ala	Ala	Tyr	Trp	Ala	
				710					715					720	
Leu	Ala	Ser	Gly	Ala	Asp	Glu	Ala	Pro	Pro	Arg	Leu	Arg	Val	Leu	
				725					730					735	

Val Ser Gly Ala	Ser Met Val Leu Pro Arg Ala Val Ala Gly Leu	740	745	750
Ala Ala Ser Gly	Leu Ala Leu Leu Leu Trp Lys Pro Val Thr Val	755	760	765
Leu Val Lys Ala	Gly Ala Gly Ala Pro Arg Thr Arg Thr Val Leu	770	775	780
Thr Pro Phe Ser	Gly Pro Pro Thr Ser Gln Ala Asp Leu Asp Tyr	785	790	795
Val Val Pro Gln	Ile Tyr Arg His Met Gln Glu Glu Phe Arg Gly	800	805	810
Arg Leu Glu Arg	Thr Lys Ser Gln Gly Pro Leu Thr Val Ala Ala	815	820	825
Tyr Gln Leu Gly	Ser Val Tyr Ser Ala Ala Met Val Thr Ala Leu	830	835	840
Thr Leu Leu Ala	Phe Pro Leu Leu Leu Leu His Ala Glu Arg Ile	845	850	855
Ser Leu Val Phe	Leu Leu Leu Phe Leu Gln Ser Phe Leu Leu Leu	860	865	870
His Leu Leu Ala	Ala Gly Ile Pro Val Thr Thr Pro Gly Pro Phe	875	880	885
Thr Val Pro Trp	Gln Ala Val Ser Ala Trp Ala Leu Met Ala Thr	890	895	900
Gln Thr Phe Tyr	Ser Thr Gly His Gln Pro Val Phe Pro Ala Ile	905	910	915
His Trp His Ala	Ala Phe Val Gly Phe Pro Glu Gly His Gly Ser	920	925	930
Cys Thr Trp Leu	Pro Ala Leu Leu Val Gly Ala Asn Thr Phe Ala	935	940	945
Ser His Leu Leu	Phe Ala Val Gly Cys Pro Leu Leu Leu Leu Trp	950	955	960
Pro Phe Leu Cys	Glu Ser Gln Gly Leu Arg Lys Arg Gln Gln Pro	965	970	975
Pro Gly Asn Glu	Ala Asp Ala Arg Val Arg Pro Glu Glu Glu Glu	980	985	990
Glu Pro Leu Met	Glu Met Arg Leu Arg Asp Ala Pro Gln His Phe	995	1000	1005
Tyr Ala Ala Leu	Leu Gln Leu Gly Leu Lys Tyr Leu Phe Ile Leu	1010	1015	1020

Gly Ile Gln Ile Leu Ala Cys Ala Leu Ala Ala Ser Ile Leu Arg		
1025	1030	1035
Arg His Leu Met Val Trp Lys Val Phe Ala Pro Lys Phe Ile Phe		
1040	1045	1050
Glu Ala Val Gly Phe Ile Val Ser Ser Val Gly Leu Leu Leu Gly		
1055	1060	1065
Ile Ala Leu Val Met Arg Val Asp Gly Ala Val Ser Ser Trp Phe		
1070	1075	1080
Arg Gln Leu Phe Leu Ala Gln Gln Arg		
1085		

<210> 103

<211> 1743

<212> DNA

<213> Homo sapiens

<400> 103

```

tgccgctgcc gccgctgctg ctgttgctcc tggcggcgcc ttggggacgg 50
gcagttccct gtgtctctgg tggtttgctt aaacctgcaa acatcacctt 100
cttatccatc aacatgaaga atgtcctaca atggactcca ccagagggtc 150
ttcaaggagt taaagttact tacactgtgc agtatttcat cacaaattgg 200
cccaccagag gtggcactga ctacagatga gaagtccatt tctgttgtcc 250
tgacagctcc agagaagtgg aagagaaatc cagaagacct tcctgtttcc 300
atgcaacaaa tatactccaa tctgaagtat aacgtgtctg tgttgaatac 350
taaatcaaac agaactgggt cccagtgtgt gaccaaccac acgctggtgc 400
tcacctggct ggagccgaac actctttact gcgtacacgt ggagtccttc 450
gtcccagggc ccctcgccg tgcctcagct tctgagaagc agtgtgccag 500
gactttgaaa gatcaatcat cagagttcaa ggctaaaatc atcttctggt 550
atgttttgcc catatctatt accgtgtttc ttttttctgt gatgggctat 600
tccatctacc gatatatcca cgttggcaaa gagaaacacc cagcaaattt 650
gattttgatt tatggaaatg aatttgacaa aagattcttt gtgcctgctg 700
aaaaaatcgt gattaacttt atcacctca atatctcgga tgattctaaa 750
atttctcatc aggatatgag tttactggga aaaagcagtg atgtatccag 800
ccttaatgat cctcagccca gcgggaacct gaggccccct caggaggaag 850
aggaggtgaa acatttaggg tatgcttcgc atttgatgga aattttttgt 900

```

gactctgaag aaaacacgga aggtacttct ctcacccagc aagagtcctt 950  
cagcagaaca atacccccgg ataaaacagt cattgaatat gaatatgatg 1000  
tcagaaccac tgacatttgt gcggggcctg aagagcagga gctcagtttg 1050  
caggaggagg tgtccacaca aggaacatta ttggagtcgc aggagcggtt 1100  
ggcagtcttg ggcccgc aaa cggttacagta ctcatacacc cctcagctcc 1150  
aagacttaga cccctggcg caggagcaca cagactcgga ggaggggccg 1200  
gaggaagagc catcgacgac cctggtcgac tgggatcccc aaactggcag 1250  
gctgtgtatt ccttcgctgt ccagcttoga ccaggattca gagggctgcg 1300  
agccttctga gggggatggg ctcggagagg agggcttct atctagactc 1350  
tatgaggagc cggctccaga caggccacca ggagaaaatg aaacctatct 1400  
catgcaattc atggaggaat gggggttata tgtgcagatg gaaaactgat 1450  
gccaacactt ccttttgcct tttgtttcct gtgcaaaca gtgagtcacc 1500  
cctttgatcc cagccataaa gtacctggga tgaaagaagt tttttccagt 1550  
ttgtcagtgt ctgtgagaat tacttatttc ttttctctat tctcatagca 1600  
cgtgtgtgat tggttcatgc atgtaggtct cttacaatg atggtgggcc 1650  
tctggagtcc aggggctggc cggttgttct atgcagagaa agcagtcaat 1700  
aatgtttgc cagactgggt gcagaattta ttcaggtggg tgt 1743

<210> 104

<211> 442

<212> PRT

<213> Homo sapiens

<400> 104

Met	Ser	Tyr	Asn	Gly	Leu	His	Gln	Arg	Val	Phe	Lys	Glu	Leu	Lys
1				5					10					15
Leu	Leu	Thr	Leu	Cys	Ser	Ile	Ser	Ser	Gln	Ile	Gly	Pro	Pro	Glu
				20					25					30
Val	Ala	Leu	Thr	Thr	Asp	Glu	Lys	Ser	Ile	Ser	Val	Val	Leu	Thr
				35					40					45
Ala	Pro	Glu	Lys	Trp	Lys	Arg	Asn	Pro	Glu	Asp	Leu	Pro	Val	Ser
				50					55					60
Met	Gln	Gln	Ile	Tyr	Ser	Asn	Leu	Lys	Tyr	Asn	Val	Ser	Val	Leu
				65					70					75
Asn	Thr	Lys	Ser	Asn	Arg	Thr	Trp	Ser	Gln	Cys	Val	Thr	Asn	His
				80					85					90

Thr	Leu	Val	Leu	Thr	Trp	Leu	Glu	Pro	Asn	Thr	Leu	Tyr	Cys	Val	95	100	105
His	Val	Glu	Ser	Phe	Val	Pro	Gly	Pro	Pro	Arg	Arg	Ala	Gln	Pro	110	115	120
Ser	Glu	Lys	Gln	Cys	Ala	Arg	Thr	Leu	Lys	Asp	Gln	Ser	Ser	Glu	125	130	135
Phe	Lys	Ala	Lys	Ile	Ile	Phe	Trp	Tyr	Val	Leu	Pro	Ile	Ser	Ile	140	145	150
Thr	Val	Phe	Leu	Phe	Ser	Val	Met	Gly	Tyr	Ser	Ile	Tyr	Arg	Tyr	155	160	165
Ile	His	Val	Gly	Lys	Glu	Lys	His	Pro	Ala	Asn	Leu	Ile	Leu	Ile	170	175	180
Tyr	Gly	Asn	Glu	Phe	Asp	Lys	Arg	Phe	Phe	Val	Pro	Ala	Glu	Lys	185	190	195
Ile	Val	Ile	Asn	Phe	Ile	Thr	Leu	Asn	Ile	Ser	Asp	Asp	Ser	Lys	200	205	210
Ile	Ser	His	Gln	Asp	Met	Ser	Leu	Leu	Gly	Lys	Ser	Ser	Asp	Val	215	220	225
Ser	Ser	Leu	Asn	Asp	Pro	Gln	Pro	Ser	Gly	Asn	Leu	Arg	Pro	Pro	230	235	240
Gln	Glu	Glu	Glu	Glu	Val	Lys	His	Leu	Gly	Tyr	Ala	Ser	His	Leu	245	250	255
Met	Glu	Ile	Phe	Cys	Asp	Ser	Glu	Glu	Asn	Thr	Glu	Gly	Thr	Ser	260	265	270
Leu	Thr	Gln	Gln	Glu	Ser	Leu	Ser	Arg	Thr	Ile	Pro	Pro	Asp	Lys	275	280	285
Thr	Val	Ile	Glu	Tyr	Glu	Tyr	Asp	Val	Arg	Thr	Thr	Asp	Ile	Cys	290	295	300
Ala	Gly	Pro	Glu	Glu	Gln	Glu	Leu	Ser	Leu	Gln	Glu	Glu	Val	Ser	305	310	315
Thr	Gln	Gly	Thr	Leu	Leu	Glu	Ser	Gln	Ala	Ala	Leu	Ala	Val	Leu	320	325	330
Gly	Pro	Gln	Thr	Leu	Gln	Tyr	Ser	Tyr	Thr	Pro	Gln	Leu	Gln	Asp	335	340	345
Leu	Asp	Pro	Leu	Ala	Gln	Glu	His	Thr	Asp	Ser	Glu	Glu	Gly	Pro	350	355	360
Glu	Glu	Glu	Pro	Ser	Thr	Thr	Leu	Val	Asp	Trp	Asp	Pro	Gln	Thr	365	370	375

Gly Arg Leu Cys Ile Pro Ser Leu Ser Ser Phe Asp Gln Asp Ser  
380 385 390

Glu Gly Cys Glu Pro Ser Glu Gly Asp Gly Leu Gly Glu Glu Gly  
395 400 405

Leu Leu Ser Arg Leu Tyr Glu Glu Pro Ala Pro Asp Arg Pro Pro  
410 415 420

Gly Glu Asn Glu Thr Tyr Leu Met Gln Phe Met Glu Glu Trp Gly  
425 430 435

Leu Tyr Val Gln Met Glu Asn  
440

<210> 105

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 105

cgctgctgct gttgctcctg g 21

<210> 106

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 106

cagtgtgccca ggactttg 18

<210> 107

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 107

agtcgcaggc agcgttgg 18

<210> 108

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 108

ctcctccgag tctgtgtgct cctgc 25

<210> 109

<211> 51

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 109

ggacgggcag ttccctgtgt ctctggtggt ttgcctaaac ctgcaaacad 50

c 51

<210> 110

<211> 1114

<212> DNA

<213> Homo sapiens

<400> 110

cggacgcgtg ggccgacgcg tgggcggacg cgtgggtctc tgcggggaga 50

cgccagcctg cgtctgccat ggggctcggg ttgaggggct ggggacgtcc 100

tctgctgact gtggccaccg ccctgatgct gcccgtaag cccccgcag 150

gtcctgggg ggcccagatc atcgggggcc acgaggtgac cccccactcc 200

agggcctaca tggcatccgt gcgcttcggg ggccaacatc actgcggagg 250

cttcctgctg cgagcccgtg ggggtgtctc ggccgcccac tgcttcagcc 300

acagagacct ccgactggc ctggtggtgc tgggcgcca cgtcctgagt 350

actgcggagc ccaccagca ggtgtttggc atcgatgctc tcaccacgca 400

ccccgactac caccatga cccacgcaa cgacatctgc ctgctgcggc 450

tgaacggctc tgctgtcctg ggccctgcag tggggctgct gaggctgcca 500

gggagaaggg ccaggcccc cacagcggg acacggtgcc gggaggctgg 550

ctggggcttc gtgtctgact ttgaggagct gccgcctgga ctgatggagg 600

ccaaggctcg agtgctggac ccggacgtct gcaacagctc ctggaagggc 650

cacctgacac ttaccatgct ctgcacccgc agtggggaca gccacagacg 700

gggcttctgc tcggccgact ccggagggcc cctggtgtgc aggaaccggg 750

ctcacggcct cgtttccttc tcgggcctct ggtgcggcga cccaagacc 800

cccgaagtgt acacgcaggt gtccgccttt gtggcctgga tctgggacgt 850

ggttcggcgg agcagtcacc agcccgccc cctgcctggg accaccaggc 900

ccccaggaga agccgcctga gccacaacct tgcggcatgc aaatgagatg 950  
 gccgctccag gcctggaatg ttccgtggct gggcccccacg ggaagcctga 1000  
 tgttcagggt tggggtggga cgggcagcgg tggggcacac ccattccaca 1050  
 tgcaaagggc agaagcaaac ccagtaaaat gttaactgac aaaaaaaaaa 1100  
 aaaaaaaaaa gaaa 1114

<210> 111  
 <211> 283  
 <212> PRT  
 <213> Homo sapiens

<400> 111  
 Met Gly Leu Gly Leu Arg Gly Trp Gly Arg Pro Leu Leu Thr Val  
 1 5 10 15  
 Ala Thr Ala Leu Met Leu Pro Val Lys Pro Pro Ala Gly Ser Trp  
 20 25 30  
 Gly Ala Gln Ile Ile Gly Gly His Glu Val Thr Pro His Ser Arg  
 35 40 45  
 Pro Tyr Met Ala Ser Val Arg Phe Gly Gly Gln His His Cys Gly  
 50 55 60  
 Gly Phe Leu Leu Arg Ala Arg Trp Val Val Ser Ala Ala His Cys  
 65 70 75  
 Phe Ser His Arg Asp Leu Arg Thr Gly Leu Val Val Leu Gly Ala  
 80 85 90  
 His Val Leu Ser Thr Ala Glu Pro Thr Gln Gln Val Phe Gly Ile  
 95 100 105  
 Asp Ala Leu Thr Thr His Pro Asp Tyr His Pro Met Thr His Ala  
 110 115 120  
 Asn Asp Ile Cys Leu Leu Arg Leu Asn Gly Ser Ala Val Leu Gly  
 125 130 135  
 Pro Ala Val Gly Leu Leu Arg Leu Pro Gly Arg Arg Ala Arg Pro  
 140 145 150  
 Pro Thr Ala Gly Thr Arg Cys Arg Val Ala Gly Trp Gly Phe Val  
 155 160 165  
 Ser Asp Phe Glu Glu Leu Pro Pro Gly Leu Met Glu Ala Lys Val  
 170 175 180  
 Arg Val Leu Asp Pro Asp Val Cys Asn Ser Ser Trp Lys Gly His  
 185 190 195  
 Leu Thr Leu Thr Met Leu Cys Thr Arg Ser Gly Asp Ser His Arg



	200		205		210
Arg Gly Phe Cys	Ser Ala Asp Ser Gly	Gly Pro Leu Val Cys	Arg		
	215	220	225		
Asn Arg Ala His	Gly Leu Val Ser Phe	Ser Gly Leu Trp Cys	Gly		
	230	235	240		
Asp Pro Lys Thr	Pro Asp Val Tyr Thr	Gln Val Ser Ala Phe	Val		
	245	250	255		
Ala Trp Ile Trp	Asp Val Val Arg Arg	Ser Ser Pro Gln Pro	Gly		
	260	265	270		
Pro Leu Pro Gly	Thr Thr Arg Pro Pro	Gly Glu Ala Ala			
	275	280			

<210> 112

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 112

gacgtctgca acagctcctg gaag 24

<210> 113

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 113

cgagaaggaa acgaggccgt gag 23

<210> 114

<211> 44

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 114

tgacacttac catgctctgc acccgcagtg gggacagcca caga 44

<210> 115

<211> 1808

<212> DNA

<213> Homo sapiens

<400> 115

gagctacca ggcggctggt gtgcagcaag ctccgcgccg actccggacg 50

cctgacgcct gacgcctgtc cccggcccgg catgagccgc tacctgctgc 100  
cgctgtcggc gctgggcacg gtagcaggcg ccgccgtgct gctcaaggac 150  
tatgtcaccg gtggggcttg ccccagcaag gccaccatcc ctgggaagac 200  
ggtcacgtg acggggcgcca acacaggcat cgggaagcag accgccttgg 250  
aactggccag gagaggaggc aacatcatcc tggcctgccg agacatggag 300  
aagtgtgagg cggcagcaaa ggacatccgc ggggagaccc tcaatcacca 350  
tgtcaacgcc cggcacctgg acttggttc cctcaagtct atccgagagt 400  
ttgcagcaaa gatcattgaa gaggaggagc gagtggacat tctaataaac 450  
aacgcgggtg tgatgcggtg cccccactgg accaccgagg acggcttcga 500  
gatgcagttt ggcgttaacc acctgggtca ctttctcttg acaaacttgc 550  
tgctggacaa gctgaaagcc tcagcccctt cgcggatcat caacctctcg 600  
tccctggccc atgttgctgg gcacatagac tttgacgact tgaactggca 650  
gacgaggaag tataacacca aagccgccta ctgccagagc aagctcgcca 700  
tcgtctctt caccaaggag ctgagccggc ggctgcaagg ctctggtgtg 750  
actgtcaacg ccctgcaccc cggcgtggcc aggacagagc tgggcagaca 800  
cacgggcac catggctcca cttctccag caccacactc gggcccatct 850  
tctggctgct ggtcaagagc cccgagctgg ccgccagcc cagcacatac 900  
ctggccgtgg cggaggaact ggcggatgtt tccggaaagt acttcgatgg 950  
actcaaacag aaggccccgg cccccgaggc tgaggatgag gaggtggccc 1000  
ggaggctttg ggctgaaagt gccgcctgg tgggcttaga ggctccctct 1050  
gtgagggagc agccctccc cagataacct ctggagcaga ttgaaagcc 1100  
aggatggcgc ctccagaccg aggacagctg tccgccatgc ccgcagcttc 1150  
ctggcactac ctgagccggg agaccagga ctggcgccg ccatgcccgc 1200  
agtaggttct agggggcggg gctggccgca gtggactggc ctgcaggtga 1250  
gcactgcccc gggctctggc tggttccgtc tgctctgctg ccagcagggg 1300  
agaggggcca tctgatgctt cccctgggaa tctaaactgg gaatggccga 1350  
ggaggaaggg gctctgtgca cttgcaggcc acgtcaggag agccagcggg 1400  
gcctgtcggg gagggttcca aggtgctccg tgaagagcat gggcaagttg 1450

tctgacactt ggtggattct tgggtccctg tgggaccttg tgcattgcatg 1500  
gtcctctctg agccttggtt tcttcagcag tgagatgctc agaataactg 1550  
ctgtctccca tgatgggtgtg gtacagcgag ctgttgctctg gctatggcat 1600  
ggctgtgccg ggggtgtttg ctgagggctt cctgtgccag agcccagcca 1650  
gagagcaggt gcaggtgtca tcccagagttc aggctctgca cggcatggag 1700  
tggaacccc accagctgct gctacaggac ctgggattgc ctgggactcc 1750  
caccttcta tcaattctca tggtagtcca aactgcagac tctcaaactt 1800  
gctcattt 1808

<210> 116

<211> 331

<212> PRT

<213> Homo sapiens

<400> 116

Met	Ser	Arg	Tyr	Leu	Leu	Pro	Leu	Ser	Ala	Leu	Gly	Thr	Val	Ala	1	5	10	15
Gly	Ala	Ala	Val	Leu	Leu	Lys	Asp	Tyr	Val	Thr	Gly	Gly	Ala	Cys	20	25	30	
Pro	Ser	Lys	Ala	Thr	Ile	Pro	Gly	Lys	Thr	Val	Ile	Val	Thr	Gly	35	40	45	
Ala	Asn	Thr	Gly	Ile	Gly	Lys	Gln	Thr	Ala	Leu	Glu	Leu	Ala	Arg	50	55	60	
Arg	Gly	Gly	Asn	Ile	Ile	Leu	Ala	Cys	Arg	Asp	Met	Glu	Lys	Cys	65	70	75	
Glu	Ala	Ala	Ala	Lys	Asp	Ile	Arg	Gly	Glu	Thr	Leu	Asn	His	His	80	85	90	
Val	Asn	Ala	Arg	His	Leu	Asp	Leu	Ala	Ser	Leu	Lys	Ser	Ile	Arg	95	100	105	
Glu	Phe	Ala	Ala	Lys	Ile	Ile	Glu	Glu	Glu	Glu	Arg	Val	Asp	Ile	110	115	120	
Leu	Ile	Asn	Asn	Ala	Gly	Val	Met	Arg	Cys	Pro	His	Trp	Thr	Thr	125	130	135	
Glu	Asp	Gly	Phe	Glu	Met	Gln	Phe	Gly	Val	Asn	His	Leu	Gly	His	140	145	150	
Phe	Leu	Leu	Thr	Asn	Leu	Leu	Leu	Asp	Lys	Leu	Lys	Ala	Ser	Ala	155	160	165	
Pro	Ser	Arg	Ile	Ile	Asn	Leu	Ser	Ser	Leu	Ala	His	Val	Ala	Gly	170	175	180	

His	Ile	Asp	Phe	Asp	Asp	Leu	Asn	Trp	Gln	Thr	Arg	Lys	Tyr	Asn	
				185					190					195	
Thr	Lys	Ala	Ala	Tyr	Cys	Gln	Ser	Lys	Leu	Ala	Ile	Val	Leu	Phe	
				200					205					210	
Thr	Lys	Glu	Leu	Ser	Arg	Arg	Leu	Gln	Gly	Ser	Gly	Val	Thr	Val	
				215					220					225	
Asn	Ala	Leu	His	Pro	Gly	Val	Ala	Arg	Thr	Glu	Leu	Gly	Arg	His	
				230					235					240	
Thr	Gly	Ile	His	Gly	Ser	Thr	Phe	Ser	Ser	Thr	Thr	Leu	Gly	Pro	
				245					250					255	
Ile	Phe	Trp	Leu	Leu	Val	Lys	Ser	Pro	Glu	Leu	Ala	Ala	Gln	Pro	
				260					265					270	
Ser	Thr	Tyr	Leu	Ala	Val	Ala	Glu	Glu	Leu	Ala	Asp	Val	Ser	Gly	
				275					280					285	
Lys	Tyr	Phe	Asp	Gly	Leu	Lys	Gln	Lys	Ala	Pro	Ala	Pro	Glu	Ala	
				290					295					300	
Glu	Asp	Glu	Glu	Val	Ala	Arg	Arg	Leu	Trp	Ala	Glu	Ser	Ala	Arg	
				305					310					315	
Leu	Val	Gly	Leu	Glu	Ala	Pro	Ser	Val	Arg	Glu	Gln	Pro	Leu	Pro	
				320					325					330	

Arg

<210> 117  
 <211> 2249  
 <212> DNA  
 <213> Homo sapiens

<400> 117  
 gaagttcgcg agcgctggca tgtggctctg gggcgcggtt ggcggcgctg 50  
 ctggcggtgc tggcgctcgg gacaggagac ccagaaaggg ctgcggctcg 100  
 gggcgacacg ttctcggcgc tgaccagcgt ggcgcgcgcc ctggcgcccg 150  
 agcgccggct gctggggctg ctgaggcgtt acctgcgcgg ggaggaggcg 200  
 cggctgcggg acctgactag attctacgac aaggctactt ctttgcata 250  
 ggattcaaca acccctgtgg ctaaccctct gcttgcattt actctcatca 300  
 aacgcctgca gtctgactgg aggaatgtgg tacatagtct ggaggccagt 350  
 gagaacatcc gagctctgaa ggatggctat gagaagggtg agcaagacct 400  
 tccagccttt gaggaccttg agggagcagc aagggccctg atgcggctgc 450

aggacgtgta catgctcaat gtgaaaggcc tggcccagg tgtctttcag 500  
agagtcaactg gctctgccat cactgacctg tacagcccca aacggctctt 550  
ttctctcaca ggggatgact gcttccaagt tggcaagggtg gcctatgaca 600  
tgggggatta ttaccatgcc attccatggc tggaggaggc tgtcagtctc 650  
ttccgaggat cttacggaga gtggaagaca gaggatgagg caagtctaga 700  
agatgccttg gatcacttgg cctttgctta tttccgggca ggaaatgttt 750  
cgtgtgccct cagcctctct cgggagtttc ttctctacag cccagataat 800  
aagaggatgg ccaggaatgt cttgaaatat gaaaggctct tggcagagag 850  
ccccaaccac gtggtagctg aggtgtcat ccagaggccc aatatacccc 900  
acctgcagac cagagacacc tacgaggggc tatgtcagac cctgggttcc 950  
cagcccactg tctaccagat ccctagcctc tactgttctt atgagaccaa 1000  
ttccaacgcc tacctgctgc tccagcccat ccggaaggag gtcattccacc 1050  
tggagcccta cattgctctc taccatgact tcgtcagtga ctcagaggct 1100  
cagaaaatta gagaacttgc agaaccatgg ctacagaggt cagtgggtggc 1150  
atcaggggag aagcagttac aagtggagta ccgcatcagc aaaagtcct 1200  
ggctgaagga cactgttgac caaaaactgg tgaccctcaa ccaccgcatt 1250  
gctgccctca caggccttga tgtccggcct ccctatgcag agtatctgca 1300  
ggtggtgaac tatggcatcg gaggacacta tgagcctcac tttgaccatg 1350  
ctacgtcacc aagcagcccc ctctacagaa tgaagtcagg aaaccgagtt 1400  
gcaacattta tgatctatct gagctcgggtg gaagctggag gagccacagc 1450  
cttcacttat gccaacctca gcgtgcctgt ggtaggaat gcagcactgt 1500  
tttggtggaa cctgcacagg agtgggtgaag gggacagtga cacacttcat 1550  
gctggctgtc ctgtcctggg gggagataag tgggtggcca acaagtggat 1600  
acatgagtat ggacaggaat tccgcagacc ctgcagctcc agccctgaag 1650  
actgaactgt tggcagagag aagctggtgg agtcctgtgg ctttccagag 1700  
aagccaggag ccaaaagctg gggtaggaga ggagaaagca gagcagcctc 1750  
ctggaagaag gccttgtcag ctttgtctgt gcctcgcaaa tcagaggcaa 1800  
gggagagggt gttaccaggg gacactgaga atgtacattt gatctgcccc 1850

agccacggaa gtcagagtag gatgcacagt acaaaggagg ggggagtgga 1900  
 ggcctgagag ggaagtttct ggagttcaga tactctctgt tgggaacagg 1950  
 acatctcaac agtctcaggt tcgatcagtg ggtcttttgg cactttgaac 2000  
 cttgaccaca gggaccaaga agtggcaatg aggacacctg caggaggggc 2050  
 tagcctgact cccagaactt taagactttc tccccactgc cttctgctgc 2100  
 agcccaagca gggagtgtcc ccctcccaga agcatatccc agatgagtgg 2150  
 tacattatat aaggattttt tttaagttga aaacaacttt cttttctttt 2200  
 tgtatgatgg tttttaaca cagtcattaa aaatgtttat aaatcaaaa 2249

<210> 118

<211> 544

<212> PRT

<213> Homo sapiens

<400> 118

Met	Gly	Pro	Gly	Ala	Arg	Leu	Ala	Ala	Leu	Leu	Ala	Val	Leu	Ala	1	5	10	15
Leu	Gly	Thr	Gly	Asp	Pro	Glu	Arg	Ala	Ala	Ala	Arg	Gly	Asp	Thr	20	25	30	
Phe	Ser	Ala	Leu	Thr	Ser	Val	Ala	Arg	Ala	Leu	Ala	Pro	Glu	Arg	35	40	45	
Arg	Leu	Leu	Gly	Leu	Leu	Arg	Arg	Tyr	Leu	Arg	Gly	Glu	Glu	Ala	50	55	60	
Arg	Leu	Arg	Asp	Leu	Thr	Arg	Phe	Tyr	Asp	Lys	Val	Leu	Ser	Leu	65	70	75	
His	Glu	Asp	Ser	Thr	Thr	Pro	Val	Ala	Asn	Pro	Leu	Leu	Ala	Phe	80	85	90	
Thr	Leu	Ile	Lys	Arg	Leu	Gln	Ser	Asp	Trp	Arg	Asn	Val	Val	His	95	100	105	
Ser	Leu	Glu	Ala	Ser	Glu	Asn	Ile	Arg	Ala	Leu	Lys	Asp	Gly	Tyr	110	115	120	
Glu	Lys	Val	Glu	Gln	Asp	Leu	Pro	Ala	Phe	Glu	Asp	Leu	Glu	Gly	125	130	135	
Ala	Ala	Arg	Ala	Leu	Met	Arg	Leu	Gln	Asp	Val	Tyr	Met	Leu	Asn	140	145	150	
Val	Lys	Gly	Leu	Ala	Arg	Gly	Val	Phe	Gln	Arg	Val	Thr	Gly	Ser	155	160	165	
Ala	Ile	Thr	Asp	Leu	Tyr	Ser	Pro	Lys	Arg	Leu	Phe	Ser	Leu	Thr	170	175	180	

Gly Asp Asp Cys Phe Gln Val Gly Lys Val Ala Tyr Asp Met Gly	185	190	195
Asp Tyr Tyr His Ala Ile Pro Trp Leu Glu Glu Ala Val Ser Leu	200	205	210
Phe Arg Gly Ser Tyr Gly Glu Trp Lys Thr Glu Asp Glu Ala Ser	215	220	225
Leu Glu Asp Ala Leu Asp His Leu Ala Phe Ala Tyr Phe Arg Ala	230	235	240
Gly Asn Val Ser Cys Ala Leu Ser Leu Ser Arg Glu Phe Leu Leu	245	250	255
Tyr Ser Pro Asp Asn Lys Arg Met Ala Arg Asn Val Leu Lys Tyr	260	265	270
Glu Arg Leu Leu Ala Glu Ser Pro Asn His Val Val Ala Glu Ala	275	280	285
Val Ile Gln Arg Pro Asn Ile Pro His Leu Gln Thr Arg Asp Thr	290	295	300
Tyr Glu Gly Leu Cys Gln Thr Leu Gly Ser Gln Pro Thr Leu Tyr	305	310	315
Gln Ile Pro Ser Leu Tyr Cys Ser Tyr Glu Thr Asn Ser Asn Ala	320	325	330
Tyr Leu Leu Leu Gln Pro Ile Arg Lys Glu Val Ile His Leu Glu	335	340	345
Pro Tyr Ile Ala Leu Tyr His Asp Phe Val Ser Asp Ser Glu Ala	350	355	360
Gln Lys Ile Arg Glu Leu Ala Glu Pro Trp Leu Gln Arg Ser Val	365	370	375
Val Ala Ser Gly Glu Lys Gln Leu Gln Val Glu Tyr Arg Ile Ser	380	385	390
Lys Ser Ala Trp Leu Lys Asp Thr Val Asp Pro Lys Leu Val Thr	395	400	405
Leu Asn His Arg Ile Ala Ala Leu Thr Gly Leu Asp Val Arg Pro	410	415	420
Pro Tyr Ala Glu Tyr Leu Gln Val Val Asn Tyr Gly Ile Gly Gly	425	430	435
His Tyr Glu Pro His Phe Asp His Ala Thr Ser Pro Ser Ser Pro	440	445	450
Leu Tyr Arg Met Lys Ser Gly Asn Arg Val Ala Thr Phe Met Ile	455	460	465

Tyr Leu Ser Ser Val Glu Ala Gly Gly Ala Thr Ala Phe Ile Tyr  
470 475 480

Ala Asn Leu Ser Val Pro Val Val Arg Asn Ala Ala Leu Phe Trp  
485 490 495

Trp Asn Leu His Arg Ser Gly Glu Gly Asp Ser Asp Thr Leu His  
500 505 510

Ala Gly Cys Pro Val Leu Val Gly Asp Lys Trp Val Ala Asn Lys  
515 520 525

Trp Ile His Glu Tyr Gly Gln Glu Phe Arg Arg Pro Cys Ser Ser  
530 535 540

Ser Pro Glu Asp

<210> 119

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 119

cgggacagga gacccagaaa ggg 23

<210> 120

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 120

ggccaagtga tccaaggcat cttc 24

<210> 121

<211> 49

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 121

ctgcgggacc tgactagatt ctacgacaag gtacttttctt tgcattgggg 49

<210> 122

<211> 1778

<212> DNA

<213> Homo sapiens



<400> 122

gagatagggga gtctggggttt aagtccctgc tccatctcag gagccccctgc 50  
tcccacccct aggaagccac cagactccac ggtgtggggc caatcagggtg 100  
gaatcgggcc tggcagggtg ggccacgagc gctggctgag ggaccgagcc 150  
ggagagcccc ggagcccccg taaccgcgc ggggagcgcc caggatgccg 200  
cgcggggact cggagcaggt gcgctactgc gcgcgcttct cctacctctg 250  
gctcaagttt tcacttatca tctattccac cgtgttctgg ctgattgggg 300  
ccctggtcct gtctgtgggc atctatgcag aggttgagcg gcagaaatat 350  
aaaacccttg aaagtgcctt cctggctcca gccatcatcc tcctcctcct 400  
ggcgctcgtc atgttcatgg tctccttcat tgggtgtgctg gcgtccctcc 450  
gtgacaacct gtaccttctc caagcattca tgtacatcct tgggatctgc 500  
ctcatcatgg agctcattgg tggcgtggtg gccttgacct tccggaacca 550  
gaccattgac ttctgaacg acaacattcg aagaggaatt gagaactact 600  
atgatgatct ggacttcaaa aacatcatgg actttgttca gaaaaagttc 650  
aagtgtgtg gcggggagga ctaccgagat tggagcaaga atcagtacca 700  
cgactgcagt gccctggac ccctggcctg tggggtgcc tacacctgct 750  
gcatcaggaa cagcacagaa gttgtcaaca ccatgtgtgg ctacaaaact 800  
atcgacaagg agcgtttcag tgtgcaggat gtcacttacg tgcggggctg 850  
caccaacgcc gtgatcatct ggttcatgga caactacacc atcatggcgt 900  
gcatcctcct gggcatcctg cttccccagt tctgggggt gctgctgacg 950  
ctgctgtaca taccgggt ggaggacatc atcatggagc actctgtcac 1000  
tgatgggctc ctggggcccc gtgccaaagg cagcgtggag gcggcaggca 1050  
cgggatgctg cttgtgtac cccaattagg gccagcctg ccatggcagc 1100  
tccaacaagg accgtctggg atagcacctc tcagtcaaca tcgtggggct 1150  
ggacagggt gcggccctc tgcccacact cagtactgac caaagccagg 1200  
gctgtgtgtg cctgtgtgta ggtcccacgg cctctgcctc ccaggggagc 1250  
agagcctggg cctcccctaa gaggtttcc ccgaggcagc tctggaatct 1300  
gtgcccacct ggggcctggg gaacaaggcc ctctttctc caggcctggg 1350  
ctacagggga gggagagcct gaggtctctg tcagggccca tttcatctct 1400

ggcagtgcct tggcgggtggt attcaaggca gttttgtagc acctgtaatt 1450  
 ggggagaggg agtgtgcccc tcggggcagg agggaagggc atctggggaa 1500  
 gggcaggagg gaagagctgt ccatgcagcc acgcccattg ccagggtggc 1550  
 ctcttctcag cctcccaggt gccttgagcc ctcttgcaag ggcggctgct 1600  
 tccttgagcc tagttttttt ttacgtgatt tttgtaacat tcattttttt 1650  
 gtacagataa caggagtttc tgactaatca aagctgggat ttccccgcat 1700  
 gtcttattct tgcccttccc ccaaccagtt tgttaatcaa acaataaaaa 1750  
 catgttttgt tttgttttta aaaaaaaaa 1778

<210> 123

<211> 294

<212> PRT

<213> Homo sapiens

<400> 123

Met	Pro	Arg	Gly	Asp	Ser	Glu	Gln	Val	Arg	Tyr	Cys	Ala	Arg	Phe
1				5					10					15
Ser	Tyr	Leu	Trp	Leu	Lys	Phe	Ser	Leu	Ile	Ile	Tyr	Ser	Thr	Val
				20					25					30
Phe	Trp	Leu	Ile	Gly	Ala	Leu	Val	Leu	Ser	Val	Gly	Ile	Tyr	Ala
				35					40					45
Glu	Val	Glu	Arg	Gln	Lys	Tyr	Lys	Thr	Leu	Glu	Ser	Ala	Phe	Leu
				50					55					60
Ala	Pro	Ala	Ile	Ile	Leu	Ile	Leu	Leu	Gly	Val	Val	Met	Phe	Met
				65					70					75
Val	Ser	Phe	Ile	Gly	Val	Leu	Ala	Ser	Leu	Arg	Asp	Asn	Leu	Tyr
				80					85					90
Leu	Leu	Gln	Ala	Phe	Met	Tyr	Ile	Leu	Gly	Ile	Cys	Leu	Ile	Met
				95					100					105
Glu	Leu	Ile	Gly	Gly	Val	Val	Ala	Leu	Thr	Phe	Arg	Asn	Gln	Thr
				110					115					120
Ile	Asp	Phe	Leu	Asn	Asp	Asn	Ile	Arg	Arg	Gly	Ile	Glu	Asn	Tyr
				125					130					135
Tyr	Asp	Asp	Leu	Asp	Phe	Lys	Asn	Ile	Met	Asp	Phe	Val	Gln	Lys
				140					145					150
Lys	Phe	Lys	Cys	Cys	Gly	Gly	Glu	Asp	Tyr	Arg	Asp	Trp	Ser	Lys
				155					160					165
Asn	Gln	Tyr	His	Asp	Cys	Ser	Ala	Pro	Gly	Pro	Leu	Ala	Cys	Gly

170	175	180
Val Pro Tyr Thr Cys Cys Ile Arg Asn Thr Thr Glu Val Val Asn		
185	190	195
Thr Met Cys Gly Tyr Lys Thr Ile Asp Lys Glu Arg Phe Ser Val		
200	205	210
Gln Asp Val Ile Tyr Val Arg Gly Cys Thr Asn Ala Val Ile Ile		
215	220	225
Trp Phe Met Asp Asn Tyr Thr Ile Met Ala Cys Ile Leu Leu Gly		
230	235	240
Ile Leu Leu Pro Gln Phe Leu Gly Val Leu Leu Thr Leu Leu Tyr		
245	250	255
Ile Thr Arg Val Glu Asp Ile Ile Met Glu His Ser Val Thr Asp		
260	265	270
Gly Leu Leu Gly Pro Gly Ala Lys Pro Ser Val Glu Ala Ala Gly		
275	280	285
Thr Gly Cys Cys Leu Cys Tyr Pro Asn		
290		

<210> 124  
 <211> 25  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 124  
 atcatctatt ccaccgtgtt ctggc 25

<210> 125  
 <211> 25  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 125  
 gacagagtgc tccatgatga tgtcc 25

<210> 126  
 <211> 50  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 126

cctgtctgtg ggcatttatg cagaggttga gcggcagaaa tataaaaccc 50

<210> 127

<211> 1636

<212> DNA

<213> Homo sapiens

<400> 127

gaggagcggg ccgaggactc cagcgtgccc aggtctggca tctgcactt 50  
gctgccctct gacacctggg aagatggccg gcccgaggac cttaccctt 100  
ctctgtggtt tgctggcagc caccttgatc caagccaccc tcagtccac 150  
tgcagttctc atcctcggcc caaaagtcac caaagaaaag ctgacacagg 200  
agctgaagga ccacaacgcc accagcatcc tgcagcagct gccgctgctc 250  
agtgccatgc gggaaaagcc agccggaggc atccctgtgc tgggcagcct 300  
ggtgaacacc gtctgaagc acatcatctg gctgaaggtc atcacagcta 350  
acatcctcca gctgcagggtg aagccctcgg ccaatgacca ggagctgcta 400  
gtcaagatcc ccctggacat ggtggctgga ttcaacacgc ccctggtaa 450  
gaccatcgtg gaggttccaca tgacgactga ggccaagcc accatccgca 500  
tggacaccag tgcaagtggc cccaccgcgc tggtcctcag tgactgtgcc 550  
accagccatg ggagcctgcg catccaactg ctgtataagc tctccttct 600  
ggtgaacgcc ttagctaagc aggtcatgaa cctcctagt ccatccctgc 650  
ccaatctagt gaaaaaccag ctgtgtcccg tgatcgaggc ttccttcaat 700  
ggcatgtatg cagacctcct gcagctgggtg aagggtgcca tttccctcag 750  
cattgaccgt ctggagtttg accttctgta tctgccatc aagggtgaca 800  
ccattcagct ctacctggg gccaaagtgt tggactcaca gggaaagggtg 850  
accaagtggg tcaataactc tgcagcttcc ctgacaatgc ccacctgga 900  
caacatcccg ttcagcctca tcgtgagtca ggacgtgggtg aaagctgcag 950  
tggctgctgt gctctctcca gaagaattca tggtcctgtt ggactctgtg 1000  
cttctgaga gtgcccatcg gctgaagtca agcatcgggc tgatcaatga 1050  
aaaggctgca gataagctgg gatctacca gatcgtgaag atcctaactc 1100  
aggacactcc cgagtttttt atagaccaag gccatgccaa ggtggcccaa 1150  
ctgatcgtgc tggaaagtgt tccctccagt gaagccctcc gccctttgtt 1200  
cacctgggc atcgaagcca gtcggaagc tcagttttac accaaagggtg 1250

accaacttat actcaacttg aataacatca gctctgatcg gatccagctg 1300  
 atgaactctg ggattggctg gttccaacct gatgttctga aaaacatcat 1350  
 cactgagatc atccactcca tctgtctgcc gaaccagaat ggcaaattaa 1400  
 gatctgggggt cccagtgtca ttggtgaagg ccttgggatt cgaggcagct 1450  
 gagtcctcac tgaccaagga tgcccttgctg cttactccag cctccttgctg 1500  
 gaaaccagc tctcctgtct cccagtgaag acttgatgg cagccatcag 1550  
 ggaaggctgg gtcccagctg ggagtatggg tgtgagctct atagaccatc 1600  
 cctctctgca atcaataaac acttgctgt gaaaaa 1636

<210> 128

<211> 484

<212> PRT

<213> Homo sapiens

<400> 128

Met	Ala	Gly	Pro	Trp	Thr	Phe	Thr	Leu	Leu	Cys	Gly	Leu	Leu	Ala
1				5					10					15

Ala	Thr	Leu	Ile	Gln	Ala	Thr	Leu	Ser	Pro	Thr	Ala	Val	Leu	Ile
			20						25					30

Leu	Gly	Pro	Lys	Val	Ile	Lys	Glu	Lys	Leu	Thr	Gln	Glu	Leu	Lys
			35						40					45

Asp	His	Asn	Ala	Thr	Ser	Ile	Leu	Gln	Gln	Leu	Pro	Leu	Leu	Ser
			50						55					60

Ala	Met	Arg	Glu	Lys	Pro	Ala	Gly	Gly	Ile	Pro	Val	Leu	Gly	Ser
			65						70					75

Leu	Val	Asn	Thr	Val	Leu	Lys	His	Ile	Ile	Trp	Leu	Lys	Val	Ile
			80						85					90

Thr	Ala	Asn	Ile	Leu	Gln	Leu	Gln	Val	Lys	Pro	Ser	Ala	Asn	Asp
			95						100					105

Gln	Glu	Leu	Leu	Val	Lys	Ile	Pro	Leu	Asp	Met	Val	Ala	Gly	Phe
			110						115					120

Asn	Thr	Pro	Leu	Val	Lys	Thr	Ile	Val	Glu	Phe	His	Met	Thr	Thr
			125						130					135

Glu	Ala	Gln	Ala	Thr	Ile	Arg	Met	Asp	Thr	Ser	Ala	Ser	Gly	Pro
			140						145					150

Thr	Arg	Leu	Val	Leu	Ser	Asp	Cys	Ala	Thr	Ser	His	Gly	Ser	Leu
			155						160					165

Arg Ile Gln Leu Leu Tyr Lys Leu Ser Phe Leu Val Asn Ala Leu

	170		175		180
Ala Lys Gln Val	Met Asn Leu Leu Val	Pro Ser Leu Pro Asn	Leu		
	185		190		195
Val Lys Asn Gln	Leu Cys Pro Val Ile	Glu Ala Ser Phe Asn	Gly		
	200		205		210
Met Tyr Ala Asp	Leu Leu Gln Leu Val	Lys Val Pro Ile Ser	Leu		
	215		220		225
Ser Ile Asp Arg	Leu Glu Phe Asp Leu	Leu Tyr Pro Ala Ile	Lys		
	230		235		240
Gly Asp Thr Ile	Gln Leu Tyr Leu Gly	Ala Lys Leu Leu Asp	Ser		
	245		250		255
Gln Gly Lys Val	Thr Lys Trp Phe Asn	Asn Ser Ala Ala Ser	Leu		
	260		265		270
Thr Met Pro Thr	Leu Asp Asn Ile Pro	Phe Ser Leu Ile Val	Ser		
	275		280		285
Gln Asp Val Val	Lys Ala Ala Val Ala	Ala Val Leu Ser Pro	Glu		
	290		295		300
Glu Phe Met Val	Leu Leu Asp Ser Val	Leu Pro Glu Ser Ala	His		
	305		310		315
Arg Leu Lys Ser	Ser Ile Gly Leu Ile	Asn Glu Lys Ala Ala	Asp		
	320		325		330
Lys Leu Gly Ser	Thr Gln Ile Val Lys	Ile Leu Thr Gln Asp	Thr		
	335		340		345
Pro Glu Phe Phe	Ile Asp Gln Gly His	Ala Lys Val Ala Gln	Leu		
	350		355		360
Ile Val Leu Glu	Val Phe Pro Ser Ser	Glu Ala Leu Arg Pro	Leu		
	365		370		375
Phe Thr Leu Gly	Ile Glu Ala Ser Ser	Glu Ala Gln Phe Tyr	Thr		
	380		385		390
Lys Gly Asp Gln	Leu Ile Leu Asn Leu	Asn Asn Ile Ser Ser	Asp		
	395		400		405
Arg Ile Gln Leu	Met Asn Ser Gly Ile	Gly Trp Phe Gln Pro	Asp		
	410		415		420
Val Leu Lys Asn	Ile Ile Thr Glu Ile	Ile His Ser Ile Leu	Leu		
	425		430		435
Pro Asn Gln Asn	Gly Lys Leu Arg Ser	Gly Val Pro Val Ser	Leu		
	440		445		450
Val Lys Ala Leu	Gly Phe Glu Ala Ala	Glu Ser Ser Leu Thr	Lys		

455

460

465

Asp Ala Leu Val Leu Thr Pro Ala Ser Leu Trp Lys Pro Ser Ser  
 470 475 480

Pro Val Ser Gln

<210> 129

<211> 2213

<212> DNA

<213> Homo sapiens

<400> 129

gagcgaacat ggcagcgcgt tggcggtttt ggtgtgtctc tgtgaccatg 50  
 gtggtggcgc tgctcatcgt ttgcgacgtt ccctcagcct ctgccc aaag 100  
 aaagaaggag atggtgttat ctgaaaagg tagtcagctg atggaatgga 150  
 ctaacaaaag acctgtaata agaataaatg gagacaagtt ccgtcgcctt 200  
 gtgaaagccc caccgagaaa ttactccgtt atcgatcatgt tcaactgctct 250  
 ccaactgcat agacagtgtg tcgtttgcaa gcaagctgat gaagaattcc 300  
 agatcctggc aaactcctgg cgatactcca gtgcattcac caacaggata 350  
 ttttttgcca tgggtggattt tgatgaaggc tctgatgtat ttcagatgct 400  
 aaacatgaat tcagctccaa ctttcatcaa ctttctctgca aaagggaaac 450  
 ccaaacgggg tgatacatat gagttacagg tgcgggggttt ttcagctgag 500  
 cagattgccc ggtggatcgc cgacagaact gatgtcaata ttagagtgat 550  
 tagaccccca aattatgctg gtccccttat gttgggattg cttttggctg 600  
 ttattgggtg acttgtgtat cttcgaagaa gtaatatgga atttctcttt 650  
 aataaaaactg gatgggcttt tgcagctttg tgttttgtgc ttgctatgac 700  
 atctggtcaa atgtggaacc atataagagg accaccatat gcccataaga 750  
 atccccacac gggacatgtg aattatatcc atggaagcag tcaagcccag 800  
 tttgtagctg aaacacacat tgttcttctg tttaatggtg gagttacctt 850  
 aggaatggtg cttttatgtg aagctgctac ctctgacatg gatattggaa 900  
 agcgaaagat aatgtgtgtg gctggtattg gacttggtgt attattcttc 950  
 agttggatgc tctctatttt tagatctaaa tatcatggct acccatacag 1000  
 ctttctgatg agttaaaaag gtcccagaga tatatagaca ctggagtact 1050  
 ggaaattgaa aaacgaaaat cgtgtgtggt tgaaaagaag aatgcaactt 1100

gtatatatttg tattacctct ttttttcaag tgatttaaag agttaatcat 1150  
 ttaaccaaag aagatgtgta gtgccttaac aagcaatcct ctgtcaaaat 1200  
 ctgaggtatt tgaaaataat tatcctctta accttctctt cccagtgaac 1250  
 tttatggaac atttaattta gtacaattaa gtatattata aaaattgtaa 1300  
 aactactact ttgttttagt tagaacaag ctcaaaacta ctttagtta 1350  
 cttggtcatc tgattttata ttgccttata caaagatggg gaaagtaagt 1400  
 cctgaccagg tggtcccaca tatgcctgtt acagataact acattaggaa 1450  
 ttcattctta gcttcttcat ctttgtgtgg atgtgtatac tttacgcac 1500  
 tttccttttg agtagagaaa ttatgtgtgt catgtggtct tctgaaaatg 1550  
 gaacaccatt cttcagagca cacgtctagc cctcagcaag acagttggtt 1600  
 ctctctctcc ttgcatattt cctactgcgc tccagcctga gtgatagagt 1650  
 gagactctgt ctcaaaaaaa agtatctcta aatacaggat tataatttct 1700  
 gcttgagtat ggtgttaact accttgtatt tagaaagatt tcagattcat 1750  
 tccatctcct tagttttctt ttaaggtgac ccatctgtga taaaaatata 1800  
 gcttagtgct aaaatcagtg taacttatac atggcctaaa atgtttctac 1850  
 aaattagagt ttgtcactta ttccatttgt acctaaagaga aaaataggct 1900  
 cagttagaaa aggactccct ggccaggcgc agtgacttac gcctgtaatc 1950  
 tcagcacttt gggaggccaa ggcaggcaga tcacgaggtc aggagttcga 2000  
 gaccatcttg gccaacatgg tgaaaccccg tctctactaa aaatataaaa 2050  
 attagctggg tgtggtggca ggagcctgta atcccagcta cacaggaggc 2100  
 tgaggcacga gaatcacttg aactcaggag atggaggttt cagtgaagccg 2150  
 agatcacgcc actgcactcc agcctggcaa cagagcgaga ctccatctca 2200  
 aaaaaaaaaa aaa 2213

<210> 130

<211> 335

<212> PRT

<213> Homo sapiens

<400> 130

Met	Ala	Ala	Arg	Trp	Arg	Phe	Trp	Cys	Val	Ser	Val	Thr	Met	Val
1				5					10				15	

Val Ala Leu Leu Ile Val Cys Asp Val Pro Ser Ala Ser Ala Gln



20										25					30				
Arg	Lys	Lys	Glu	Met	Val	Leu	Ser	Glu	Lys	Val	Ser	Gln	Leu	Met					
35										40					45				
Glu	Trp	Thr	Asn	Lys	Arg	Pro	Val	Ile	Arg	Met	Asn	Gly	Asp	Lys					
50										55					60				
Phe	Arg	Arg	Leu	Val	Lys	Ala	Pro	Pro	Arg	Asn	Tyr	Ser	Val	Ile					
65										70					75				
Val	Met	Phe	Thr	Ala	Leu	Gln	Leu	His	Arg	Gln	Cys	Val	Val	Cys					
80										85					90				
Lys	Gln	Ala	Asp	Glu	Glu	Phe	Gln	Ile	Leu	Ala	Asn	Ser	Trp	Arg					
95										100					105				
Tyr	Ser	Ser	Ala	Phe	Thr	Asn	Arg	Ile	Phe	Phe	Ala	Met	Val	Asp					
110										115					120				
Phe	Asp	Glu	Gly	Ser	Asp	Val	Phe	Gln	Met	Leu	Asn	Met	Asn	Ser					
125										130					135				
Ala	Pro	Thr	Phe	Ile	Asn	Phe	Pro	Ala	Lys	Gly	Lys	Pro	Lys	Arg					
140										145					150				
Gly	Asp	Thr	Tyr	Glu	Leu	Gln	Val	Arg	Gly	Phe	Ser	Ala	Glu	Gln					
155										160					165				
Ile	Ala	Arg	Trp	Ile	Ala	Asp	Arg	Thr	Asp	Val	Asn	Ile	Arg	Val					
170										175					180				
Ile	Arg	Pro	Pro	Asn	Tyr	Ala	Gly	Pro	Leu	Met	Leu	Gly	Leu	Leu					
185										190					195				
Leu	Ala	Val	Ile	Gly	Gly	Leu	Val	Tyr	Leu	Arg	Arg	Ser	Asn	Met					
200										205					210				
Glu	Phe	Leu	Phe	Asn	Lys	Thr	Gly	Trp	Ala	Phe	Ala	Ala	Leu	Cys					
215										220					225				
Phe	Val	Leu	Ala	Met	Thr	Ser	Gly	Gln	Met	Trp	Asn	His	Ile	Arg					
230										235					240				
Gly	Pro	Pro	Tyr	Ala	His	Lys	Asn	Pro	His	Thr	Gly	His	Val	Asn					
245										250					255				
Tyr	Ile	His	Gly	Ser	Ser	Gln	Ala	Gln	Phe	Val	Ala	Glu	Thr	His					
260										265					270				
Ile	Val	Leu	Leu	Phe	Asn	Gly	Gly	Val	Thr	Leu	Gly	Met	Val	Leu					
275										280					285				
Leu	Cys	Glu	Ala	Ala	Thr	Ser	Asp	Met	Asp	Ile	Gly	Lys	Arg	Lys					
290										295					300				
Ile	Met	Cys	Val	Ala	Gly	Ile	Gly	Leu	Val	Val	Leu	Phe	Phe	Ser					

	305		310		315
Trp Met Leu Ser Ile Phe Arg Ser Lys Tyr His Gly Tyr Pro Tyr					
	320		325		330
Ser Phe Leu Met Ser					
	335				

<210> 131

<211> 2476

<212> DNA

<213> Homo sapiens

<400> 131

```

aagcaaccaa actgcaagct ttgggagttg ttcgctgtcc ctgccctgct 50
ctgctaggga gagaacgcca gagggaggcg gctggcccgg cggcaggctc 100
tcagaaccgc taccggcgat gctactgctg tgggtgtcgg tggtcgcagc 150
cttggcgctg gcggtactgg ccccgaggagc aggggagcag aggcggagag 200
cagccaaagc gcccaatgtg gtgctggtcg tgagcgactc cttcgatgga 250
aggttaacat ttcattccagg aagtcaggta gtgaaacttc cttttatcaa 300
ctttatgaag acacgtggga cttcctttct gaatgcctac acaaactctc 350
caatttggtg cccatcacgc gcagcaatgt ggagtggcct cttcactcac 400
ttaacagaat cttggaataa ttttaagggc ctagatccaa attatacaac 450
atggatggat gtcatggaga ggcatggcta ccgaacacag aaatttgga 500
aactggacta tacttcagga catcactcca ttagtaatcg tgtggaagcg 550
tggaacaagag atgttgcttt cttactcaga caagaaggca ggcccatggt 600
taatcttatc cgtaacagga ctaaagtcag agtcatggaa agggattggc 650
agaatacaga caaagcagta aactgggtta gaaaggaagc aattaattac 700
actgaaccat ttgttattta cttgggatta aatttaccac acccttacct 750
ttcaccatct tctggagaaa attttggatc ttcaacattt cacacatctc 800
tttattggct tgaaaaagtg tctcatgatg ccatcaaaat cccaaagtgg 850
tcacctttgt cagaaatgca cctgtgatg tattactctt cttatacaaa 900
aaactgcact ggaagattta caaaaaaaga aattaagaat attagagcat 950
tttattatgc tatgtgtgct gagacagatg ccatgcttgg tgaaattatt 1000
ttggcccttc atcaattaga tcttcttcag aaaactattg tcatatactc 1050
ctcagaccat ggagagctgg ccatggaaca tcgacagttt tataaaatga 1100

```

gcattgtacga ggctagtgc catgttccgc ttttgatgat gggaccagga 1150  
attaaagccg gcctacaagt atcaaagtgtg gtttctcttg tggatattta 1200  
ccctaccatg cttgatattg ctggaattcc tctgcctcag aacctgagtg 1250  
gatactcttt gttgccgtta tcatcagaaa catttaagaa tgaacataaa 1300  
gtcaaaaacc tgcattccacc ctggattctg agtgaattcc atggatgtaa 1350  
tgtgaatgcc tccacctaca tgcttcgaac taaccactgg aaatatatag 1400  
cctattcgga tggatcatca atattgcctc aactctttga tctttcctcg 1450  
gatccagatg aattaacaaa tgttgctgta aaatttccag aaattactta 1500  
ttctttggat cagaagcttc attccattat aaactaccct aaagtttctg 1550  
cttctgtcca ccagtataat aaagagcagt ttatcaagtg gaaacaaagt 1600  
ataggacaga attattcaaa cgttatagca aatcttaggt ggcaccaaga 1650  
ctggcagaag gaaccaagga agtatgaaaa tgcaattgat cagtggctta 1700  
aaacccatat gaatccaaga gcagtttgaa caaaaagttt aaaaatagtg 1750  
ttctagagat acatataaat atattacaag atcataatta tgtattttta 1800  
atgaaacagt ttaataaatt accaagtttt ggccgggcac agtgggtcac 1850  
acctgtaatc ccaggacttt gggaggctga ggaaagcaga tcacaaggtc 1900  
aagagattga gaccatcctg gccaacatgg tgaaaccctg tctctactaa 1950  
aaatacaaaa attagctggg cgcggtggtg cacacctata gtctcagcta 2000  
ctcagaggct gaggcaggag gatcgcttga acccgggagg cagcagttgc 2050  
agtgaagctga gattgcgcca ctgtactcca gcctggcaac agagtgaagc 2100  
tgtgtcgcaa aaaaataaaa ataaaataat aataattacc aatttttcat 2150  
tattttgtaa gaatgtagtg tattttaaga taaaatgcca atgattataa 2200  
aatcacatat ttcaaaaaat ggttattatt taggcctttg tacaatttct 2250  
aacaatttag tggaagtatc aaaaggattg aagcaaatac tgtaacagtt 2300  
atgttccttt aaataataga gaatataaaa tattgtaata atatgtatca 2350  
taaaatagtt gtatgtgagc atttgatggt gaaaaaaaaa aaaaaaaaaa 2400  
aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 2450  
aaaaaaaaaa aaaaaaaaaa aaaaaa 2476

<210> 132

<211> 536

<212> PRT

<213> Homo sapiens

<400> 132

Met	Leu	Leu	Leu	Trp	Val	Ser	Val	Val	Ala	Ala	Leu	Ala	Leu	Ala
1				5					10					15

Val	Leu	Ala	Pro	Gly	Ala	Gly	Glu	Gln	Arg	Arg	Arg	Ala	Ala	Lys
				20					25					30

Ala	Pro	Asn	Val	Val	Leu	Val	Val	Ser	Asp	Ser	Phe	Asp	Gly	Arg
				35					40					45

Leu	Thr	Phe	His	Pro	Gly	Ser	Gln	Val	Val	Lys	Leu	Pro	Phe	Ile
				50					55					60

Asn	Phe	Met	Lys	Thr	Arg	Gly	Thr	Ser	Phe	Leu	Asn	Ala	Tyr	Thr
				65					70					75

Asn	Ser	Pro	Ile	Cys	Cys	Pro	Ser	Arg	Ala	Ala	Met	Trp	Ser	Gly
				80					85					90

Leu	Phe	Thr	His	Leu	Thr	Glu	Ser	Trp	Asn	Asn	Phe	Lys	Gly	Leu
				95					100					105

Asp	Pro	Asn	Tyr	Thr	Thr	Trp	Met	Asp	Val	Met	Glu	Arg	His	Gly
				110					115					120

Tyr	Arg	Thr	Gln	Lys	Phe	Gly	Lys	Leu	Asp	Tyr	Thr	Ser	Gly	His
				125					130					135

His	Ser	Ile	Ser	Asn	Arg	Val	Glu	Ala	Trp	Thr	Arg	Asp	Val	Ala
				140					145					150

Phe	Leu	Leu	Arg	Gln	Glu	Gly	Arg	Pro	Met	Val	Asn	Leu	Ile	Arg
				155					160					165

Asn	Arg	Thr	Lys	Val	Arg	Val	Met	Glu	Arg	Asp	Trp	Gln	Asn	Thr
				170					175					180

Asp	Lys	Ala	Val	Asn	Trp	Leu	Arg	Lys	Glu	Ala	Ile	Asn	Tyr	Thr
				185					190					195

Glu	Pro	Phe	Val	Ile	Tyr	Leu	Gly	Leu	Asn	Leu	Pro	His	Pro	Tyr
				200					205					210

Pro	Ser	Pro	Ser	Ser	Gly	Glu	Asn	Phe	Gly	Ser	Ser	Thr	Phe	His
				215					220					225

Thr	Ser	Leu	Tyr	Trp	Leu	Glu	Lys	Val	Ser	His	Asp	Ala	Ile	Lys
				230					235					240

Ile	Pro	Lys	Trp	Ser	Pro	Leu	Ser	Glu	Met	His	Pro	Val	Asp	Tyr
				245					250					255

Tyr Ser Ser Tyr	Thr Lys Asn Cys Thr	Gly Arg Phe Thr	Lys Lys
	260	265	270
Glu Ile Lys Asn	Ile Arg Ala Phe Tyr	Tyr Ala Met Cys Ala	Glu
	275	280	285
Thr Asp Ala Met	Leu Gly Glu Ile Ile	Leu Ala Leu His Gln	Leu
	290	295	300
Asp Leu Leu Gln	Lys Thr Ile Val Ile	Tyr Ser Ser Asp His	Gly
	305	310	315
Glu Leu Ala Met	Glu His Arg Gln Phe	Tyr Lys Met Ser Met	Tyr
	320	325	330
Glu Ala Ser Ala	His Val Pro Leu Leu	Met Met Gly Pro Gly	Ile
	335	340	345
Lys Ala Gly Leu	Gln Val Ser Asn Val	Val Ser Leu Val Asp	Ile
	350	355	360
Tyr Pro Thr Met	Leu Asp Ile Ala Gly	Ile Pro Leu Pro Gln	Asn
	365	370	375
Leu Ser Gly Tyr	Ser Leu Leu Pro Leu	Ser Ser Glu Thr Phe	Lys
	380	385	390
Asn Glu His Lys	Val Lys Asn Leu His	Pro Pro Trp Ile Leu	Ser
	395	400	405
Glu Phe His Gly	Cys Asn Val Asn Ala	Ser Thr Tyr Met Leu	Arg
	410	415	420
Thr Asn His Trp	Lys Tyr Ile Ala Tyr	Ser Asp Gly Ala Ser	Ile
	425	430	435
Leu Pro Gln Leu	Phe Asp Leu Ser Ser	Asp Pro Asp Glu Leu	Thr
	440	445	450
Asn Val Ala Val	Lys Phe Pro Glu Ile	Thr Tyr Ser Leu Asp	Gln
	455	460	465
Lys Leu His Ser	Ile Ile Asn Tyr Pro	Lys Val Ser Ala Ser	Val
	470	475	480
His Gln Tyr Asn	Lys Glu Gln Phe Ile	Lys Trp Lys Gln Ser	Ile
	485	490	495
Gly Gln Asn Tyr	Ser Asn Val Ile Ala	Asn Leu Arg Trp His	Gln
	500	505	510
Asp Trp Gln Lys	Glu Pro Arg Lys Tyr	Glu Asn Ala Ile Asp	Gln
	515	520	525
Trp Leu Lys Thr	His Met Asn Pro Arg	Ala Val	
	530	535	

<210> 133  
<211> 1475  
<212> DNA  
<213> Homo sapiens

<400> 133

gagagaagtc agcctggcag agagactctg aaatgagga ttagaggtgt 50  
tcaaggagca agagcttcag cctgaagaca agggagcagt ccctgaagac 100  
gcttctactg agaggtctgc catggcctct cttggcctcc aacttgtggg 150  
ctacatccta ggccttctgg ggcttttggg cacactggtt gccatgctgc 200  
tccccagctg gaaaacaagt tcttatgtcg gtgccagcat tgtgacagca 250  
gttggtcttct ccaagggcct ctggatggaa tgtgccacac acagcacagg 300  
catcaccag tgtgacatct atagcaccct tctgggcctg cccgctgaca 350  
tccaggctgc ccaggccatg atggtgacat ccagtgaat ctctccctg 400  
gcctgcatta tctctgtggt gggcatgaga tgcacagtct tctgccagga 450  
atcccgagcc aaagacagag tggcggtagc aggtggagtc ttttcatcc 500  
ttggaggcct cctgggattc attcctgttg cctggaatct tcatgggatc 550  
ctacgggact tctactcacc actggtgcct gacagcatga aatttgagat 600  
tgagagaggct ctttacttgg gcattatttc ttccctgttc tccctgatag 650  
ctggaatcat cctctgcttt tctgtctcat ccagagaaa tcgctccaac 700  
tactacgatg cctaccaagc ccaacctctt gccacaagga gctctccaag 750  
gcctggtcaa cctcccaaag tcaagagtga gttcaattcc tacagcctga 800  
cagggtatgt gtgaagaacc aggggccaga gctggggggg ggctgggtct 850  
gtgaaaaaca gtggacagca ccccgagggc cacaggtgag ggacactacc 900  
actggatcgt gtcagaaggt gctgctgagg atagactgac tttggccatt 950  
ggattgagca aaggcagaaa tgggggctag tgtaacagca tgcaggttga 1000  
attgccaagg atgctcgcca tgccagcctt tctgttttcc tcaccttgct 1050  
gctcccctgc cctaagtccc caaccctcaa cttgaaacct cattccctta 1100  
agccaggact cagaggatcc ctttgccttc tggtttacct gggactccat 1150  
ccccaaacct actaatcaca tccactgac tgaccctctg tgatcaaaga 1200  
ccctctctct ggctgaggtt ggctcttagc tcattgctgg ggatgggaag 1250  
gagaagcagt ggcttttgtg ggcattgctc taacctactt ctcaagcttc 1300

cctccaaaga aactgattgg ccctggaacc tccatccac tcttggtatg 1350  
 actccacagt gtccagacta atttgtgcat gaactgaaat aaaaccatcc 1400  
 tacggtatcc agggaaacaga aagcaggatg caggatggga ggacaggaag 1450  
 gcagcctggg acatttaaaa aaata 1475

<210> 134  
 <211> 230  
 <212> PRT  
 <213> Homo sapiens

<400> 134

Met	Ala	Ser	Leu	Gly	Leu	Gln	Leu	Val	Gly	Tyr	Ile	Leu	Gly	Leu	1	5	10	15
Leu	Gly	Leu	Leu	Gly	Thr	Leu	Val	Ala	Met	Leu	Leu	Pro	Ser	Trp	20	25	30	
Lys	Thr	Ser	Ser	Tyr	Val	Gly	Ala	Ser	Ile	Val	Thr	Ala	Val	Gly	35	40	45	
Phe	Ser	Lys	Gly	Leu	Trp	Met	Glu	Cys	Ala	Thr	His	Ser	Thr	Gly	50	55	60	
Ile	Thr	Gln	Cys	Asp	Ile	Tyr	Ser	Thr	Leu	Leu	Gly	Leu	Pro	Ala	65	70	75	
Asp	Ile	Gln	Ala	Ala	Gln	Ala	Met	Met	Val	Thr	Ser	Ser	Ala	Ile	80	85	90	
Ser	Ser	Leu	Ala	Cys	Ile	Ile	Ser	Val	Val	Gly	Met	Arg	Cys	Thr	95	100	105	
Val	Phe	Cys	Gln	Glu	Ser	Arg	Ala	Lys	Asp	Arg	Val	Ala	Val	Ala	110	115	120	
Gly	Gly	Val	Phe	Phe	Ile	Leu	Gly	Gly	Leu	Leu	Gly	Phe	Ile	Pro	125	130	135	
Val	Ala	Trp	Asn	Leu	His	Gly	Ile	Leu	Arg	Asp	Phe	Tyr	Ser	Pro	140	145	150	
Leu	Val	Pro	Asp	Ser	Met	Lys	Phe	Glu	Ile	Gly	Glu	Ala	Leu	Tyr	155	160	165	
Leu	Gly	Ile	Ile	Ser	Ser	Leu	Phe	Ser	Leu	Ile	Ala	Gly	Ile	Ile	170	175	180	
Leu	Cys	Phe	Ser	Cys	Ser	Ser	Gln	Arg	Asn	Arg	Ser	Asn	Tyr	Tyr	185	190	195	
Asp	Ala	Tyr	Gln	Ala	Gln	Pro	Leu	Ala	Thr	Arg	Ser	Ser	Pro	Arg	200	205	210	

Pro Gly Gln Pro Pro Lys Val Lys Ser Glu Phe Asn Ser Tyr Ser  
 215 220 225

Leu Thr Gly Tyr Val  
 230

<210> 135

<211> 610

<212> DNA

<213> Homo sapiens

<400> 135

gcactgctgc tgtcccatca gctgctctga agctccatgg tgcccagaat 50  
 cttcgctcct gcttatgtgt cagtctgtct cctcctcttg tgtccaaggg 100  
 aagtcacgc tcccgtggc tcagaacct ggctgtgcca gccggcacc 150  
 aggtgtggag acaagatcta caacccttg gagcagtgt gttacaatga 200  
 cgccatcgtg tccctgagcg agaccgcga atgtgggtccc ccctgcacct 250  
 tctggccctg ctttgagctc tgctgtcttg attcctttgg cctcacaaac 300  
 gattttgttg tgaagctgaa gggtcaggg gtgaattccc agtgccactc 350  
 atctcccatc tccagtaa atgtgaaagc aagacgtttt ccctgagaag 400  
 acatagaaag aaaatcaact ttcactaagg catctcagaa acataggcta 450  
 aggtaatatg tgtaccagta gagaagcctg aggaatttac aaaatgatgc 500  
 agctccaagc cattgtatgg cccatgtggg agactgatgg gacatggaga 550  
 atgacagtag attatcagga aataaataaa gtgggttttc caatgtacac 600  
 acctgtaaaa 610

<210> 136

<211> 119

<212> PRT

<213> Homo sapiens

<400> 136

Met Val Pro Arg Ile Phe Ala Pro Ala Tyr Val Ser Val Cys Leu  
 1 5 10 15  
 Leu Leu Leu Cys Pro Arg Glu Val Ile Ala Pro Ala Gly Ser Glu  
 20 25 30  
 Pro Trp Leu Cys Gln Pro Ala Pro Arg Cys Gly Asp Lys Ile Tyr  
 35 40 45  
 Asn Pro Leu Glu Gln Cys Cys Tyr Asn Asp Ala Ile Val Ser Leu  
 50 55 60  
 Ser Glu Thr Arg Gln Cys Gly Pro Pro Cys Thr Phe Trp Pro Cys



	65		70		75
Phe Glu Leu Cys Cys Leu Asp Ser Phe Gly Leu Thr Asn Asp Phe					
	80		85		90
Val Val Lys Leu Lys Val Gln Gly Val Asn Ser Gln Cys His Ser					
	95		100		105
Ser Pro Ile Ser Ser Lys Cys Glu Ser Arg Arg Arg Phe Pro					
	110		115		

<210> 137  
 <211> 771  
 <212> DNA  
 <213> Homo sapiens

<400> 137  
 ctccactgca accacccaga gccatggctc cccgaggctg catcgtagct 50  
 gtctttgcca ttttctgcat ctccaggctc ctctgctcac acggagcccc 100  
 agtggccccc atgactcctt acctgatgct gtgccagcca cacaagagat 150  
 gtggggacaa gttctacgac ccctgcagc actgttgcta tgatgatgcc 200  
 gtcgtgccct tggccaggac ccagacgtgt ggaaactgca ccttcagagt 250  
 ctgctttgag cagtgtctgcc cctggacctt catggtgaag ctgataaacc 300  
 agaactgcga ctacgcccgg acctcggatg acaggctttg tcgcagtgtc 350  
 agctaattga acatcagggg aacgatgact cctggattct ccttctctggg 400  
 tgggcctgga gaaagaggct ggtgttacct gagatctggg atgctgagtg 450  
 gctgtttggg ggccagagaa acacacactc aactgccac ttcattctgt 500  
 gacctgtctg aggcccaccc tgcagctgcc ctgaggaggc ccacaggtcc 550  
 ccttctagaa ttctggacag catgagatgc gtgtgctgat gggggcccag 600  
 ggactctgaa cctcctgat gaccctatg gccaacatca acccggcacc 650  
 accccaaggc tggctgggga acccttcacc cttctgtgag attttccatc 700  
 atctcaagtt ctcttctatc caggagcaaa gcacaggatc ataataaatt 750  
 tatgtacttt ataaatgaaa a 771

<210> 138  
 <211> 110  
 <212> PRT  
 <213> Homo sapiens

<400> 138  
 Met Ala Pro Arg Gly Cys Ile Val Ala Val Phe Ala Ile Phe Cys  
 1 5 10 15

Ile	Ser	Arg	Leu	Leu	Cys	Ser	His	Gly	Ala	Pro	Val	Ala	Pro	Met	
				20					25					30	
Thr	Pro	Tyr	Leu	Met	Leu	Cys	Gln	Pro	His	Lys	Arg	Cys	Gly	Asp	
			35						40					45	
Lys	Phe	Tyr	Asp	Pro	Leu	Gln	His	Cys	Cys	Tyr	Asp	Asp	Ala	Val	
				50					55					60	
Val	Pro	Leu	Ala	Arg	Thr	Gln	Thr	Cys	Gly	Asn	Cys	Thr	Phe	Arg	
				65					70					75	
Val	Cys	Phe	Glu	Gln	Cys	Cys	Pro	Trp	Thr	Phe	Met	Val	Lys	Leu	
				80					85					90	
Ile	Asn	Gln	Asn	Cys	Asp	Ser	Ala	Arg	Thr	Ser	Asp	Asp	Arg	Leu	
				95					100					105	
Cys	Arg	Ser	Val	Ser											
				110											

<210> 139

<211> 2044

<212> DNA

<213> Homo sapiens

<400> 139

```

ggggggcgggt gcctggagca cggcgctggg gccgcccga gcgctcactc 50
gctcgactc agtcgcgga ggcttccccg cgcggccgc gtcccgccc 100
ctccccgga ccagaagttc ctctgcgcgt ccgacggcga catgggcgtc 150
cccacggccc tggaggccgg cagctggcgc tggggatccc tgctcttcgc 200
tctcttctg gctgcgtccc taggtccggt ggcagccttc aaggtcgcca 250
cgccgtattc cctgtatgtc tgtcccgagg ggcagaacgt caccctcacc 300
tgcaggctct tgggccctgt ggacaaaggg cacgatgtga cttctacaa 350
gacgtggtac cgcagctcga ggggcgaggt gcagacctgc tcagagcgcc 400
ggcccatccg caacctcagc ttccaggacc ttacactgca ccatggaggc 450
caccaggctg ccaacaccag ccacgacctg gctcagcgcc acgggctgga 500
gtcggcctcc gaccacatg gcaacttctc catcaccatg cgcaacctga 550
ccctgctgga tagcggcctc tactgctgcc tgggtggtgga gatcaggcac 600
caccactcgg agcacagggt ccatggtgcc atggagctgc aggtgcagac 650
aggcaaagat gcaccatcca actgtgtggt gtacccatcc tcctcccagg 700
atagtgaata catcacggct gcagccctgg ctacgggtgc ctgcatcgta 750

```

ggaatcctct gcctccccct catcctgctc ctggtctaca agcaaaggca 800  
 ggagcctcc aaccgccgtg cccaggagct ggtgcggatg gacagcaaca 850  
 ttcaagggat tgaaaacccc ggctttgaag cctcaccacc tgcccagggg 900  
 ataccgagg ccaaagtcag gcacccccctg tcctatgtgg cccagcggca 950  
 gccttctgag tctgggcggc atctgctttc ggagcccagc acccccctgt 1000  
 ctctccagg ccccgagagc gtcttcttcc catccctgga ccctgtccct 1050  
 gactctcaa actttgaggt catctagccc agctggggga cagtgggctg 1100  
 ttgtggctgg gtctggggca ggtgcatttg agccagggtt ggctctgtga 1150  
 gtggcctcct tggcctcggc cctgggtccc tccctcctgc tctgggctca 1200  
 gatactgtga catcccagaa gcccgacccc tcaaccctc tggatgctac 1250  
 atggggatgc tggacggctc agcccctgtt ccaaggattt tggggtgctg 1300  
 agattctccc ctagagacct gaaattcacc agctacagat gccaaatgac 1350  
 ttacatctta agaagtctca gaacgtccag cccttcagca gctctcgttc 1400  
 tgagacatga gccttgggat gtggcagcat cagtgggaca agatggacac 1450  
 tgggccaccc tcccaggcac cagacacagg gcacgggtga gagacttctc 1500  
 ccccgtaggc gccttggctc ccccgttttg cccgaggctg ctcttctgtc 1550  
 agacttcctc tttgtaccac agtggctctg gggccaggcc tgctgccc 1600  
 ctggccatcg ccaccttccc cagctgcctc ctaccagcag tttctctgaa 1650  
 gatctgtcaa cagggttaagt caatctgggg cttccactgc ctgcattcca 1700  
 gtccccagag cttggtggtc ccgaaacggg aagtacatat tggggcatgg 1750  
 tggcctccgt gagcaaattg tgtcttgggc aatctgaggc caggacagat 1800  
 gttgccccac ccactggaga tggtgctgag ggaggtgggt ggggccttct 1850  
 gggaaggatga gtggagaggg gcacctgccc cccgccctcc ccatccccta 1900  
 ctcccactgc tcagcgcggg ccattgcaag ggtgccacac aatgtcttgt 1950  
 ccaccctggg acacttctga gtatgaagcg ggatgctatt aaaaactaca 2000  
 tggggaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaga 2044

<210> 140

<211> 311

<212> PRT

<213> Homo sapiens

<400> 140

Met	Gly	Val	Pro	Thr	Ala	Leu	Glu	Ala	Gly	Ser	Trp	Arg	Trp	Gly	
1				5					10					15	
Ser	Leu	Leu	Phe	Ala	Leu	Phe	Leu	Ala	Ala	Ser	Leu	Gly	Pro	Val	
				20					25					30	
Ala	Ala	Phe	Lys	Val	Ala	Thr	Pro	Tyr	Ser	Leu	Tyr	Val	Cys	Pro	
				35					40					45	
Glu	Gly	Gln	Asn	Val	Thr	Leu	Thr	Cys	Arg	Leu	Leu	Gly	Pro	Val	
				50					55					60	
Asp	Lys	Gly	His	Asp	Val	Thr	Phe	Tyr	Lys	Thr	Trp	Tyr	Arg	Ser	
				65					70					75	
Ser	Arg	Gly	Glu	Val	Gln	Thr	Cys	Ser	Glu	Arg	Arg	Pro	Ile	Arg	
				80					85					90	
Asn	Leu	Thr	Phe	Gln	Asp	Leu	His	Leu	His	His	Gly	Gly	His	Gln	
				95					100					105	
Ala	Ala	Asn	Thr	Ser	His	Asp	Leu	Ala	Gln	Arg	His	Gly	Leu	Glu	
				110					115					120	
Ser	Ala	Ser	Asp	His	His	Gly	Asn	Phe	Ser	Ile	Thr	Met	Arg	Asn	
				125					130					135	
Leu	Thr	Leu	Leu	Asp	Ser	Gly	Leu	Tyr	Cys	Cys	Leu	Val	Val	Glu	
				140					145					150	
Ile	Arg	His	His	His	Ser	Glu	His	Arg	Val	His	Gly	Ala	Met	Glu	
				155					160					165	
Leu	Gln	Val	Gln	Thr	Gly	Lys	Asp	Ala	Pro	Ser	Asn	Cys	Val	Val	
				170					175					180	
Tyr	Pro	Ser	Ser	Ser	Gln	Asp	Ser	Glu	Asn	Ile	Thr	Ala	Ala	Ala	
				185					190					195	
Leu	Ala	Thr	Gly	Ala	Cys	Ile	Val	Gly	Ile	Leu	Cys	Leu	Pro	Leu	
				200					205					210	
Ile	Leu	Leu	Leu	Val	Tyr	Lys	Gln	Arg	Gln	Ala	Ala	Ser	Asn	Arg	
				215					220					225	
Arg	Ala	Gln	Glu	Leu	Val	Arg	Met	Asp	Ser	Asn	Ile	Gln	Gly	Ile	
				230					235					240	
Glu	Asn	Pro	Gly	Phe	Glu	Ala	Ser	Pro	Pro	Ala	Gln	Gly	Ile	Pro	
				245					250					255	
Glu	Ala	Lys	Val	Arg	His	Pro	Leu	Ser	Tyr	Val	Ala	Gln	Arg	Gln	
				260					265					270	
Pro	Ser	Glu	Ser	Gly	Arg	His	Leu	Leu	Ser	Glu	Pro	Ser	Thr	Pro	

	275		280		285
Leu Ser Pro Pro Gly Pro Gly Asp Val Phe Phe Pro Ser Leu Asp					
	290		295		300
Pro Val Pro Asp Ser Pro Asn Phe Glu Val Ile					
	305		310		

<210> 141  
 <211> 1732  
 <212> DNA  
 <213> Homo sapiens

<400> 141  
 cccacgcgtc cgcgcctctc ccttctgctg gaccttcctt cgtctctcca 50  
 tctctccctc ctttccccgc gttctctttc cacctttctc ttcttccac 100  
 cttagacctc ccttcctgcc ctcttttctt gccaccgct gcttctggc 150  
 ctttctccga ccccgctcta gcagcagacc tcctggggtc tgtgggtga 200  
 tctgtggccc ctgtgcctcc gtgtcctttt cgtctccctt cctcccgaact 250  
 ccgctcccg accagcggcc tgacctggg gaaaggatgg ttcccagagt 300  
 gagggctctc tcctccttgc tgggactcgc gctgctctgg tccccctgg 350  
 actcccacgc tcgagcccg ccagacatgt tctgcctttt ccatgggaag 400  
 agatactccc ccggcgagag ctggcacccc tacttgagc cacaaggcct 450  
 gatgtactgc ctgcgctgta cctgctcaga gggcgcccat gtgagttgtt 500  
 accgcctcca ctgtccgcct gtccactgcc cccagcctgt gacggagcca 550  
 cagcaatgct gtcccaagtg tgtggaacct cacactccct ctggactccg 600  
 ggccccacca aagtcctgcc agcacaacgg gacctgtac caacacggag 650  
 agatcttcag tgcccatgag ctgttccct cccgcctgcc caaccagtgt 700  
 gtctctgca gctgcacaga gggccagatc tactgcggcc tcacaacctg 750  
 ccccgaacca ggctgcccag caccctccc actgccagac tcctgctgcc 800  
 aagcctgcaa agatgaggca agtgagcaat cggatgaaga ggacagtgtg 850  
 cagtcgctcc atggggtgag acatcctcag gatccatgtt ccagtgatgc 900  
 tgggagaaag agaggcccg gcacccagc cccactggc ctgagcgccc 950  
 ctctgagctt catccctcgc cacttcagac ccaagggagc aggcagcaca 1000  
 actgtcaaga tcgtcctgaa ggagaaacat aagaaagcct gtgtgcatgg 1050  
 cgggaagacg tactccacg gggaggtgtg gcaccggcc ttccgtgcct 1100

tcggccccctt gccctgcatc ctatgcacct gtgaggatgg ccgccaggac 1150  
 tgccagcgtg tgacctgtcc caccgagtac ccctgccgtc accccgagaa 1200  
 agtggctggg aagtgtgca agatttgccc agaggacaaa gcagaccctg 1250  
 gccacagtga gatcagttct accaggtgtc ccaaggcacc gggccgggtc 1300  
 ctcgccaca catcggtatc cccaagccca gacaacctgc gtcgctttgc 1350  
 cctggaacac gaggcctcgg acttggtgga gatctacctc tggaagctgg 1400  
 taaaagatga ggaaactgag gctcagagag gtgaagtacc tggcccaagg 1450  
 ccacacagcc agaatcttcc acttgactca gatcaagaaa gtcaggaagc 1500  
 aagacttcca gaaagaggca cagcacttcc gactgctcgc tggccccac 1550  
 gaaggtcact ggaacgtctt cctagcccag accctggagc tgaaggtcac 1600  
 ggccagtcca gacaaagtga ccaagacata acaaagacct aacagttgca 1650  
 gatatgagct gtataattgt tgttattata tattaataaa taagaagttg 1700  
 cattaccctc aaaaaaaaaa aaaaaaaaaa aa 1732

<210> 142

<211> 451

<212> PRT

<213> Homo sapiens

<400> 142

Met	Val	Pro	Glu	Val	Arg	Val	Leu	Ser	Ser	Leu	Leu	Gly	Leu	Ala
1				5				10						15
Leu	Leu	Trp	Phe	Pro	Leu	Asp	Ser	His	Ala	Arg	Ala	Arg	Pro	Asp
				20				25						30
Met	Phe	Cys	Leu	Phe	His	Gly	Lys	Arg	Tyr	Ser	Pro	Gly	Glu	Ser
				35				40						45
Trp	His	Pro	Tyr	Leu	Glu	Pro	Gln	Gly	Leu	Met	Tyr	Cys	Leu	Arg
				50				55						60
Cys	Thr	Cys	Ser	Glu	Gly	Ala	His	Val	Ser	Cys	Tyr	Arg	Leu	His
				65				70						75
Cys	Pro	Pro	Val	His	Cys	Pro	Gln	Pro	Val	Thr	Glu	Pro	Gln	Gln
				80				85						90
Cys	Cys	Pro	Lys	Cys	Val	Glu	Pro	His	Thr	Pro	Ser	Gly	Leu	Arg
				95				100						105
Ala	Pro	Pro	Lys	Ser	Cys	Gln	His	Asn	Gly	Thr	Met	Tyr	Gln	His
				110				115						120

Gly Glu Ile Phe Ser Ala His Glu Leu Phe Pro Ser Arg Leu Pro	125	130	135
Asn Gln Cys Val Leu Cys Ser Cys Thr Glu Gly Gln Ile Tyr Cys	140	145	150
Gly Leu Thr Thr Cys Pro Glu Pro Gly Cys Pro Ala Pro Leu Pro	155	160	165
Leu Pro Asp Ser Cys Cys Gln Ala Cys Lys Asp Glu Ala Ser Glu	170	175	180
Gln Ser Asp Glu Glu Asp Ser Val Gln Ser Leu His Gly Val Arg	185	190	195
His Pro Gln Asp Pro Cys Ser Ser Asp Ala Gly Arg Lys Arg Gly	200	205	210
Pro Gly Thr Pro Ala Pro Thr Gly Leu Ser Ala Pro Leu Ser Phe	215	220	225
Ile Pro Arg His Phe Arg Pro Lys Gly Ala Gly Ser Thr Thr Val	230	235	240
Lys Ile Val Leu Lys Glu Lys His Lys Lys Ala Cys Val His Gly	245	250	255
Gly Lys Thr Tyr Ser His Gly Glu Val Trp His Pro Ala Phe Arg	260	265	270
Ala Phe Gly Pro Leu Pro Cys Ile Leu Cys Thr Cys Glu Asp Gly	275	280	285
Arg Gln Asp Cys Gln Arg Val Thr Cys Pro Thr Glu Tyr Pro Cys	290	295	300
Arg His Pro Glu Lys Val Ala Gly Lys Cys Cys Lys Ile Cys Pro	305	310	315
Glu Asp Lys Ala Asp Pro Gly His Ser Glu Ile Ser Ser Thr Arg	320	325	330
Cys Pro Lys Ala Pro Gly Arg Val Leu Val His Thr Ser Val Ser	335	340	345
Pro Ser Pro Asp Asn Leu Arg Arg Phe Ala Leu Glu His Glu Ala	350	355	360
Ser Asp Leu Val Glu Ile Tyr Leu Trp Lys Leu Val Lys Asp Glu	365	370	375
Glu Thr Glu Ala Gln Arg Gly Glu Val Pro Gly Pro Arg Pro His	380	385	390
Ser Gln Asn Leu Pro Leu Asp Ser Asp Gln Glu Ser Gln Glu Ala	395	400	405

Arg Leu Pro Glu Arg Gly Thr Ala Leu Pro Thr Ala Arg Trp Pro  
410 415 420

Pro Arg Arg Ser Leu Glu Arg Leu Pro Ser Pro Asp Pro Gly Ala  
425 430 435

Glu Gly His Gly Gln Ser Arg Gln Ser Asp Gln Asp Ile Thr Lys  
440 445 450

Thr

<210> 143

<211> 693

<212> DNA

<213> Homo sapiens

<400> 143

ctagcctgcg ccaaggggta gtgagaccgc gcggcaacag cttgcggctg 50

cggggagctc ccgtgggcgc tccgctggct gtgcaggcgg ccatggattc 100

cttgcggaaa atgctgatct cagtcgcaat gctgggcgca ggggctggcg 150

tgggctacgc gtcctcggtt atcgtgaccc cgaggagagcg gcggaagcag 200

gaaatgctaa aggagatgcc actgcaggac ccaaggagca gggaggaggc 250

ggccaggacc cagcagctat tgctggccac tctgcaggag gcagcgacca 300

cgcaggagaa cgtggcctgg aggaagaact ggatggttgg cggcgaaggc 350

ggcgccagcg ggaggtcacc gtgagaccgg acttgccctcc gtgggcgccg 400

gaccttggtt tgggcgcagg aatccgaggc agcctttctc cttcgtgggc 450

ccagcggaga gtccggaccg agataccatg ccaggactct ccggggtcct 500

gtgagctgcc gtcgggtgag cacgtttccc ccaaaccctg gactgactgc 550

tttaaggtcc gcaaggcggg ccagggccga gacgcgagtc ggatgtggtg 600

aactgaaaga accaataaaa tcatgttcct ccaaaaaaaaaa aaaaaaaaaa 650

aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaa 693

<210> 144

<211> 93

<212> PRT

<213> Homo sapiens

<400> 144

Met Asp Ser Leu Arg Lys Met Leu Ile Ser Val Ala Met Leu Gly  
1 5 10 15

Ala Gly Ala Gly Val Gly Tyr Ala Leu Leu Val Ile Val Thr Pro  
20 25 30



Gly	Glu	Arg	Arg	Lys	Gln	Glu	Met	Leu	Lys	Glu	Met	Pro	Leu	Gln
				35					40					45
Asp	Pro	Arg	Ser	Arg	Glu	Glu	Ala	Ala	Arg	Thr	Gln	Gln	Leu	Leu
				50					55					60
Leu	Ala	Thr	Leu	Gln	Glu	Ala	Ala	Thr	Thr	Gln	Glu	Asn	Val	Ala
				65					70					75
Trp	Arg	Lys	Asn	Trp	Met	Val	Gly	Gly	Glu	Gly	Gly	Ala	Ser	Gly
				80					85					90
Arg Ser Pro														

<210> 145

<211> 1883

<212> DNA

<213> Homo sapiens

<400> 145

```

caggagagaa ggcaccgccc ccaccccgcc tccaaagcta accctcgggc 50
ttgaggggaa gaggctgact gtacgttcct tctactctgg caccactctc 100
caggctgcca tggggcccag caccctctc ctcactttgt tccttttgtc 150
atggtcggga cccctccaag gacagcagca ccaccttggt gagtacatgg 200
aacgccgact agctgcttta gaggaacggc tggcccagtg ccaggaccag 250
agtagtcggc atgctgctga gctgcgggac ttcaagaaca agatgctgcc 300
actgctggag gtggcagaga aggagcggga ggcactcaga actgaggccg 350
acaccatctc cgggagagtg gatcgtctgg agcgggaggt agactatctg 400
gagacccaga acccagctct gccctgtgta gagtttgatg agaaggtgac 450
tggaggccct gggaccaaag gcaagggaag aaggaatgag aagtacgata 500
tggtgacaga ctgtggctac acaatctctc aagtgagatc aatgaagatt 550
ctgaagcgat ttggtggccc agctgggtcta tggaccaagg atccactggg 600
gcaaacagag aagatctacg tgtagatgg gacacagaat gacacagcct 650
ttgtcttccc aaggctgctg gacttcaccc ttgccatggc tgcccggaaa 700
gcttcccag tccgggtgcc cttcccctgg gtaggcacag ggcagctggt 750
atatggtggc tttctttatt ttgctcggag gcctcctgga agacctggtg 800
gaggtggtga gatggagaac actttgcagc taatcaaatt ccacctggca 850
aaccgaacag tgggtggacag ctcaagtatt ccagcagagg ggctgatccc 900

```

cccctacggc ttgacagcag acacctacat cgacctggta gctgatgagg 950  
 aaggtctttg ggctgtctat gccacccggg aggatgacag gcacttgtgt 1000  
 ctggccaagt tagatccaca gacactggac acagagcagc agtgggacac 1050  
 accatgtccc agagagaatg ctgaggctgc ctttgtcatc tgtgggaccc 1100  
 tctatgtcgt ctataacacc cgtcctgcca gtcggggccg catccagtgc 1150  
 tcctttgatg ccagcggcac cctgacccct gaacgggcag cactccctta 1200  
 ttttccccgc agatatggtg cccatgccag cctccgctat aacccccgag 1250  
 aacgccagct ctatgcctgg gatgatggct accagattgt ctataagctg 1300  
 gagatgagga agaaagagga ggaggtttga ggagctagcc ttgttttttg 1350  
 catctttctc actcccatac atttatatta tatccccact aaatttcttg 1400  
 ttctcattc ttcaaatgtg ggccagttgt ggctcaaata ctctatattt 1450  
 ttagccaatg gcaatcaaat tctttcagct cctttgtttc atacggaact 1500  
 ccagatcctg agtaatcctt ttagagcccg aagagtcaaa accctcaatg 1550  
 ttccctcctg ctctcctgcc ccatgtcaac aaatttcagg ctaaggatgc 1600  
 cccagaccca gggctctaac cttgtatgcg ggcaggccca gggagcaggc 1650  
 agcagtgttc ttcccctcag agtgacttgg ggagggagaa ataggaggag 1700  
 acgtccagct ctgtcctctc ttctcactc ctcccttcag tgtcctgagg 1750  
 aacaggactt tctccacatt gttttgtatt gcaacatttt gcattaaaag 1800  
 gaaaatccac aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 1850  
 aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaa 1883

<210> 146

<211> 406

<212> PRT

<213> Homo sapiens

<400> 146

Met	Gly	Pro	Ser	Thr	Pro	Leu	Leu	Ile	Leu	Phe	Leu	Leu	Ser	Trp
1				5				10					15	

Ser	Gly	Pro	Leu	Gln	Gly	Gln	Gln	His	His	Leu	Val	Glu	Tyr	Met
				20				25						30

Glu	Arg	Arg	Leu	Ala	Ala	Leu	Glu	Glu	Arg	Leu	Ala	Gln	Cys	Gln
				35				40						45

Asp	Gln	Ser	Ser	Arg	His	Ala	Ala	Glu	Leu	Arg	Asp	Phe	Lys	Asn
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

	50		55		60
Lys Met Leu Pro	Leu Leu Glu Val Ala	Glu Lys Glu Arg Glu Ala			
	65		70		75
Leu Arg Thr Glu	Ala Asp Thr Ile Ser	Gly Arg Val Asp Arg Leu			
	80		85		90
Glu Arg Glu Val	Asp Tyr Leu Glu Thr	Gln Asn Pro Ala Leu Pro			
	95		100		105
Cys Val Glu Phe	Asp Glu Lys Val Thr	Gly Gly Pro Gly Thr Lys			
	110		115		120
Gly Lys Gly Arg	Arg Asn Glu Lys Tyr	Asp Met Val Thr Asp Cys			
	125		130		135
Gly Tyr Thr Ile	Ser Gln Val Arg Ser	Met Lys Ile Leu Lys Arg			
	140		145		150
Phe Gly Gly Pro	Ala Gly Leu Trp Thr	Lys Asp Pro Leu Gly Gln			
	155		160		165
Thr Glu Lys Ile	Tyr Val Leu Asp Gly	Thr Gln Asn Asp Thr Ala			
	170		175		180
Phe Val Phe Pro	Arg Leu Arg Asp Phe	Thr Leu Ala Met Ala Ala			
	185		190		195
Arg Lys Ala Ser	Arg Val Arg Val Pro	Phe Pro Trp Val Gly Thr			
	200		205		210
Gly Gln Leu Val	Tyr Gly Gly Phe Leu	Tyr Phe Ala Arg Arg Pro			
	215		220		225
Pro Gly Arg Pro	Gly Gly Gly Gly Glu	Met Glu Asn Thr Leu Gln			
	230		235		240
Leu Ile Lys Phe	His Leu Ala Asn Arg	Thr Val Val Asp Ser Ser			
	245		250		255
Val Phe Pro Ala	Glu Gly Leu Ile Pro	Pro Tyr Gly Leu Thr Ala			
	260		265		270
Asp Thr Tyr Ile	Asp Leu Val Ala Asp	Glu Glu Gly Leu Trp Ala			
	275		280		285
Val Tyr Ala Thr	Arg Glu Asp Asp Arg	His Leu Cys Leu Ala Lys			
	290		295		300
Leu Asp Pro Gln	Thr Leu Asp Thr Glu	Gln Gln Trp Asp Thr Pro			
	305		310		315
Cys Pro Arg Glu	Asn Ala Glu Ala Ala	Phe Val Ile Cys Gly Thr			
	320		325		330
Leu Tyr Val Val	Tyr Asn Thr Arg Pro	Ala Ser Arg Ala Arg Ile			

	335		340		345
Gln Cys Ser Phe	Asp Ala Ser Gly Thr Leu Thr Pro Glu Arg Ala				
	350		355		360
Ala Leu Pro Tyr	Phe Pro Arg Arg Tyr Gly Ala His Ala Ser Leu				
	365		370		375
Arg Tyr Asn Pro	Arg Glu Arg Gln Leu Tyr Ala Trp Asp Asp Gly				
	380		385		390
Tyr Gln Ile Val	Tyr Lys Leu Glu Met Arg Lys Lys Glu Glu Glu				
	395		400		405

Val

<210> 147

<211> 2052

<212> DNA

<213> Homo sapiens

<400> 147

```

gacagctgtg tctcgatgga gtagactctc agaacagcgc agtttgcct 50
ccgctcacgc agagcctctc cgtggcttcc gcaccttgag cattaggcca 100
gttctcctct tctctctaat ccatccgtca cctctcctgt catccgtttc 150
catgccgtga ggtccattca cagaacacat ccatggctct catgctcagt 200
ttggttctga gtctcctcaa gctgggatca gggcagtggc aggtgtttgg 250
gccagacaag cctgtccagg ccttggtggg ggaggacgca gcattctcct 300
gtttcctgtc tcctaagacc aatgcagagg ccatggaagt gcggttcttc 350
agggggccagt tctctagcgt ggtccacctc tacagggacg ggaaggacca 400
gccatttatg cagatgccac agtatcaagg caggacaaaa ctggtgaagg 450
attctattgc ggaggggcgc atctctctga ggctggaaaa cattactgtg 500
ttggatgctg gcctctatgg gtgcaggatt agttcccagt cttactacca 550
gaaggccatc tgggagctac aggtgtcagc actgggctca gttcctctca 600
tttccatcac gggatatgtt gatagagaca tccagctact ctgtcagtcc 650
tcgggctggt tccccggcc cacagcgaag tggaaaggtc cacaaggaca 700
ggatttgtcc acagactcca ggacaaacag agacatgcat ggcctgtttg 750
atgtggagat ctctctgacc gtccaagaga acgccgggag catatcctgt 800
tccatgcggc atgctcatct gagccgagag gtggaatcca gggtacagat 850

```

aggagatacc tttttcgagc ctatatcgtg gcacctggct accaaagtac 900  
 tgggaatact ctgctgtggc ctatTTTTTg gcattgttgg actgaagatt 950  
 ttcttctcca aattccagtg gaaaatccag gcggaactgg actggagaag 1000  
 aaagcacgga caggcagaat tgagagacgc ccggaacac gcagtggagg 1050  
 tgactctgga tccagagacg gctcaccoga agctctgctt ttctgatctg 1100  
 aaaactgtaa cccatagaaa agctccccag gaggtgcctc actctgagaa 1150  
 gagatttaca aggaagagtg tgggtggcttc tcagagtttc caagcaggga 1200  
 aacattactg ggaggtggac ggaggacaca ataaaaggtg gcgctggga 1250  
 gtgtgccggg atgatgtgga caggaggaag gagtacgtga ctttgtctcc 1300  
 cgatcatggg tactgggtcc tcagactgaa tggagaacat ttgtatttca 1350  
 cattaaatcc ccgttttatc agcgtcttcc ccaggacccc acctacaaaa 1400  
 ataggggtct tcctggacta tgagtgtggg accatctcct tcttcaacat 1450  
 aaatgaccag tcccttattt atacctgac atgtcggttt gaaggcttat 1500  
 tgaggcccta cattgagtat ccgtcctata atgagcaaaa tggaactccc 1550  
 atagtcatct gccagtcac ccaggaatca gagaaagagg cctcttggca 1600  
 aagggcctct gcaatcccag agacaagcaa cagtgagtcc tcctcacagg 1650  
 caaccacgcc ctctctcccc aggggtgaaa tgtaggatga atcacatccc 1700  
 acattcttct ttagggatat taaggctctt ctcccagatc caaagtcccg 1750  
 cagcagccgg ccaaggtggc ttccagatga agggggactg gcctgtccac 1800  
 atgggagtca ggtgtcatgg ctgccctgag ctgggaggga agaaggctga 1850  
 cattacattt agtttgctct cactccatct ggctaagtga tcttgaaata 1900  
 ccacctctca ggtgaagaac cgtcaggaat tcccatctca caggctgtgg 1950  
 tntagattaa gtagacaagg aatgtgaata atgcttagat cttattgatg 2000  
 acagagtgta tcctaattgg ttgttcatta tattacactt tcagtaaaaa 2050

aa 2052

<210> 148

<211> 500

<212> PRT

<213> Homo sapiens

<400> 148

Met Ala Leu Met Leu Ser Leu Val Leu Ser Leu Leu Lys Leu Gly

1	5	10	15
Ser Gly Gln Trp	Gln Val Phe Gly Pro	Asp Lys Pro Val	Gln Ala
	20	25	30
Leu Val Gly Glu	Asp Ala Ala Phe Ser	Cys Phe Leu Ser	Pro Lys
	35	40	45
Thr Asn Ala Glu	Ala Met Glu Val Arg	Phe Phe Arg Gly	Gln Phe
	50	55	60
Ser Ser Val Val	His Leu Tyr Arg Asp	Gly Lys Asp Gln	Pro Phe
	65	70	75
Met Gln Met Pro	Gln Tyr Gln Gly Arg	Thr Lys Leu Val	Lys Asp
	80	85	90
Ser Ile Ala Glu	Gly Arg Ile Ser Leu	Arg Leu Glu Asn	Ile Thr
	95	100	105
Val Leu Asp Ala	Gly Leu Tyr Gly Cys	Arg Ile Ser Ser	Gln Ser
	110	115	120
Tyr Tyr Gln Lys	Ala Ile Trp Glu Leu	Gln Val Ser Ala	Leu Gly
	125	130	135
Ser Val Pro Leu	Ile Ser Ile Thr Gly	Tyr Val Asp Arg	Asp Ile
	140	145	150
Gln Leu Leu Cys	Gln Ser Ser Gly Trp	Phe Pro Arg Pro	Thr Ala
	155	160	165
Lys Trp Lys Gly	Pro Gln Gly Gln Asp	Leu Ser Thr Asp	Ser Arg
	170	175	180
Thr Asn Arg Asp	Met His Gly Leu Phe	Asp Val Glu Ile	Ser Leu
	185	190	195
Thr Val Gln Glu	Asn Ala Gly Ser Ile	Ser Cys Ser Met	Arg His
	200	205	210
Ala His Leu Ser	Arg Glu Val Glu Ser	Arg Val Gln Ile	Gly Asp
	215	220	225
Thr Phe Phe Glu	Pro Ile Ser Trp His	Leu Ala Thr Lys	Val Leu
	230	235	240
Gly Ile Leu Cys	Cys Gly Leu Phe Phe	Gly Ile Val Gly	Leu Lys
	245	250	255
Ile Phe Phe Ser	Lys Phe Gln Trp Lys	Ile Gln Ala Glu	Leu Asp
	260	265	270
Trp Arg Arg Lys	His Gly Gln Ala Glu	Leu Arg Asp Ala	Arg Lys
	275	280	285
His Ala Val Glu	Val Thr Leu Asp Pro	Glu Thr Ala His	Pro Lys

290	295	300
Leu Cys Val Ser Asp Leu Lys Thr Val	Thr His Arg Lys Ala Pro	
305	310	315
Gln Glu Val Pro His Ser Glu Lys Arg	Phe Thr Arg Lys Ser Val	
320	325	330
Val Ala Ser Gln Ser Phe Gln Ala Gly	Lys His Tyr Trp Glu Val	
335	340	345
Asp Gly Gly His Asn Lys Arg Trp Arg	Val Gly Val Cys Arg Asp	
350	355	360
Asp Val Asp Arg Arg Lys Glu Tyr Val	Thr Leu Ser Pro Asp His	
365	370	375
Gly Tyr Trp Val Leu Arg Leu Asn Gly	Glu His Leu Tyr Phe Thr	
380	385	390
Leu Asn Pro Arg Phe Ile Ser Val Phe	Pro Arg Thr Pro Pro Thr	
395	400	405
Lys Ile Gly Val Phe Leu Asp Tyr Glu	Cys Gly Thr Ile Ser Phe	
410	415	420
Phe Asn Ile Asn Asp Gln Ser Leu Ile	Tyr Thr Leu Thr Cys Arg	
425	430	435
Phe Glu Gly Leu Leu Arg Pro Tyr Ile	Glu Tyr Pro Ser Tyr Asn	
440	445	450
Glu Gln Asn Gly Thr Pro Ile Val Ile	Cys Pro Val Thr Gln Glu	
455	460	465
Ser Glu Lys Glu Ala Ser Trp Gln Arg	Ala Ser Ala Ile Pro Glu	
470	475	480
Thr Ser Asn Ser Glu Ser Ser Ser Gln	Ala Thr Thr Pro Phe Leu	
485	490	495
Pro Arg Gly Glu Met		
500		

<210> 149

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 149

gcgtggtcca cctctacagg gacg 24

<210> 150

<211> 23

<212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Synthetic oligonucleotide probe  
  
 <400> 150  
 ggaactgacc cagtgtgac acc 23  
  
 <210> 151  
 <211> 45  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Synthetic oligonucleotide probe  
  
 <400> 151  
 gcagatgcc cagtatcaag gcaggacaaa actggtgaag gattc 45  
  
 <210> 152  
 <211> 2294  
 <212> DNA  
 <213> Homo sapiens  
  
 <400> 152  
 gcgatggtgc gcccggtggc ggtggcggcg gcggttgccg aggcttcctt 50  
 ggtcggattg caacgaggag aagatgactg accaaccgac tggctgaatg 100  
 aatgaatggc ggagccgagc gcgccatgag gagcctgccg agcctgggcg 150  
 gcctcgccct gttgtgctgc gccgccgccg ccgccgccgt cgcctcagcc 200  
 gcctcggcgg ggaatgtcac cggcggcggc ggggccgcgg ggcaggtgga 250  
 cgcgtcgccg ggccccgggt tgcggggcga gccagccac cccttccta 300  
 gggcgacggc tcccacggcc caggccccga ggaccgggcc cccgcgcgcc 350  
 accgtccacc gacccttggc tgcgacttct ccagcccagt ccccgagac 400  
 caccctctt tgggcgactg ctggaccctc ttccaccacc tttcaggcgc 450  
 cgctcggccc ctgcgcgacc acccctccgg cggcggaacg cacttcgacc 500  
 acctctcagg cgccgaccag acccgcgccg accacccttt cgacgaccac 550  
 tggcccggcg ccgaccaccc ctgtagcgac caccgtaccg gcgcccacga 600  
 ctccccggac cccgaccccc gatctcccca gcagcagcaa cagcagcgtc 650  
 ctccccaccc cacctgccac cgaggcccc tcttcgcctc ctccagagta 700  
 tgtatgtaac tgctctgtgg ttggaagcct gaatgtgaat cgctgcaacc 750  
 agaccacagg gcagtgtgag tgtcggccag gttatcagg gcttcactgt 800



gaaacctgca aagagggctt ttacctaaat tacacttctg ggctctgtca 850  
gccatgtgac tgtagtccac atggagctct cagcataccg tgcaacaggt 900  
aagcaacaga ggggtggaact gaagtttatt ttatttttagc aagggaaaaa 950  
aaaaggctgc tactctcaag gaccatactg gtttaaaciaa aggaggatga 1000  
gggtcataga ttacaaaaat attttatata cttttattct cttactttat 1050  
atgttatatt taatgtcagg atttaaaaac atctaattta ctgatttagt 1100  
tcttcaaaag cactagagtc gccaatTTTT ctctgggata atttctgtaa 1150  
atttcatggg aaaaaattat tgaagaataa atctgctttc tggaagggt 1200  
ttcaggcatg aaacctgcta ggaggtttag aaatgttctt atgtttatta 1250  
atataccatt ggagtttgag gaaatttggt gtttggttta tttttctctc 1300  
taatcaaaat tctacatttg tttctttgga catctaaagc ttaacctggg 1350  
ggtagcctaa tttatttaac tagtggttag tagactggtt ttactctatt 1400  
taccagtaca tttttgagac caaaagtaga ttaagcagga attatcttta 1450  
aactattatg ttatttgag gtaatttaat ctagtggaat aatgtactgt 1500  
tatctaagca ttgacctgt actgcactga aagtaattat tctttgacct 1550  
tatgtgaggc acttggtttt ttgtggacc caagtcaaaa aactgaagag 1600  
acagtattaa ataataaaaa aaataatgac aggttatact cagtgttaacc 1650  
tggttataac ccaagatctg ctgccactta cgagctgtgt tccttgggca 1700  
agtaatttcc tttcactgag cttgtttctt ctcaagggtt ttgtgaagat 1750  
taaagaggt gatatatata aaatgcctag cacatgtcac tcaataaatt 1800  
ctggtttggt ttaatttcaa aggaatatta tggactgaaa tgagagaaca 1850  
tgttttaaga acttttagct cttgacaaa gaagtgttt atacttttagc 1900  
actaaatatt ttaaagtctt tataaatgat attatactgt tatggaatat 1950  
tgtatcatat tgtagtttat taaaaatgta gaagaggctg ggcgcggtgg 2000  
ctcacgctg taatcctagc actttgggag gccaaaggcg gtggatcact 2050  
tgaggccagg agttctagat gagcctggcc agcacagtga aacccgtct 2100  
ctactaaaaa tacaaacaaa ttagctgggc gtggtggcac acacctgtag 2150  
tcccagctac tcgggagggt gaggcaggag aatcggttga acccgaggag 2200

tggaggttgc agtgagctga gatcgcgccca ctgcactcca gcctggtgag 2250

agaggggagac tctgtcttaa aaaaaaaaaa aaaaaaaaaa aaaa 2294

<210> 153

<211> 258

<212> PRT

<213> Homo sapiens

<400> 153

Met	Arg	Ser	Leu	Pro	Ser	Leu	Gly	Gly	Leu	Ala	Leu	Leu	Cys	Cys
1				5					10					15

Ala	Ala	Ala	Ala	Ala	Ala	Val	Ala	Ser	Ala	Ala	Ser	Ala	Gly	Asn
				20					25					30

Val	Thr	Gly	Gly	Gly	Gly	Ala	Ala	Gly	Gln	Val	Asp	Ala	Ser	Pro
				35					40					45

Gly	Pro	Gly	Leu	Arg	Gly	Glu	Pro	Ser	His	Pro	Phe	Pro	Arg	Ala
				50					55					60

Thr	Ala	Pro	Thr	Ala	Gln	Ala	Pro	Arg	Thr	Gly	Pro	Pro	Arg	Ala
				65					70					75

Thr	Val	His	Arg	Pro	Leu	Ala	Ala	Thr	Ser	Pro	Ala	Gln	Ser	Pro
				80					85					90

Glu	Thr	Thr	Pro	Leu	Trp	Ala	Thr	Ala	Gly	Pro	Ser	Ser	Thr	Thr
				95					100					105

Phe	Gln	Ala	Pro	Leu	Gly	Pro	Ser	Pro	Thr	Thr	Pro	Pro	Ala	Ala
				110					115					120

Glu	Arg	Thr	Ser	Thr	Thr	Ser	Gln	Ala	Pro	Thr	Arg	Pro	Ala	Pro
				125					130					135

Thr	Thr	Leu	Ser	Thr	Thr	Thr	Gly	Pro	Ala	Pro	Thr	Thr	Pro	Val
				140					145					150

Ala	Thr	Thr	Val	Pro	Ala	Pro	Thr	Thr	Pro	Arg	Thr	Pro	Thr	Pro
				155					160					165

Asp	Leu	Pro	Ser	Ser	Ser	Asn	Ser	Ser	Val	Leu	Pro	Thr	Pro	Pro
				170					175					180

Ala	Thr	Glu	Ala	Pro	Ser	Ser	Pro	Pro	Pro	Glu	Tyr	Val	Cys	Asn
				185					190					195

Cys	Ser	Val	Val	Gly	Ser	Leu	Asn	Val	Asn	Arg	Cys	Asn	Gln	Thr
				200					205					210

Thr	Gly	Gln	Cys	Glu	Cys	Arg	Pro	Gly	Tyr	Gln	Gly	Leu	His	Cys
				215					220					225

Glu	Thr	Cys	Lys	Glu	Gly	Phe	Tyr	Leu	Asn	Tyr	Thr	Ser	Gly	Leu
				230					235					240

Cys Gln Pro Cys Asp Cys Ser Pro His Gly Ala Leu Ser Ile Pro  
245 250 255

Cys Asn Arg

<210> 154

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 154

aactgctctg tggttggaag cctg 24

<210> 155

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 155

cagtcacatg gctgacagac ccac 24

<210> 156

<211> 38

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 156

aggttatcag gggcttcact gtgaaacctg caaagagg 38

<210> 157

<211> 689

<212> DNA

<213> Homo sapiens

<400> 157

tgcggcgacg tgtagacctg ggaggatggg cggcctgctg ctggctgctt 50

ttctggcttt ggtctcggtg cccagggccc aggccgtgtg gttgggaaga 100

ctggaccctg agcagcttct tgggccctgg tacgtgcttg cggtggcctc 150

ccgggaaaag ggctttgcc aaggagaagga catgaagaac gtcgtggggg 200

tggtgggtgac cctcactcca gaaaacaacc tgcggacgct gtcctctcag 250

cacgggctgg gaggggtgtga ccagagtgtc atggacctga taaagcgaaa 300

ctccggatgg gtgtttgaga atccctcaat aggcgtgctg gagctctggg 350  
 tgctggccac caacttcaga gactatgcc aatctttcac tcagctggag 400  
 ttcggggacg agcccttcaa caccgtggag ctgtacagtc tgacggagac 450  
 agccagccag gaggccatgg ggctcttcac caagtggagc aggagcctgg 500  
 gcttcctgtc acagtagcag gccagctgc agaaggacct cacctgtgct 550  
 cacaagatcc ttctgtgagt gctgcgtccc cagtagggat ggcgccaca 600  
 gggtcctgtg acctcgcca gtgtccaccc acctcgctca gcggctcccg 650  
 gggcccagca ccagctcaga ataaagcgat tccacagca 689

<210> 158

<211> 163

<212> PRT

<213> Homo sapiens

<400> 158

Met	Gly	Gly	Leu	Leu	Leu	Ala	Ala	Phe	Leu	Ala	Leu	Val	Ser	Val
1				5					10					15

Pro	Arg	Ala	Gln	Ala	Val	Trp	Leu	Gly	Arg	Leu	Asp	Pro	Glu	Gln
			20						25					30

Leu	Leu	Gly	Pro	Trp	Tyr	Val	Leu	Ala	Val	Ala	Ser	Arg	Glu	Lys
			35						40					45

Gly	Phe	Ala	Met	Glu	Lys	Asp	Met	Lys	Asn	Val	Val	Gly	Val	Val
			50						55					60

Val	Thr	Leu	Thr	Pro	Glu	Asn	Asn	Leu	Arg	Thr	Leu	Ser	Ser	Gln
			65						70					75

His	Gly	Leu	Gly	Gly	Cys	Asp	Gln	Ser	Val	Met	Asp	Leu	Ile	Lys
			80						85					90

Arg	Asn	Ser	Gly	Trp	Val	Phe	Glu	Asn	Pro	Ser	Ile	Gly	Val	Leu
			95						100					105

Glu	Leu	Trp	Val	Leu	Ala	Thr	Asn	Phe	Arg	Asp	Tyr	Ala	Ile	Ile
			110						115					120

Phe	Thr	Gln	Leu	Glu	Phe	Gly	Asp	Glu	Pro	Phe	Asn	Thr	Val	Glu
			125						130					135

Leu	Tyr	Ser	Leu	Thr	Glu	Thr	Ala	Ser	Gln	Glu	Ala	Met	Gly	Leu
			140						145					150

Phe	Thr	Lys	Trp	Ser	Arg	Ser	Leu	Gly	Phe	Leu	Ser	Gln
			155						160			

<210> 159

<211> 1665

<212> DNA

<213> Homo sapiens

<400> 159

aacagacgtt ccctcgcggc cctggcacct ctaaccccag acatgctgct 50  
gctgctgctg cccctgctct gggggaggga gagggcggaa ggacagacaa 100  
gtaaactgct gacgatgcag agttccgtga cggatgcagga aggcctgtgt 150  
gtccatgtgc cctgctcctt ctccctacccc tcgcatggct ggatttacct 200  
tggcccagta gttcatggct actggttccg ggaagggggc aatacagacc 250  
aggatgctcc agtggccaca aacaacccag ctccgggcagt gtgggaggag 300  
actcgggacc gattccacct ccttggggac ccacatacca agaattgcac 350  
cctgagcatc agagatgcc aagaagtga tgcggggaga tacttctttc 400  
gtatggagaa aggaagtata aaatggaatt ataaacatca ccggctctct 450  
gtgaatgtga cagccttgac ccacaggccc aacatcctca tcccaggcac 500  
cctggagtcc ggctgcccc agaatctgac ctgctctgtg ccctgggcct 550  
gtgagcaggg gacaccccct atgatctcct ggataggagc ctccgtgtcc 600  
cccctggacc cctccaccac ccgctcctcg gtgctcacc tcaccccaca 650  
gccccaggac catggcacca gcctcacctg tcaggtgacc ttccctgggg 700  
ccagcgtgac cacgaacaag accgtccatc tcaacgtgtc ctacccgcct 750  
cagaacttga ccatgactgt cttccaagga gacggcacag tatccacagt 800  
cttgggaaat ggctcatctc tgtcactccc agagggccag tctctgcgc 850  
tggtctgtgc agttgatgca gttgacagca atccccctgc caggctgagc 900  
ctgagctgga gaggcctgac cctgtgcccc tcacagccct caaacccggg 950  
ggtgctggag ctgccttggg tgcacctgag ggatgcagct gaattcacct 1000  
gcagagctca gaaccctctc ggctctcagc aggtctacct gaacgtctcc 1050  
ctgcagagca aagccacatc aggagtgact caggggggtg tcgggggagc 1100  
tgaggctctg caggaagaaa tcggcaaggc cagcagcggg cgtgggagat 1200  
acgggcatag aggatgcaaa cgctgtcagg ggttcagcct ctacggggcc 1250  
cctgactgaa ccttgggcag aagacagtcc ccagaccag cctccccag 1300

cttctgccccg ctcctcagtg ggggaaggag agctccagta tgcattccctc 1350  
agcttccaga tggatgaagcc ttgggactcg cggggacagg aggccactga 1400  
caccgagtac tcggagatca agatccacag atgagaaact gcagagactc 1450  
accctgattg agggatcaca gcccctccag gcaagggaga agtcagaggc 1500  
tgattcttgt agaattaaca gccctcaacg tgatgagcta tgataacact 1550  
atgaattatg tgcagagtga aaagcacaca ggcttttagag tcaaagtatc 1600  
tcaaacctga atccacactg tgccctccct tttatTTTTT taactaaaag 1650  
acagacaaat tccta 1665

<210> 160

<211> 463

<212> PRT

<213> Homo sapiens

<400> 160

Met	Leu	Leu	Leu	Leu	Leu	Pro	Leu	Leu	Trp	Gly	Arg	Glu	Arg	Ala
1				5					10					15

Glu	Gly	Gln	Thr	Ser	Lys	Leu	Leu	Thr	Met	Gln	Ser	Ser	Val	Thr
				20					25					30

Val	Gln	Glu	Gly	Leu	Cys	Val	His	Val	Pro	Cys	Ser	Phe	Ser	Tyr
				35					40					45

Pro	Ser	His	Gly	Trp	Ile	Tyr	Pro	Gly	Pro	Val	Val	His	Gly	Tyr
				50					55					60

Trp	Phe	Arg	Glu	Gly	Ala	Asn	Thr	Asp	Gln	Asp	Ala	Pro	Val	Ala
				65					70					75

Thr	Asn	Asn	Pro	Ala	Arg	Ala	Val	Trp	Glu	Glu	Thr	Arg	Asp	Arg
				80					85					90

Phe	His	Leu	Leu	Gly	Asp	Pro	His	Thr	Lys	Asn	Cys	Thr	Leu	Ser
				95					100					105

Ile	Arg	Asp	Ala	Arg	Arg	Ser	Asp	Ala	Gly	Arg	Tyr	Phe	Phe	Arg
				110					115					120

Met	Glu	Lys	Gly	Ser	Ile	Lys	Trp	Asn	Tyr	Lys	His	His	Arg	Leu
				125					130					135

Ser	Val	Asn	Val	Thr	Ala	Leu	Thr	His	Arg	Pro	Asn	Ile	Leu	Ile
				140					145					150

Pro	Gly	Thr	Leu	Glu	Ser	Gly	Cys	Pro	Gln	Asn	Leu	Thr	Cys	Ser
				155					160					165

Val	Pro	Trp	Ala	Cys	Glu	Gln	Gly	Thr	Pro	Pro	Met	Ile	Ser	Trp
				170					175					180

Ile Gly Thr Ser	Val Ser Pro Leu Asp	Pro Ser Thr Thr Arg Ser
185	190	195
Ser Val Leu Thr	Leu Ile Pro Gln Pro	Gln Asp His Gly Thr Ser
200	205	210
Leu Thr Cys Gln	Val Thr Phe Pro Gly	Ala Ser Val Thr Thr Asn
215	220	225
Lys Thr Val His	Leu Asn Val Ser Tyr	Pro Pro Gln Asn Leu Thr
230	235	240
Met Thr Val Phe	Gln Gly Asp Gly Thr	Val Ser Thr Val Leu Gly
245	250	255
Asn Gly Ser Ser	Leu Ser Leu Pro Glu	Gly Gln Ser Leu Arg Leu
260	265	270
Val Cys Ala Val	Asp Ala Val Asp Ser	Asn Pro Pro Ala Arg Leu
275	280	285
Ser Leu Ser Trp	Arg Gly Leu Thr Leu	Cys Pro Ser Gln Pro Ser
290	295	300
Asn Pro Gly Val	Leu Glu Leu Pro Trp	Val His Leu Arg Asp Ala
305	310	315
Ala Glu Phe Thr	Cys Arg Ala Gln Asn	Pro Leu Gly Ser Gln Gln
320	325	330
Val Tyr Leu Asn	Val Ser Leu Gln Ser	Lys Ala Thr Ser Gly Val
335	340	345
Thr Gln Gly Val	Val Gly Gly Ala Gly	Ala Thr Ala Leu Val Phe
350	355	360
Leu Ser Phe Cys	Val Ile Phe Val Val	Val Arg Ser Cys Arg Lys
365	370	375
Lys Ser Ala Arg	Pro Ala Ala Gly Val	Gly Asp Thr Gly Ile Glu
380	385	390
Asp Ala Asn Ala	Val Arg Gly Ser Ala	Ser Gln Gly Pro Leu Thr
395	400	405
Glu Pro Trp Ala	Glu Asp Ser Pro Pro	Asp Gln Pro Pro Pro Ala
410	415	420
Ser Ala Arg Ser	Ser Val Gly Glu Gly	Glu Leu Gln Tyr Ala Ser
425	430	435
Leu Ser Phe Gln	Met Val Lys Pro Trp	Asp Ser Arg Gly Gln Glu
440	445	450
Ala Thr Asp Thr	Glu Tyr Ser Glu Ile	Lys Ile His Arg
455	460	

<210> 161  
<211> 739  
<212> DNA  
<213> Homo sapiens

<400> 161  
gacgcccagt gacctgccga ggtcggcagc acagagctct ggagatgaag 50  
accctgttcc tgggtgtcac gctcggcctg gccgctgccc tgtccttcac 100  
cctggaggag gaggatatca cagggacctg gtacgtgaag gccatggtgg 150  
tcgataagga ctttccggag gacaggaggc ccaggaaggt gtccccagtg 200  
aaggtgacag ccctgggcgg tgggaagttg gaagccacgt tcaccttcat 250  
gagggaggat cgggtgcatcc agaagaaaat cctgatgcgg aagacggagg 300  
agcctggcaa atacagcgcc tatgggggca ggaagctcat gtacctgcag 350  
gagctgcccc ggaggggacca ctacatcttt tactgcaaag accagcacca 400  
tgggggcctg ctccacatgg gaaagcttgt gggtaggaat tctgatacca 450  
accgggaggc cctggaagaa ttttaagaaat tgggtgcagcg caagggactc 500  
tcggaggagg acattttcac gccctgcag acgggaagct gcgttccga 550  
acactaggca gccccgggt ctgcacctcc agagcccacc ctaccaccag 600  
acacagagcc cggaccacct ggacctaccc tccagccatg acccttcctt 650  
gctcccaccc acctgactcc aaataaagtc cttttcccc aaaaaaaaaa 700  
aaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 739

<210> 162  
<211> 170  
<212> PRT  
<213> Homo sapiens

<400> 162  
Met Lys Thr Leu Phe Leu Gly Val Thr Leu Gly Leu Ala Ala Ala  
1 5 10 15  
Leu Ser Phe Thr Leu Glu Glu Glu Asp Ile Thr Gly Thr Trp Tyr  
20 25 30  
Val Lys Ala Met Val Val Asp Lys Asp Phe Pro Glu Asp Arg Arg  
35 40 45  
Pro Arg Lys Val Ser Pro Val Lys Val Thr Ala Leu Gly Gly Gly  
50 55 60  
Lys Leu Glu Ala Thr Phe Thr Phe Met Arg Glu Asp Arg Cys Ile  
65 70 75



Gln	Lys	Lys	Ile	Leu	Met	Arg	Lys	Thr	Glu	Glu	Pro	Gly	Lys	Tyr	
				80					85					90	
Ser	Ala	Tyr	Gly	Gly	Arg	Lys	Leu	Met	Tyr	Leu	Gln	Glu	Leu	Pro	
				95					100					105	
Arg	Arg	Asp	His	Tyr	Ile	Phe	Tyr	Cys	Lys	Asp	Gln	His	His	Gly	
				110					115					120	
Gly	Leu	Leu	His	Met	Gly	Lys	Leu	Val	Gly	Arg	Asn	Ser	Asp	Thr	
				125					130					135	
Asn	Arg	Glu	Ala	Leu	Glu	Glu	Phe	Lys	Lys	Leu	Val	Gln	Arg	Lys	
				140					145					150	
Gly	Leu	Ser	Glu	Glu	Asp	Ile	Phe	Thr	Pro	Leu	Gln	Thr	Gly	Ser	
				155					160					165	
Cys	Val	Pro	Glu	His											
				170											

<210> 163  
 <211> 22  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 163  
 ggagatgaag accctgttcc tg 22

<210> 164  
 <211> 26  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 164  
 ggagatgaag accctgttcc tgggtg 26

<210> 165  
 <211> 21  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 165  
 gtcctccgga aagtccttat c 21

<210> 166  
 <211> 25

<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 166  
gcctagtgtt cggaacgca gcttc 25

<210> 167  
<211> 50  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 167  
cagggacctg gtacgtgaag gccatggtgg tcgataagga ctttcggag 50

<210> 168  
<211> 45  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 168  
ctgtccttca ccctggagga ggaggatc acagggacct ggtac 45

<210> 169  
<211> 1204  
<212> DNA  
<213> Homo sapiens

<400> 169  
gttccgcaga tgcagaggtt gaggtggctg cgggactgga agtcacgagg 50  
cagaggtctc acagcagcca aggaacctgg ggcccgtcc tccccctcc 100  
aggccatgag gattctgcag ttaatcctgc ttgctctggc aacagggctt 150  
gtagggggag agaccaggat catcaagggg ttcgagtgc agcctcactc 200  
ccagccctgg caggcagccc tggtcgagaa gacgcggcta ctctgtggg 250  
cgacgctcat cgccccaga tggctcctga cagcagccca ctgcctcaag 300  
ccccgctaca tagttcacct ggggcagcac aacctccaga aggaggagg 350  
ctgtgagcag acccgacag cactgagtc cttccccac cccggcttca 400  
acaacagcct cccaacaaa gaccaccgca atgacatcat gctggtgaag 450  
atggcatcgc cagtctccat cacctgggct gtgcgacccc tcaccctctc 500

ctcacgctgt gtcactgctg gcaccagctg cctcatttcc ggctggggca 550  
 gcacgtccag cccccagtta cgctgcctc acaccttgcg atgcgccaac 600  
 atcaccatca ttgagcacca gaagtgtgag aacgcctacc ccggcaacat 650  
 cacagacacc atggtgtgtg ccagcgtgca ggaagggggc aaggactcct 700  
 gccaggggtga ctccgggggc cctctggtct gtaaccagtc tcttcaaggc 750  
 attatctcct ggggccagga tccgtgtgcg atcacccgaa agcctggtgt 800  
 ctacacgaaa gtctgcaa atgtggactg gatccaggag acgatgaaga 850  
 acaattagac tggaccacc caccacagcc catcacctc catttccact 900  
 tgggtgtttgg ttcctgttca ctctgttaat aagaaaccct aagccaagac 950  
 cctctacgaa cattctttgg gcctcctgga ctacaggaga tgctgtcact 1000  
 taataatcaa cctgggggttc gaaatcagtg agacctggat tcaaattctg 1050  
 ccttgaaata ttgtgactct gggaatgaca acacctggtt tggtctctgt 1100  
 tgtatcccca gccc aaaga cagctcctgg ccatatatca aggtttcaat 1150  
 aaatatttgc taaatgaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 1200  
 aaaa 1204

<210> 170  
 <211> 250  
 <212> PRT  
 <213> Homo sapiens

<400> 170  
 Met Arg Ile Leu Gln Leu Ile Leu Leu Ala Leu Ala Thr Gly Leu  
 1 5 10 15  
 Val Gly Gly Glu Thr Arg Ile Ile Lys Gly Phe Glu Cys Lys Pro  
 20 25 30  
 His Ser Gln Pro Trp Gln Ala Ala Leu Phe Glu Lys Thr Arg Leu  
 35 40 45  
 Leu Cys Gly Ala Thr Leu Ile Ala Pro Arg Trp Leu Leu Thr Ala  
 50 55 60  
 Ala His Cys Leu Lys Pro Arg Tyr Ile Val His Leu Gly Gln His  
 65 70 75  
 Asn Leu Gln Lys Glu Glu Gly Cys Glu Gln Thr Arg Thr Ala Thr  
 80 85 90  
 Glu Ser Phe Pro His Pro Gly Phe Asn Asn Ser Leu Pro Asn Lys  
 95 100 105

Asp	His	Arg	Asn	Asp	Ile	Met	Leu	Val	Lys	Met	Ala	Ser	Pro	Val	
				110					115					120	
Ser	Ile	Thr	Trp	Ala	Val	Arg	Pro	Leu	Thr	Leu	Ser	Ser	Arg	Cys	
				125					130					135	
Val	Thr	Ala	Gly	Thr	Ser	Cys	Leu	Ile	Ser	Gly	Trp	Gly	Ser	Thr	
				140					145					150	
Ser	Ser	Pro	Gln	Leu	Arg	Leu	Pro	His	Thr	Leu	Arg	Cys	Ala	Asn	
				155					160					165	
Ile	Thr	Ile	Ile	Glu	His	Gln	Lys	Cys	Glu	Asn	Ala	Tyr	Pro	Gly	
				170					175					180	
Asn	Ile	Thr	Asp	Thr	Met	Val	Cys	Ala	Ser	Val	Gln	Glu	Gly	Gly	
				185					190					195	
Lys	Asp	Ser	Cys	Gln	Gly	Asp	Ser	Gly	Gly	Pro	Leu	Val	Cys	Asn	
				200					205					210	
Gln	Ser	Leu	Gln	Gly	Ile	Ile	Ser	Trp	Gly	Gln	Asp	Pro	Cys	Ala	
				215					220					225	
Ile	Thr	Arg	Lys	Pro	Gly	Val	Tyr	Thr	Lys	Val	Cys	Lys	Tyr	Val	
				230					235					240	
Asp	Trp	Ile	Gln	Glu	Thr	Met	Lys	Asn	Asn						
				245					250						

<210> 171

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 171

ggctgcgggga ctggaagtca tcggg 25

<210> 172

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 172

ctccaggcca tgaggattct gcag 24

<210> 173

<211> 18

<212> DNA

<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe  
  
<400> 173  
cctctgggtct gtaaccag 18  
  
<210> 174  
<211> 24  
<212> DNA  
<213> Artificial Sequence  
  
<220>  
<223> Synthetic oligonucleotide probe  
  
<400> 174  
tctgtgatgt tgccggggta ggcg 24  
  
<210> 175  
<211> 25  
<212> DNA  
<213> Artificial Sequence  
  
<220>  
<223> Synthetic oligonucleotide probe  
  
<400> 175  
cgtgtagaca ccaggctttc gggcg 25  
  
<210> 176  
<211> 18  
<212> DNA  
<213> Artificial Sequence  
  
<220>  
<223> Synthetic oligonucleotide probe  
  
<400> 176  
cccttgatga tcctgggc 18  
  
<210> 177  
<211> 50  
<212> DNA  
<213> Artificial Sequence  
  
<220>  
<223> Synthetic oligonucleotide probe  
  
<400> 177  
aggccatgag gattctgcag ttaatcctgc ttgctctggc aacagggctt 50  
  
<210> 178  
<211> 43  
<212> DNA  
<213> Artificial Sequence  
  
<220>  
<223> Synthetic oligonucleotide probe

<400> 178  
gagagaccag gatcatcaag gggttcgagt gcaagcctca ctc 43

<210> 179  
<211> 907  
<212> DNA  
<213> Homo sapiens

<400> 179  
gagcagtgtt ctgctggagc cgatgccaaa aaccatgcat ttcttattca 50  
gattcattgt tttcttttat ctgtggggcc tttttactgc tcagagacaa 100  
aagaaagagg agagcaccga agaagtgaag atagaagttt tgcacgtcc 150  
agaaaactgc tctaagacaa gcaagaagg agacctacta aatgcccatt 200  
atgacggcta cctggctaaa gacggctcga aattctactg cagccggaca 250  
caaatgaag gccaccccaa atgggttggt cttggtgttg ggcaagtcac 300  
aaaaggccta gacattgcta tgacagatat gtgccctgga gaaaagcgaa 350  
aagtagttat acccccttca tttgcatacg gaaaggaagg ctatgcagaa 400  
ggcaagattc caccggatgc tacattgatt tttgagattg aactttatgc 450  
tgtgaccaa ggcacacgga gcattgagac atttaacaa atagacatgg 500  
acaatgacag gcagctctct aaagccgaga taaacctcta cttgcaaagg 550  
gaatttgaaa aagatgagaa gccacgtgac aagtcataac aggatgcagt 600  
tttagaagat atttttaaga agaatgacca tgatggtgat ggcttcattt 650  
ctccaagga atacaatgta taccaacacg atgaactata gcatatttgt 700  
atttctactt ttttttttta gctatttact gtactttatg tataaaacaa 750  
agtcactttt ctccaagttg tatttgctat ttttcccta tgagaagata 800  
tttgatctc cccaatacat tgattttggt ataataaatg tgaggctgtt 850  
ttgcaaaactt aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 900  
aaaaaaa 907

<210> 180  
<211> 222  
<212> PRT  
<213> Homo sapiens

<400> 180  
Met Pro Lys Thr Met His Phe Leu Phe Arg Phe Ile Val Phe Phe  
1 5 10 15

Tyr	Leu	Trp	Gly	Leu	Phe	Thr	Ala	Gln	Arg	Gln	Lys	Lys	Glu	Glu	
				20					25					30	
Ser	Thr	Glu	Glu	Val	Lys	Ile	Glu	Val	Leu	His	Arg	Pro	Glu	Asn	
				35					40					45	
Cys	Ser	Lys	Thr	Ser	Lys	Lys	Gly	Asp	Leu	Leu	Asn	Ala	His	Tyr	
				50					55					60	
Asp	Gly	Tyr	Leu	Ala	Lys	Asp	Gly	Ser	Lys	Phe	Tyr	Cys	Ser	Arg	
				65					70					75	
Thr	Gln	Asn	Glu	Gly	His	Pro	Lys	Trp	Phe	Val	Leu	Gly	Val	Gly	
				80					85					90	
Gln	Val	Ile	Lys	Gly	Leu	Asp	Ile	Ala	Met	Thr	Asp	Met	Cys	Pro	
				95					100					105	
Gly	Glu	Lys	Arg	Lys	Val	Val	Ile	Pro	Pro	Ser	Phe	Ala	Tyr	Gly	
				110					115					120	
Lys	Glu	Gly	Tyr	Ala	Glu	Gly	Lys	Ile	Pro	Pro	Asp	Ala	Thr	Leu	
				125					130					135	
Ile	Phe	Glu	Ile	Glu	Leu	Tyr	Ala	Val	Thr	Lys	Gly	Pro	Arg	Ser	
				140					145					150	
Ile	Glu	Thr	Phe	Lys	Gln	Ile	Asp	Met	Asp	Asn	Asp	Arg	Gln	Leu	
				155					160					165	
Ser	Lys	Ala	Glu	Ile	Asn	Leu	Tyr	Leu	Gln	Arg	Glu	Phe	Glu	Lys	
				170					175					180	
Asp	Glu	Lys	Pro	Arg	Asp	Lys	Ser	Tyr	Gln	Asp	Ala	Val	Leu	Glu	
				185					190					195	
Asp	Ile	Phe	Lys	Lys	Asn	Asp	His	Asp	Gly	Asp	Gly	Phe	Ile	Ser	
				200					205					210	
Pro	Lys	Glu	Tyr	Asn	Val	Tyr	Gln	His	Asp	Glu	Leu				
				215					220						

<210> 181

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 181

gtgttctgct ggagccgatg cc 22

<210> 182

<211> 18

<212> DNA

<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 182  
gacatggaca atgacagg 18

<210> 183  
<211> 18  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 183  
cctttcagga tgtaggag 18

<210> 184  
<211> 18  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 184  
gatgtctgcc accccaag 18

<210> 185  
<211> 27  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 185  
gcacacctgat atgacttgac acgtggc 27

<210> 186  
<211> 24  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 186  
tacaagaggg aagaggagtt gcac 24

<210> 187  
<211> 52  
<212> DNA  
<213> Artificial Sequence

<220>



<223> Synthetic oligonucleotide probe

<400> 187

gcccattatg acggtacct ggctaaagac ggctcgaaat tctactgcag 50

cc 52

<210> 188

<211> 573

<212> DNA

<213> Homo sapiens

<400> 188

cagaaatgca gggaccattg cttcttccag gcctctgctt tctgctgagc 50

ctctttggag ctgtgactca gaaaaccaa acttcctgtg ctaagtgcc 100

cccaaatgct tcctgtgtca ataactactca ctgcacctgc aaccatggat 150

atacttctgg atctgggcag aaactattca cattccccctt ggagacatgt 200

aacgccaggc atggtggctc gcgcctgtaa tcccagttct ttgggaagcc 250

aaggcagggtg gatcacctga ggtcaggagt ttgagaccag cctggccaac 300

atagtgaac ccctgtgtcta ctaaaaatac aaaaatcagc cgggcgtggt 350

ggtgcatgcc tgcaatccca gttactcggg aggctgaggc aggagaatcg 400

cttgaactca ggaggcagaa gttgcagtga acccagatcc tgccattgca 450

ctccagcatg gatgacagag caagactccg tctcaaaaag aaaagatagt 500

ttcttgtttc atttcgcgac tgccctctca gtgtttcctg ggatcccctc 550

ccaaataaag tacttatatt ctc 573

<210> 189

<211> 74

<212> PRT

<213> Homo sapiens

<400> 189

Met	Gln	Gly	Pro	Leu	Leu	Leu	Pro	Gly	Leu	Cys	Phe	Leu	Leu	Ser
1				5					10					15

Leu	Phe	Gly	Ala	Val	Thr	Gln	Lys	Thr	Lys	Thr	Ser	Cys	Ala	Lys
				20					25					30

Cys	Pro	Pro	Asn	Ala	Ser	Cys	Val	Asn	Asn	Thr	His	Cys	Thr	Cys
				35					40					45

Asn	His	Gly	Tyr	Thr	Ser	Gly	Ser	Gly	Gln	Lys	Leu	Phe	Thr	Phe
				50					55					60

Pro	Leu	Glu	Thr	Cys	Asn	Ala	Arg	His	Gly	Gly	Ser	Arg	Leu
				65					70				

<210> 190  
<211> 24  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 190  
agggaccatt gcttcttcca ggcc 24

<210> 191  
<211> 24  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 191  
cgttacatgt ctccaagggg aatg 24

<210> 192  
<211> 50  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 192  
cctgtgctaa gtgcccccca aatgcttcct gtgtcaataa cactcactgc 50

<210> 193  
<211> 1091  
<212> DNA  
<213> Homo sapiens

<400> 193  
caagcagggtc atccccttgg tgaccttcaa agagaagcag agagggcaga 50  
gggtggggggc acagggaaag ggtgacctct gagattcccc ttttccccca 100  
gactttggaa gtgaccacc atggggctca gcatcttttt gctcctgtgt 150  
gttcttgggc tcagccaggc agccacaccg aagattttca atggcactga 200  
gtgtgggcgt aactcacagc cgtggcaggt ggggctgttt gagggcacca 250  
gcctgcgctg cggggggtgtc cttattgacc acaggtgggt cctcacagcg 300  
gctcactgca gcggcagcag gtactgggtg cgctggggg aacacagcct 350  
cagccagctc gactggaccg agcagatccg gcacagcggc ttctctgtga 400  
cccatcccgg ctacctggga gcctcgacga gccacgagca cgacctccgg 450

ctgctgcggc tgcgcctgcc cgtccgcgta accagcagcg ttcaaccctt 500  
 gcccctgccc aatgactgtg caaccgctgg caccgagtgc cacgtctcag 550  
 gctggggcat caccaaccac ccacggaacc cattcccgga tctgctccag 600  
 tgcctcaacc tctccatcgt ctcccatgcc acctgccatg gtgtgtatcc 650  
 cgggagaatc acgagcaaca tgggtgtgtgc aggcggcgtc ccggggcagg 700  
 atgcctgcca ggggtgattct gggggccccc tgggtgtgtgg gggagtcctt 750  
 caaggctctgg tgtcctgggg gtctgtgggg ccctgtggac aagatggcat 800  
 ccctggagtc tacacctata tttgcaagta tgtggactgg atccggatga 850  
 tcatgaggaa caactgacct gtttctcca cctccacccc cacccttaa 900  
 cttgggtacc cctctggccc tcagagcacc aatatctcct ccatcacttc 950  
 ccctagctcc actcttggtg gcctgggaac ttcttggaac tttaactcct 1000  
 gccagccctt ctaagacca cgagcggggg gagagaagtg tgcaatagtc 1050  
 tggaataaat ataatgaag gaggggcaaa aaaaaaaaaa a 1091

<210> 194  
 <211> 248  
 <212> PRT  
 <213> Homo sapiens

<400> 194  
 Met Gly Leu Ser Ile Phe Leu Leu Leu Cys Val Leu Gly Leu Ser  
 1 5 10 15  
 Gln Ala Ala Thr Pro Lys Ile Phe Asn Gly Thr Glu Cys Gly Arg  
 20 25 30  
 Asn Ser Gln Pro Trp Gln Val Gly Leu Phe Glu Gly Thr Ser Leu  
 35 40 45  
 Arg Cys Gly Gly Val Leu Ile Asp His Arg Trp Val Leu Thr Ala  
 50 55 60  
 Ala His Cys Ser Gly Ser Arg Tyr Trp Val Arg Leu Gly Glu His  
 65 70 75  
 Ser Leu Ser Gln Leu Asp Trp Thr Glu Gln Ile Arg His Ser Gly  
 80 85 90  
 Phe Ser Val Thr His Pro Gly Tyr Leu Gly Ala Ser Thr Ser His  
 95 100 105  
 Glu His Asp Leu Arg Leu Leu Arg Leu Arg Leu Pro Val Arg Val  
 110 115 120

Thr	Ser	Ser	Val	Gln	Pro	Leu	Pro	Leu	Pro	Asn	Asp	Cys	Ala	Thr	
				125					130					135	
Ala	Gly	Thr	Glu	Cys	His	Val	Ser	Gly	Trp	Gly	Ile	Thr	Asn	His	
				140					145					150	
Pro	Arg	Asn	Pro	Phe	Pro	Asp	Leu	Leu	Gln	Cys	Leu	Asn	Leu	Ser	
				155					160					165	
Ile	Val	Ser	His	Ala	Thr	Cys	His	Gly	Val	Tyr	Pro	Gly	Arg	Ile	
				170					175					180	
Thr	Ser	Asn	Met	Val	Cys	Ala	Gly	Gly	Val	Pro	Gly	Gln	Asp	Ala	
				185					190					195	
Cys	Gln	Gly	Asp	Ser	Gly	Gly	Pro	Leu	Val	Cys	Gly	Gly	Val	Leu	
				200					205					210	
Gln	Gly	Leu	Val	Ser	Trp	Gly	Ser	Val	Gly	Pro	Cys	Gly	Gln	Asp	
				215					220					225	
Gly	Ile	Pro	Gly	Val	Tyr	Thr	Tyr	Ile	Cys	Lys	Tyr	Val	Asp	Trp	
				230					235					240	
Ile	Arg	Met	Ile	Met	Arg	Asn	Asn								
				245											

<210> 195

<211> 1485

<212> DNA

<213> Homo sapiens

<400> 195

```

gcggccacac gcagctagcc ggagcccgga ccaggcgcct gtgcctcctc 50
ctcgtccctc gccgcgtccg cgaagcctgg agccggcggg agccccgcgc 100
tcgccatgtc gggcgagctc agcaacaggt tccaaggagg gaaggcgttc 150
ggcttgctca aagcccggca ggagaggagg ctggccgaga tcaaccggga 200
gtttctgtgt gaccagaagt acagtgatga agagaacctt ccagaaaagc 250
tcacagcctt caaagagaag tacatggagt ttgacctgaa caatgaaggc 300
gagattgacc tgatgtcttt aaagaggatg atggagaagc ttggtgtccc 350
caagaccac ctggagatga agaagatgat ctgagaggtg acaggagggg 400
tcagtgcac tatatcctac cgagactttg tgaacatgat gctggggaaa 450
cggtcggctg tcctcaagtt agtcatgatg tttgaaggaa aagccaacga 500
gagcagcccc aagccagttg gccccctcc agagagagac attgctagcc 550
tgccctgagg accccgcctg gactccccag ccttcccacc ccatactcc 600

```

ctcccgatct tgctgccctt cttgacacac tgtgatctct ctctctctca 650  
 tttgttttgt cattgagggg ttgttttgtt tttcatcaat gtctttgtaa 700  
 agcaciaaatt atctgcctta aaggggctct gggtcgggga atcctgagcc 750  
 ttgggtcccc tccctctctt cttccctcct tccccgctcc ctgtgcagaa 800  
 gggctgatat caaaccaaaa actagagggg gcagggccag ggcagggagg 850  
 cttccagcct gtgttccctt cacttggagg aaccagcact ctccatcctt 900  
 tcagaaagtc tccaagccaa gttcaggctc actgacctgg ctctgacgag 950  
 gaccccaggc cactctgaga agaccttga gtagggacaa ggctgcaggg 1000  
 cctctttcgg gtttccttgg acagtgccat ggttccagtg ctctggtgtc 1050  
 acccaggaca cagccactcg gggccccgct gccccagctg atccccactc 1100  
 attccacacc tcttctcatc ctcaagtatg tgaaggtggg aaggaaagga 1150  
 gcttggcatt gggagccctt caagaaggta ccagaaggaa ccctccagtc 1200  
 ctgctctctg gccacacctg tgcaggcagc tgagaggcag cgtgcagccc 1250  
 tactgtccct tactggggca gcagagggct tcggaggcag aagtgaggcc 1300  
 tggggtttgg ggggaaaggt cagctcagtg ctgttcacc ttttagggag 1350  
 gatactgagg ggaccaggat gggagaatga ggagtaaaat gctcacggca 1400  
 aagtcagcag cactggtaag ccaagactga gaaatacaag gttgcttgtc 1450  
 tgacccaat ctgcttgaaa aaaaaaaaaa aaaaa 1485

<210> 196

<211> 150

<212> PRT

<213> Homo sapiens

<400> 196

Met	Ser	Gly	Glu	Leu	Ser	Asn	Arg	Phe	Gln	Gly	Gly	Lys	Ala	Phe
1				5					10					15
Gly	Leu	Leu	Lys	Ala	Arg	Gln	Glu	Arg	Arg	Leu	Ala	Glu	Ile	Asn
			20						25					30
Arg	Glu	Phe	Leu	Cys	Asp	Gln	Lys	Tyr	Ser	Asp	Glu	Glu	Asn	Leu
			35						40					45
Pro	Glu	Lys	Leu	Thr	Ala	Phe	Lys	Glu	Lys	Tyr	Met	Glu	Phe	Asp
			50						55					60
Leu	Asn	Asn	Glu	Gly	Glu	Ile	Asp	Leu	Met	Ser	Leu	Lys	Arg	Met
			65						70					75

Met	Glu	Lys	Leu	Gly	Val	Pro	Lys	Thr	His	Leu	Glu	Met	Lys	Lys
				80					85					90
Met	Ile	Ser	Glu	Val	Thr	Gly	Gly	Val	Ser	Asp	Thr	Ile	Ser	Tyr
				95					100					105
Arg	Asp	Phe	Val	Asn	Met	Met	Leu	Gly	Lys	Arg	Ser	Ala	Val	Leu
				110					115					120
Lys	Leu	Val	Met	Met	Phe	Glu	Gly	Lys	Ala	Asn	Glu	Ser	Ser	Pro
				125					130					135
Lys	Pro	Val	Gly	Pro	Pro	Pro	Glu	Arg	Asp	Ile	Ala	Ser	Leu	Pro
				140					145					150

<210> 197

<211> 4842

<212> DNA

<213> Homo sapiens

<400> 197

```

cgcgctcccc ggcgcgcctcc tcgggctcca cgcgtcttgc cccgcagagg 50
cagcctcctc caggagcggg gccctgcaca ccatggcccc cgggtgggca 100
ggggtcggcg ccgccgtgcg cgccgcctg gcgctggcct tggcgctggc 150
gagcgtcctg agtgggcctc cagccgtcgc ctgccccacc aagtgtacct 200
gctccgctgc cagcgtggac tgccacgggc tgggcctccg cgcggttcct 250
cggggcatcc cccgcaacgc tgagcgcctt gacctggaca gaaataatat 300
caccaggatc accaagatgg acttcgctgg gctcaagaac ctccgagtct 350
tgcatctgga agacaaccag gtcagcgtca tcgagagagg cgccttcag 400
gacctgaagc agctagagcg actgcgcctg aacaagaata agctgcaagt 450
ccttcagaa ttgcttttcc agagcacgcc gaagctcacc agactagatt 500
tgagtgaaaa ccagatccag gggatccga ggaaggcgtt ccgcggcatc 550
accgatgtga agaacctgca actggacaac aaccacatca gctgcattga 600
agatggagcc ttccgagcgc tgcgcgattt ggagatcctt accctcaaca 650
acaacaacat cagtcgcctc ctggctacca gcttcaacca catgccgaag 700
atccgaactc tgcgcctcca ctccaaccac ctctactgcg actgccacct 750
ggcctggctc tcggattggc tgcgacagcg acggacagtt ggccagttca 800
cactctgcat ggctcctgtg catttgaggg gcttcaacgt ggcgatgtg 850
cagaagaagg agtacgtgtg ccagccccc cactcggagc ccccatcctg 900

```

caatgccaac tccatctcct gcccttcgcc ctgcacgtgc agcaataaca 950  
tcgtggactg tcgaggaaag ggcttgatgg agattcctgc caacttgccg 1000  
gagggcatcg tcgaaatacg cctagaacag aactccatca aagccatccc 1050  
tgcaggagcc ttcacccagt acaagaaact gaagcgaata gacatcagca 1100  
agaatcagat atcggatatt gctccagatg ccttccaggg cctgaaatca 1150  
ctcacatcgc tggctctgta tgggaacaag atcaccgaga ttgccaaggg 1200  
actgtttgat gggctggtgt ccctacagct gctcctcctc aatgccaaaca 1250  
agatcaactg cctgcgggtg aacacgtttc aggacctgca gaacctcaac 1300  
ttgctctccc tgtatgacaa caagctgcag accatcagca aggggctctt 1350  
cgcccctctg cagtccatcc agacactcca cttagcccaa aacctatttg 1400  
tgtgcgactg ccacttgaag tggctggccg actacctcca ggacaacccc 1450  
atcgagacaa gcggggcccg ctgcagcagc ccgcgcgcgac tcgccaacaa 1500  
gcgcatcagc cagatcaaga gcaagaagtt ccgctgctca ggctccgagg 1550  
attaccgcag caggttcagc agcgagtgtc tcatggacct cgtgtgcccc 1600  
gagaagtgtc gctgtgaggg cacgattgtg gactgctcca accagaagct 1650  
ggtccgcata ccaagccacc tccctgaata tgtcaccgac ctgcgactga 1700  
atgacaatga ggtatctggt ctggaggcca ctggcatctt caagaagttg 1750  
cccaacctgc ggaaaataaa tctgagtaac aataagatca aggagggtgcg 1800  
agaggagct ttcgatggag cagccagcgt gcaggagctg atgctgacag 1850  
ggaaccagct ggagaccgtg cacgggcgcg tgttccgtgg cctcagtggc 1900  
ctcaaaacct tgatgctgag gagtaacttg atcagctgtg tgagtaatga 1950  
cacctttgcc ggctgagtt cggtgagact gctgtccctc tatgacaatc 2000  
ggatcaccac catcaccctt ggggccttca ccacgcttgt ctccctgtcc 2050  
accataaacc tctgttccaa ccccttcaac tgcaactgcc acctggcctg 2100  
gctcggcaag tggttgagga agaggcggat cgtcagtggg aaccctaggt 2150  
gccagaagcc atttttcctc aaggagattc ccatccagga tgtggccatc 2200  
caggacttca cctgtgatgg caacgaggag agtagctgcc agctgagccc 2250  
gcgctgcccg gagcagtgca cctgtatgga gacagtgggt cgatgcagca 2300  
acaaggggct ccgcgcctc ccagaggca tgcccaagga tgtgaccgag 2350

ctgtacctgg aaggaaacca cctaacagcc gtgccagag agctgtccgc 2400  
cctccgacac ctgacgctta ttgacctgag caacaacagc atcagcatgc 2450  
tgaccaatta caccttcagt aacatgtctc acctotccac tctgatcctg 2500  
agctacaacc ggctgaggtg catccccgtc cacgccttca acgggctgcg 2550  
gtccctgcga gtgctaaccc tccatggcaa tgacatttcc agcgttcctg 2600  
aaggctcctt caacgacctc acatctcttt cccatctggc gctgggaacc 2650  
aaccactcc actgtgactg cagtcttcgg tggctgtcgg agtgggtgaa 2700  
ggcgggttac aaggagcctg gcatcgcccg ctgcagtagc cctgagccca 2750  
tggctgacag gctcctgctc accaccccaa cccaccgctt ccagtgcaaa 2800  
gggccagtgg acatcaacat tgtggccaaa tgcaatgcct gcctctccag 2850  
cccgtgcaag aataacggga catgcaccca ggaccctgtg gagctgtacc 2900  
gctgtgcctg cccctacagc tacaagggca aggactgcac tgtgcccatc 2950  
aacacctgca tccagaaccc ctgtcagcat ggaggcacct gccacctgag 3000  
tgacagccac aaggatgggt tcagctgctc ctgccctctg ggctttgagg 3050  
ggcagcgggtg tgagatcaac ccagatgact gtgaggacaa cgactgcgaa 3100  
aacaatgcca cctgcgtgga cgggatcaac aactacgtgt gtatctgtcc 3150  
gcctaactac acaggtgagc tatgcgacga ggtgattgac cactgtgtgc 3200  
ctgagctgaa cctctgtcag catgaggcca agtgcacccc cctggacaaa 3250  
ggattcagct gcgagtggtg ccctggctac agcgggaagc tctgtgagac 3300  
agacaatgat gactgtgtgg ccacaaagtg ccgccacggg gccagtgcg 3350  
tggacacaat caatggctac acatgcacct gccccaggc cttcagtgga 3400  
cccttctgtg aacaccccc acccatggtc ctactgcaga ccagcccatg 3450  
cgaccagtac gagtgccaga acggggccca gtgcatcgtg gtgcagcagg 3500  
agcccacctg ccgtgcca ccaggcttcg ccggccccag atgcgagaag 3550  
ctcatcactg tcaacttcgt gggcaaagac tcctacgtgg aactggcctc 3600  
cgccaaggtc cgaccccagg ccaacatctc cctgcaggtg gccactgaca 3650  
aggacaacgg catccttctc taaaaggag acaatgaccc cctggcactg 3700  
gagctgtacc agggccacgt gcggctggtc tatgacagcc tgagttcccc 3750



tccaaccaca gtgtacagtg tggagacagt gaatgatggg cagtttcaca 3800  
 gtgtggagct ggtgacgcta aaccagaccc tgaacctagt agtggacaaa 3850  
 ggaactccaa agagcctggg gaagctccag aagcagccag cagtgggcat 3900  
 caacagcccc ctctaccttg gaggcattcc cacctccacc ggctctctcg 3950  
 ccttgcgcca gggcacggac cggcctctag gcggcttcca cggatgcatt 4000  
 catgaggtgc gcatcaacaa cgagctgcag gacttcaagg ccctcccacc 4050  
 acagtccctg ggggtgtcac caggctgcaa gtctctgcacc gtgtgcaagc 4100  
 acggcctgtg ccgctccgtg gagaaggaca gcgtgggtgtg cgagtgccgc 4150  
 ccaggctgga ccggcccaact ctgcgaccag gagggccggg acccctgcct 4200  
 cggccacaga tgccaccatg gaaaatgtgt ggcaactggg acctcataca 4250  
 tgtgcaagtg tgccgagggc tatggagggg acttgtgtga caacaagaat 4300  
 gactctgcca atgcctgctc agccttcaag tgtcaccatg ggcagtgcc 4350  
 catctcagac caaggggagc cctactgcct gtgccagccc ggcttttagc 4400  
 gcgagcaactg ccaacaagag aatccgtgcc tgggacaagt agtccgagag 4450  
 gtgatccgcc gccagaaagg ttatgcatca tgtgccacag cctccaaggt 4500  
 gcccatcatg gaatgtcgtg ggggctgtgg gcccagtgcc tgccagccca 4550  
 cccgcagcaa gcggcgga aa tacgtcttcc agtgcacgga cggctcctcg 4600  
 tttgtagaag aggtggagag acacttagag tgcggctgcc tcgctgttcc 4650  
 ctaagcccct gcccgctgc ctgccacctc tcggactcca gcttgatgga 4700  
 gttgggacag ccatgtggga ccccttgtg attcagcatg aaggaaatga 4750  
 agctggagag gaaggtaaag aagaagagaa tattaagtat attgtaaaat 4800  
 aaacaaaaaa tagaacttaa aaaaaaaaaa aaaaaaaaaa aa 4842

<210> 198  
 <211> 1523  
 <212> PRT  
 <213> Homo sapiens

<400> 198  
 Met Ala Pro Gly Trp Ala Gly Val Gly Ala Ala Val Arg Ala Arg  
 1 5 10 15  
 Leu Ala Leu Ala Leu Ala Leu Ala Ser Val Leu Ser Gly Pro Pro  
 20 25 30  
 Ala Val Ala Cys Pro Thr Lys Cys Thr Cys Ser Ala Ala Ser Val

35										40					45				
Asp	Cys	His	Gly	Leu	Gly	Leu	Arg	Ala	Val	Pro	Arg	Gly	Ile	Pro					
50										55					60				
Arg	Asn	Ala	Glu	Arg	Leu	Asp	Leu	Asp	Arg	Asn	Asn	Ile	Thr	Arg					
65										70					75				
Ile	Thr	Lys	Met	Asp	Phe	Ala	Gly	Leu	Lys	Asn	Leu	Arg	Val	Leu					
80										85					90				
His	Leu	Glu	Asp	Asn	Gln	Val	Ser	Val	Ile	Glu	Arg	Gly	Ala	Phe					
95										100					105				
Gln	Asp	Leu	Lys	Gln	Leu	Glu	Arg	Leu	Arg	Leu	Asn	Lys	Asn	Lys					
110										115					120				
Leu	Gln	Val	Leu	Pro	Glu	Leu	Leu	Phe	Gln	Ser	Thr	Pro	Lys	Leu					
125										130					135				
Thr	Arg	Leu	Asp	Leu	Ser	Glu	Asn	Gln	Ile	Gln	Gly	Ile	Pro	Arg					
140										145					150				
Lys	Ala	Phe	Arg	Gly	Ile	Thr	Asp	Val	Lys	Asn	Leu	Gln	Leu	Asp					
155										160					165				
Asn	Asn	His	Ile	Ser	Cys	Ile	Glu	Asp	Gly	Ala	Phe	Arg	Ala	Leu					
170										175					180				
Arg	Asp	Leu	Glu	Ile	Leu	Thr	Leu	Asn	Asn	Asn	Asn	Ile	Ser	Arg					
185										190					195				
Ile	Leu	Val	Thr	Ser	Phe	Asn	His	Met	Pro	Lys	Ile	Arg	Thr	Leu					
200										205					210				
Arg	Leu	His	Ser	Asn	His	Leu	Tyr	Cys	Asp	Cys	His	Leu	Ala	Trp					
215										220					225				
Leu	Ser	Asp	Trp	Leu	Arg	Gln	Arg	Arg	Thr	Val	Gly	Gln	Phe	Thr					
230										235					240				
Leu	Cys	Met	Ala	Pro	Val	His	Leu	Arg	Gly	Phe	Asn	Val	Ala	Asp					
245										250					255				
Val	Gln	Lys	Lys	Glu	Tyr	Val	Cys	Pro	Ala	Pro	His	Ser	Glu	Pro					
260										265					270				
Pro	Ser	Cys	Asn	Ala	Asn	Ser	Ile	Ser	Cys	Pro	Ser	Pro	Cys	Thr					
275										280					285				
Cys	Ser	Asn	Asn	Ile	Val	Asp	Cys	Arg	Gly	Lys	Gly	Leu	Met	Glu					
290										295					300				
Ile	Pro	Ala	Asn	Leu	Pro	Glu	Gly	Ile	Val	Glu	Ile	Arg	Leu	Glu					
305										310					315				
Gln	Asn	Ser	Ile	Lys	Ala	Ile	Pro	Ala	Gly	Ala	Phe	Thr	Gln	Tyr					

				320						325					330
Lys	Lys	Leu	Lys	Arg	Ile	Asp	Ile	Ser	Lys	Asn	Gln	Ile	Ser	Asp	
				335					340					345	
Ile	Ala	Pro	Asp	Ala	Phe	Gln	Gly	Leu	Lys	Ser	Leu	Thr	Ser	Leu	
				350					355					360	
Val	Leu	Tyr	Gly	Asn	Lys	Ile	Thr	Glu	Ile	Ala	Lys	Gly	Leu	Phe	
				365					370					375	
Asp	Gly	Leu	Val	Ser	Leu	Gln	Leu	Leu	Leu	Leu	Asn	Ala	Asn	Lys	
				380					385					390	
Ile	Asn	Cys	Leu	Arg	Val	Asn	Thr	Phe	Gln	Asp	Leu	Gln	Asn	Leu	
				395					400					405	
Asn	Leu	Leu	Ser	Leu	Tyr	Asp	Asn	Lys	Leu	Gln	Thr	Ile	Ser	Lys	
				410					415					420	
Gly	Leu	Phe	Ala	Pro	Leu	Gln	Ser	Ile	Gln	Thr	Leu	His	Leu	Ala	
				425					430					435	
Gln	Asn	Pro	Phe	Val	Cys	Asp	Cys	His	Leu	Lys	Trp	Leu	Ala	Asp	
				440					445					450	
Tyr	Leu	Gln	Asp	Asn	Pro	Ile	Glu	Thr	Ser	Gly	Ala	Arg	Cys	Ser	
				455					460					465	
Ser	Pro	Arg	Arg	Leu	Ala	Asn	Lys	Arg	Ile	Ser	Gln	Ile	Lys	Ser	
				470					475					480	
Lys	Lys	Phe	Arg	Cys	Ser	Gly	Ser	Glu	Asp	Tyr	Arg	Ser	Arg	Phe	
				485					490					495	
Ser	Ser	Glu	Cys	Phe	Met	Asp	Leu	Val	Cys	Pro	Glu	Lys	Cys	Arg	
				500					505					510	
Cys	Glu	Gly	Thr	Ile	Val	Asp	Cys	Ser	Asn	Gln	Lys	Leu	Val	Arg	
				515					520					525	
Ile	Pro	Ser	His	Leu	Pro	Glu	Tyr	Val	Thr	Asp	Leu	Arg	Leu	Asn	
				530					535					540	
Asp	Asn	Glu	Val	Ser	Val	Leu	Glu	Ala	Thr	Gly	Ile	Phe	Lys	Lys	
				545					550					555	
Leu	Pro	Asn	Leu	Arg	Lys	Ile	Asn	Leu	Ser	Asn	Asn	Lys	Ile	Lys	
				560					565					570	
Glu	Val	Arg	Glu	Gly	Ala	Phe	Asp	Gly	Ala	Ala	Ser	Val	Gln	Glu	
				575					580					585	
Leu	Met	Leu	Thr	Gly	Asn	Gln	Leu	Glu	Thr	Val	His	Gly	Arg	Val	
				590					595					600	
Phe	Arg	Gly	Leu	Ser	Gly	Leu	Lys	Thr	Leu	Met	Leu	Arg	Ser	Asn	

605					610					615				
Leu	Ile	Ser	Cys	Val	Ser	Asn	Asp	Thr	Phe	Ala	Gly	Leu	Ser	Ser
				620					625					630
Val	Arg	Leu	Leu	Ser	Leu	Tyr	Asp	Asn	Arg	Ile	Thr	Thr	Ile	Thr
				635					640					645
Pro	Gly	Ala	Phe	Thr	Thr	Leu	Val	Ser	Leu	Ser	Thr	Ile	Asn	Leu
				650					655					660
Leu	Ser	Asn	Pro	Phe	Asn	Cys	Asn	Cys	His	Leu	Ala	Trp	Leu	Gly
				665					670					675
Lys	Trp	Leu	Arg	Lys	Arg	Arg	Ile	Val	Ser	Gly	Asn	Pro	Arg	Cys
				680					685					690
Gln	Lys	Pro	Phe	Phe	Leu	Lys	Glu	Ile	Pro	Ile	Gln	Asp	Val	Ala
				695					700					705
Ile	Gln	Asp	Phe	Thr	Cys	Asp	Gly	Asn	Glu	Glu	Ser	Ser	Cys	Gln
				710					715					720
Leu	Ser	Pro	Arg	Cys	Pro	Glu	Gln	Cys	Thr	Cys	Met	Glu	Thr	Val
				725					730					735
Val	Arg	Cys	Ser	Asn	Lys	Gly	Leu	Arg	Ala	Leu	Pro	Arg	Gly	Met
				740					745					750
Pro	Lys	Asp	Val	Thr	Glu	Leu	Tyr	Leu	Glu	Gly	Asn	His	Leu	Thr
				755					760					765
Ala	Val	Pro	Arg	Glu	Leu	Ser	Ala	Leu	Arg	His	Leu	Thr	Leu	Ile
				770					775					780
Asp	Leu	Ser	Asn	Asn	Ser	Ile	Ser	Met	Leu	Thr	Asn	Tyr	Thr	Phe
				785					790					795
Ser	Asn	Met	Ser	His	Leu	Ser	Thr	Leu	Ile	Leu	Ser	Tyr	Asn	Arg
				800					805					810
Leu	Arg	Cys	Ile	Pro	Val	His	Ala	Phe	Asn	Gly	Leu	Arg	Ser	Leu
				815					820					825
Arg	Val	Leu	Thr	Leu	His	Gly	Asn	Asp	Ile	Ser	Ser	Val	Pro	Glu
				830					835					840
Gly	Ser	Phe	Asn	Asp	Leu	Thr	Ser	Leu	Ser	His	Leu	Ala	Leu	Gly
				845					850					855
Thr	Asn	Pro	Leu	His	Cys	Asp	Cys	Ser	Leu	Arg	Trp	Leu	Ser	Glu
				860					865					870
Trp	Val	Lys	Ala	Gly	Tyr	Lys	Glu	Pro	Gly	Ile	Ala	Arg	Cys	Ser
				875					880					885
Ser	Pro	Glu	Pro	Met	Ala	Asp	Arg	Leu	Leu	Leu	Thr	Thr	Pro	Thr

890										895					900				
His	Arg	Phe	Gln	Cys	Lys	Gly	Pro	Val	Asp	Ile	Asn	Ile	Val	Ala					
				905					910					915					
Lys	Cys	Asn	Ala	Cys	Leu	Ser	Ser	Pro	Cys	Lys	Asn	Asn	Gly	Thr					
				920					925					930					
Cys	Thr	Gln	Asp	Pro	Val	Glu	Leu	Tyr	Arg	Cys	Ala	Cys	Pro	Tyr					
				935					940					945					
Ser	Tyr	Lys	Gly	Lys	Asp	Cys	Thr	Val	Pro	Ile	Asn	Thr	Cys	Ile					
				950					955					960					
Gln	Asn	Pro	Cys	Gln	His	Gly	Gly	Thr	Cys	His	Leu	Ser	Asp	Ser					
				965					970					975					
His	Lys	Asp	Gly	Phe	Ser	Cys	Ser	Cys	Pro	Leu	Gly	Phe	Glu	Gly					
				980					985					990					
Gln	Arg	Cys	Glu	Ile	Asn	Pro	Asp	Asp	Cys	Glu	Asp	Asn	Asp	Cys					
				995					1000					1005					
Glu	Asn	Asn	Ala	Thr	Cys	Val	Asp	Gly	Ile	Asn	Asn	Tyr	Val	Cys					
				1010					1015					1020					
Ile	Cys	Pro	Pro	Asn	Tyr	Thr	Gly	Glu	Leu	Cys	Asp	Glu	Val	Ile					
				1025					1030					1035					
Asp	His	Cys	Val	Pro	Glu	Leu	Asn	Leu	Cys	Gln	His	Glu	Ala	Lys					
				1040					1045					1050					
Cys	Ile	Pro	Leu	Asp	Lys	Gly	Phe	Ser	Cys	Glu	Cys	Val	Pro	Gly					
				1055					1060					1065					
Tyr	Ser	Gly	Lys	Leu	Cys	Glu	Thr	Asp	Asn	Asp	Asp	Cys	Val	Ala					
				1070					1075					1080					
His	Lys	Cys	Arg	His	Gly	Ala	Gln	Cys	Val	Asp	Thr	Ile	Asn	Gly					
				1085					1090					1095					
Tyr	Thr	Cys	Thr	Cys	Pro	Gln	Gly	Phe	Ser	Gly	Pro	Phe	Cys	Glu					
				1100					1105					1110					
His	Pro	Pro	Pro	Met	Val	Leu	Leu	Gln	Thr	Ser	Pro	Cys	Asp	Gln					
				1115					1120					1125					
Tyr	Glu	Cys	Gln	Asn	Gly	Ala	Gln	Cys	Ile	Val	Val	Gln	Gln	Glu					
				1130					1135					1140					
Pro	Thr	Cys	Arg	Cys	Pro	Pro	Gly	Phe	Ala	Gly	Pro	Arg	Cys	Glu					
				1145					1150					1155					
Lys	Leu	Ile	Thr	Val	Asn	Phe	Val	Gly	Lys	Asp	Ser	Tyr	Val	Glu					
				1160					1165					1170					
Leu	Ala	Ser	Ala	Lys	Val	Arg	Pro	Gln	Ala	Asn	Ile	Ser	Leu	Gln					

1175	1180	1185
Val Ala Thr Asp Lys Asp Asn Gly Ile Leu Leu Tyr Lys Gly Asp 1190	1195	1200
Asn Asp Pro Leu Ala Leu Glu Leu Tyr Gln Gly His Val Arg Leu 1205	1210	1215
Val Tyr Asp Ser Leu Ser Ser Pro Pro Thr Thr Val Tyr Ser Val 1220	1225	1230
Glu Thr Val Asn Asp Gly Gln Phe His Ser Val Glu Leu Val Thr 1235	1240	1245
Leu Asn Gln Thr Leu Asn Leu Val Val Asp Lys Gly Thr Pro Lys 1250	1255	1260
Ser Leu Gly Lys Leu Gln Lys Gln Pro Ala Val Gly Ile Asn Ser 1265	1270	1275
Pro Leu Tyr Leu Gly Gly Ile Pro Thr Ser Thr Gly Leu Ser Ala 1280	1285	1290
Leu Arg Gln Gly Thr Asp Arg Pro Leu Gly Gly Phe His Gly Cys 1295	1300	1305
Ile His Glu Val Arg Ile Asn Asn Glu Leu Gln Asp Phe Lys Ala 1310	1315	1320
Leu Pro Pro Gln Ser Leu Gly Val Ser Pro Gly Cys Lys Ser Cys 1325	1330	1335
Thr Val Cys Lys His Gly Leu Cys Arg Ser Val Glu Lys Asp Ser 1340	1345	1350
Val Val Cys Glu Cys Arg Pro Gly Trp Thr Gly Pro Leu Cys Asp 1355	1360	1365
Gln Glu Ala Arg Asp Pro Cys Leu Gly His Arg Cys His His Gly 1370	1375	1380
Lys Cys Val Ala Thr Gly Thr Ser Tyr Met Cys Lys Cys Ala Glu 1385	1390	1395
Gly Tyr Gly Gly Asp Leu Cys Asp Asn Lys Asn Asp Ser Ala Asn 1400	1405	1410
Ala Cys Ser Ala Phe Lys Cys His His Gly Gln Cys His Ile Ser 1415	1420	1425
Asp Gln Gly Glu Pro Tyr Cys Leu Cys Gln Pro Gly Phe Ser Gly 1430	1435	1440
Glu His Cys Gln Gln Glu Asn Pro Cys Leu Gly Gln Val Val Arg 1445	1450	1455
Glu Val Ile Arg Arg Gln Lys Gly Tyr Ala Ser Cys Ala Thr Ala		

1460	1465	1470
Ser Lys Val Pro Ile Met Glu Cys Arg Gly Gly Cys Gly Pro Gln		
1475	1480	1485
Cys Cys Gln Pro Thr Arg Ser Lys Arg Arg Lys Tyr Val Phe Gln		
1490	1495	1500
Cys Thr Asp Gly Ser Ser Phe Val Glu Glu Val Glu Arg His Leu		
1505	1510	1515
Glu Cys Gly Cys Leu Ala Cys Ser		
1520		

<210> 199

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 199

atggagattc ctgccaaactt gccg 24

<210> 200

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 200

ttgttggcat tgaggaggag cagc 24

<210> 201

<211> 50

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 201

gagggcatcg tcgaaatacg cctagaacag aactccatca aagccatccc 50

<210> 202

<211> 753

<212> DNA

<213> Homo sapiens

<400> 202

ggatgcagga cgctccoctg agctgcctgt caccgactag gtggagcagt 50

gtttcttccg cagactcaac tgagaagtca gcctctgggg caggcaccag 100

gaatctgcct tttcagttct gtctccggca ggctttgagg atgaaggctg 150  
 cgggcattct gaccctcatt ggctgcctgg tcacaggcgc cgagtccaaa 200  
 atctacactc gttgcaaact ggcaaaaata ttctcgaggg ctggcctgga 250  
 caattactgg ggcttcagcc ttggaaactg gatctgcatg gcatattatg 300  
 agagcggcta caacaccaca gcccgcaggg tcctggatga cggcagcatc 350  
 gactatggca tcttccagat caacagcttc gcgtggtgca gacgcggaaa 400  
 gctgaaggag aacaaccact gccatgtcgc ctgctcagcc ttgatcactg 450  
 atgacctcac agatgcaatt atctgtgcca ggaaaattgt taaagagaca 500  
 caaggaatga actattggca aggctggaag aaacattgtg agggcagaga 550  
 cctgtccgag tggaaaaaag gctgtgaggt ttcttaaact ggaactggac 600  
 ccaggatgct ttgcagcaac gccctaggat ttgcagtga tgtccaaatg 650  
 cctgtgtcat cttgtcccgt ttctcccaa tattccttct caaacttgga 700  
 gagggaaaat taagctatac ttttaagaaa ataaatattt ccatttaa 750  
 gtc 753

<210> 203

<211> 148

<212> PRT

<213> Homo sapiens

<400> 203

Met	Lys	Ala	Ala	Gly	Ile	Leu	Thr	Leu	Ile	Gly	Cys	Leu	Val	Thr
1				5					10				15	
Gly	Ala	Glu	Ser	Lys	Ile	Tyr	Thr	Arg	Cys	Lys	Leu	Ala	Lys	Ile
				20					25				30	
Phe	Ser	Arg	Ala	Gly	Leu	Asp	Asn	Tyr	Trp	Gly	Phe	Ser	Leu	Gly
				35					40				45	
Asn	Trp	Ile	Cys	Met	Ala	Tyr	Tyr	Glu	Ser	Gly	Tyr	Asn	Thr	Thr
				50					55				60	
Ala	Pro	Thr	Val	Leu	Asp	Asp	Gly	Ser	Ile	Asp	Tyr	Gly	Ile	Phe
				65					70				75	
Gln	Ile	Asn	Ser	Phe	Ala	Trp	Cys	Arg	Arg	Gly	Lys	Leu	Lys	Glu
				80					85				90	
Asn	Asn	His	Cys	His	Val	Ala	Cys	Ser	Ala	Leu	Ile	Thr	Asp	Asp
				95					100				105	
Leu	Thr	Asp	Ala	Ile	Ile	Cys	Ala	Arg	Lys	Ile	Val	Lys	Glu	Thr
				110					115				120	



Gln Gly Met Asn Tyr Trp Gln Gly Trp Lys Lys His Cys Glu Gly  
125 130 135

Arg Asp Leu Ser Glu Trp Lys Lys Gly Cys Glu Val Ser  
140 145

<210> 204

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 204

gcaggctttg aggatgaagg ctgc 24

<210> 205

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 205

ctcattggct gcctggtcac aggc 24

<210> 206

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 206

ccagtcggac aggtctctcc cctc 24

<210> 207

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 207

tcagtgaacca aggctgagca ggcg 24

<210> 208

<211> 47

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 208

ctacactcgt tgcaaactgg caaaaatatt ctcgagggct ggcctgg 47

<210> 209

<211> 1648

<212> DNA

<213> Homo sapiens

<400> .209

caggccattt gcatccact gtccttgtgt tcggagccag gccacaccgt 50  
cctcagcagt gtcattgtgt aaaaacgcca agctgaatat atcatgcccc 100  
tattaaaact tgtacatggc tccccattgg tttttggaga aaagttcaag 150  
ctttttacct tgggtgtctgc ctgtatccca gtgttcaggc tggctagacg 200  
gcggaagaag atcctatatt actgtcaact ccagatctg cttctcacca 250  
agagagattc ttttcttaaa cgactataca gggccccaat tgactggata 300  
gaggaataca ccacaggcat ggcagactgc atcttagtca acagccagtt 350  
cacagctgct gtttttaagg aaacattcaa gtccctgtct cacatagacc 400  
ctgatgtcct ctatccatct ctaaattgtca ccagctttga ctcagttgtt 450  
cctgaaaagc tggatgacct agtccccaag gggaaaaaat tcctgctgct 500  
ctccatcaac agatacgaaa ggaagaaaaa tctgactttg gcactggaag 550  
ccctagtaca gctgcgtgga agattgacat cccaagattg ggagagggtt 600  
catctgatcg tggcagggtg ttatgacgag agagtcctgg agaattgtga 650  
acattatcag gaattgaaga aaatgggtcca acagtccgac cttggccagt 700  
atgtgacctt cttgaggtct ttctcagaca aacagaaaat ctccctctc 750  
cacagctgca cgtgtgtgct ttacacacca agcaatgagc actttggcat 800  
tgtccctctg gaagccatgt acatgcagtg ccagtcatt gctgttaatt 850  
cgggtggacc cttggagtcc attgaccaca gtgtcacagg gtttctgtgt 900  
gagcctgacc cgggtgcact ctcagaagca atagaaaagt tcatccgtga 950  
accttcctta aaagccacca tgggcctggc tggaagagcc agagtgaagg 1000  
aaaaattttc ccctgaagca ttacagaac agctctaccg atatgttacc 1050  
aaactgctgg tataatcaga ttgtttttaa gatctccatt aatgtcattt 1100  
ttatggattg tagaccagtt tttgaaacca aaaaagaaac ctagaatcta 1150

atgcagaaga gatcttttaa aaaataaact tgagtcttga atgtgagcca 1200  
 ctttcctata taccacacct ccctgtccac ttttcagaaa aaccatgtct 1250  
 tttatgctat aatcattcca aattttgccca gtggttaagtt acaaagtggg 1300  
 tgtcattcca tgttcagcag agtatTTTTAA ttatatTTTc tcgggattat 1350  
 tgctcttctg tctataaatt ttgaatgata ctgtgcctta attggTTTTc 1400  
 atagtttaag tgtgtatcat tatcaaagtt gattaatttg gcttcatagt 1450  
 ataatgagag cagggctatt gtagttccca gattcaatcc accgaagtgt 1500  
 tcaactgcat ctggttagga atttttgttt gtctgtctt tgcctggatc 1550  
 catagcgaga gtgctctgta ttttttttaa gataatttgt atttttgcac 1600  
 actgagatat aataaaaggt gtttatcata aaaaaaaaaa aaaaaaaaa 1648

<210> 210

<211> 323

<212> PRT

<213> Homo sapiens

<400> 210

Met	Pro	Leu	Leu	Lys	Leu	Val	His	Gly	Ser	Pro	Leu	Val	Phe	Gly
1				5					10					15

Glu	Lys	Phe	Lys	Leu	Phe	Thr	Leu	Val	Ser	Ala	Cys	Ile	Pro	Val
			20						25					30

Phe	Arg	Leu	Ala	Arg	Arg	Arg	Lys	Lys	Ile	Leu	Phe	Tyr	Cys	His
			35						40					45

Phe	Pro	Asp	Leu	Leu	Leu	Thr	Lys	Arg	Asp	Ser	Phe	Leu	Lys	Arg
			50						55					60

Leu	Tyr	Arg	Ala	Pro	Ile	Asp	Trp	Ile	Glu	Glu	Tyr	Thr	Thr	Gly
			65						70					75

Met	Ala	Asp	Cys	Ile	Leu	Val	Asn	Ser	Gln	Phe	Thr	Ala	Ala	Val
			80						85					90

Phe	Lys	Glu	Thr	Phe	Lys	Ser	Leu	Ser	His	Ile	Asp	Pro	Asp	Val
			95						100					105

Leu	Tyr	Pro	Ser	Leu	Asn	Val	Thr	Ser	Phe	Asp	Ser	Val	Val	Pro
			110						115					120

Glu	Lys	Leu	Asp	Asp	Leu	Val	Pro	Lys	Gly	Lys	Lys	Phe	Leu	Leu
			125						130					135

Leu	Ser	Ile	Asn	Arg	Tyr	Glu	Arg	Lys	Lys	Asn	Leu	Thr	Leu	Ala
			140						145					150

Leu	Glu	Ala	Leu	Val	Gln	Leu	Arg	Gly	Arg	Leu	Thr	Ser	Gln	Asp
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

	155	160	165
Trp Glu Arg Val	His Leu Ile Val Ala	Gly Gly Tyr Asp Glu Arg	
	170	175	180
Val Leu Glu Asn	Val Glu His Tyr Gln	Glu Leu Lys Lys Met Val	
	185	190	195
Gln Gln Ser Asp	Leu Gly Gln Tyr Val	Thr Phe Leu Arg Ser Phe	
	200	205	210
Ser Asp Lys Gln	Lys Ile Ser Leu Leu	His Ser Cys Thr Cys Val	
	215	220	225
Leu Tyr Thr Pro	Ser Asn Glu His Phe	Gly Ile Val Pro Leu Glu	
	230	235	240
Ala Met Tyr Met	Gln Cys Pro Val Ile	Ala Val Asn Ser Gly Gly	
	245	250	255
Pro Leu Glu Ser	Ile Asp His Ser Val	Thr Gly Phe Leu Cys Glu	
	260	265	270
Pro Asp Pro Val	His Phe Ser Glu Ala	Ile Glu Lys Phe Ile Arg	
	275	280	285
Glu Pro Ser Leu	Lys Ala Thr Met Gly	Leu Ala Gly Arg Ala Arg	
	290	295	300
Val Lys Glu Lys	Phe Ser Pro Glu Ala	Phe Thr Glu Gln Leu Tyr	
	305	310	315
Arg Tyr Val Thr	Lys Leu Leu Val		
	320		

<210> 211  
 <211> 1554  
 <212> DNA  
 <213> Homo sapiens

<400> 211  
 gactacgccg atccgagacg tggctccctg ggcggcagaa ccatgttgga 50  
 cttcgcgata ttgcgcgtta ccttcttgct ggcgttggtg ggagccgtgc 100  
 tctacctcta tccggcttcc agacaagctg caggaattcc agggattact 150  
 ccaactgaag aaaaagatgg taatcttcca gatattgtga atagtggaag 200  
 tttgcatgag ttcttggtta atttgcata gagatatggg cctgtggtct 250  
 ccttctggtt tggcaggcgc ctcgtgggta gtttgggcac tggtgatgta 300  
 ctgaagcagc atatcaatcc caataagaca tcggaccctt ttgaaaccat 350  
 gctgaagtca ttattaaggt atcaatctgg tgggtggcagt gtgagtgaaa 400

accacatgag gaaaaaattg tatgaaaatg gtgtgactga ttctctgaag 450  
 agtaactttg cctcctcct aaagctttca gaagaattat tagataaatg 500  
 gctctcctac ccagagaccc agcacgtgcc cctcagccag catatgcttg 550  
 gttttgctat gaagtctgtt acacagatgg taatgggtag tacatttgaa 600  
 gatgatcagg aagtcattcg cttccagaag aatcatggca cagtttggtc 650  
 tgagattgga aaaggctttc tagatgggtc acttgataaa aacatgactc 700  
 ggaaaaaaca atatgaagat gccctcatgc aactggagtc tgttttaagg 750  
 aacatcataa aagaacgaaa aggaaggaac ttcagtcaac atattttcat 800  
 tgactcctta gtacaaggga accttaatga ccaacagatc ctagaagaca 850  
 gtatgatatt ttctctggcc agttgcataa taactgcaaa attgtgtacc 900  
 tgggcaatct gttttttaac cacctctgaa gaagttcaaa aaaaattata 950  
 tgaagagata aaccaagttt ttggaaatgg tcctgttact ccagagaaaa 1000  
 ttgagcagct cagatattgt cagcatgtgc tttgtgaaac tgttcgaact 1050  
 gccaaactga ctccagtttc tgcccagctt caagatattg aaggaaaaat 1100  
 tgaccgattt attattccta gagagacct cgtcctttat gcccttggtg 1150  
 tggacttca ggatcctaact acttggccat ctccacacaa gtttgatcca 1200  
 gatcggtttg atgatgaatt agtaatgaaa actttttcct cacttggtt 1250  
 ctcaggcaca caggagtgtc cagagttgag gtttgcatat atggtgacca 1300  
 cagtacttct tagtgtattg gtgaagagac tgcacctact ttctgtggag 1350  
 ggacaggtta ttgaaacaaa gtatgaactg gtaacatcat caagggaaga 1400  
 agcttggtatc actgtctcaa agagatatta aaattttata catttaaaat 1450  
 cattgttaaa ttgattgagg aaaacaacca tttaaaaaaa atctatgttg 1500  
 aatcctttta taaaccagta tcactttgta atataaacac ctatttgtac 1550  
 ttaa 1554

<210> 212  
 <211> 462  
 <212> PRT  
 <213> Homo sapiens

<400> 212  
 Met Leu Asp Phe Ala Ile Phe Ala Val Thr Phe Leu Leu Ala Leu  
 1 5 10 15

Val Gly Ala Val	Leu Tyr Leu Tyr	Pro Ala Ser Arg	Gln Ala Ala	
	20	25	30	
Gly Ile Pro Gly	Ile Thr Pro Thr	Glu Glu Lys Asp	Gly Asn Leu	
	35	40	45	
Pro Asp Ile Val	Asn Ser Gly Ser	Leu His Glu Phe	Leu Val Asn	
	50	55	60	
Leu His Glu Arg	Tyr Gly Pro Val	Val Ser Phe Trp	Phe Gly Arg	
	65	70	75	
Arg Leu Val Val	Ser Leu Gly Thr	Val Asp Val Leu	Lys Gln His	
	80	85	90	
Ile Asn Pro Asn	Lys Thr Ser Asp	Pro Phe Glu Thr	Met Leu Lys	
	95	100	105	
Ser Leu Leu Arg	Tyr Gln Ser Gly	Gly Glu Ser Val	Ser Glu Asn	
	110	115	120	
His Met Arg Lys	Lys Leu Tyr Glu	Asn Gly Val Thr	Asp Ser Leu	
	125	130	135	
Lys Ser Asn Phe	Ala Leu Leu Leu	Lys Leu Ser Glu	Glu Leu Leu	
	140	145	150	
Asp Lys Trp Leu	Ser Tyr Pro Glu	Thr Gln His Val	Pro Leu Ser	
	155	160	165	
Gln His Met Leu	Gly Phe Ala Met	Lys Ser Val Thr	Gln Met Val	
	170	175	180	
Met Gly Ser Thr	Phe Glu Asp Asp	Gln Glu Val Ile	Arg Phe Gln	
	185	190	195	
Lys Asn His Gly	Thr Val Trp Ser	Glu Ile Gly Lys	Gly Phe Leu	
	200	205	210	
Asp Gly Ser Leu	Asp Lys Asn Met	Thr Arg Lys Lys	Gln Tyr Glu	
	215	220	225	
Asp Ala Leu Met	Gln Leu Glu Ser	Val Leu Arg Asn	Ile Ile Lys	
	230	235	240	
Glu Arg Lys Gly	Arg Asn Phe Ser	Gln His Ile Phe	Ile Asp Ser	
	245	250	255	
Leu Val Gln Gly	Asn Leu Asn Asp	Gln Gln Ile Leu	Glu Asp Ser	
	260	265	270	
Met Ile Phe Ser	Leu Ala Ser Cys	Ile Ile Thr Ala	Lys Leu Cys	
	275	280	285	
Thr Trp Ala Ile	Cys Phe Leu Thr	Thr Ser Glu Glu	Val Gln Lys	
	290	295	300	

Lys	Leu	Tyr	Glu	Glu	Ile	Asn	Gln	Val	Phe	Gly	Asn	Gly	Pro	Val	
				305						310				315	
Thr	Pro	Glu	Lys	Ile	Glu	Gln	Leu	Arg	Tyr	Cys	Gln	His	Val	Leu	
				320						325				330	
Cys	Glu	Thr	Val	Arg	Thr	Ala	Lys	Leu	Thr	Pro	Val	Ser	Ala	Gln	
				335						340				345	
Leu	Gln	Asp	Ile	Glu	Gly	Lys	Ile	Asp	Arg	Phe	Ile	Ile	Pro	Arg	
				350						355				360	
Glu	Thr	Leu	Val	Leu	Tyr	Ala	Leu	Gly	Val	Val	Leu	Gln	Asp	Pro	
				365						370				375	
Asn	Thr	Trp	Pro	Ser	Pro	His	Lys	Phe	Asp	Pro	Asp	Arg	Phe	Asp	
				380						385				390	
Asp	Glu	Leu	Val	Met	Lys	Thr	Phe	Ser	Ser	Leu	Gly	Phe	Ser	Gly	
				395						400				405	
Thr	Gln	Glu	Cys	Pro	Glu	Leu	Arg	Phe	Ala	Tyr	Met	Val	Thr	Thr	
				410						415				420	
Val	Leu	Leu	Ser	Val	Leu	Val	Lys	Arg	Leu	His	Leu	Leu	Ser	Val	
				425						430				435	
Glu	Gly	Gln	Val	Ile	Glu	Thr	Lys	Tyr	Glu	Leu	Val	Thr	Ser	Ser	
				440						445				450	
Arg	Glu	Glu	Ala	Trp	Ile	Thr	Val	Ser	Lys	Arg	Tyr				
				455						460					

<210> 213  
 <211> 759  
 <212> DNA  
 <213> Homo sapiens

<400> 213  
 ctagatttgt cggcttgccg ggagacttca ggagtcgctg tctctgaact 50  
 tccagcctca gagaccgccg cccttgctcc cgagggccat gggccgggtc 100  
 tcagggttg tgccctctcg ctctctgacg ctctggcgc atctggtggt 150  
 cgtcatcacc ttattctggt cccgggacag caacatacag gctgcctgc 200  
 ctctcacgtt ccccccgag gagtatgaca agcaggacat tcagctggtg 250  
 gccgcgctct ctgtaccct gggcctcttt gcagtggagc tggccggttt 300  
 cctctcagga gtctccatgt tcaacagcac ccagagcctc atctccattg 350  
 gggctcaactg tagtgcatcc gtggccctgt cttcttcat attcgagcgt 400  
 tgggagtgc a ctacgtattg gtacatTTTT gtcttctgca gtgcccttcc 450

agctgtcact gaaatggctt tattcgtcac cgtctttggg ctgaaaaaga 500  
 aacccttctg attaccttca tgacgggaac ctaaggacga agcctacagg 550  
 ggcaagggcc gcttcgtatt cctggaagaa ggaaggcata ggcttcggtt 600  
 ttcccctcgg aaactgcttc tgctggagga tatgtgttgg aataattacg 650  
 tcttgagtct gggattatcc gcattgtatt tagtgctttg taataaaata 700  
 tgttttgtag taacattaag acttatatac agttttaggg gacaattaa 750  
 aaaaaaaaa 759

<210> 214  
 <211> 140  
 <212> PRT  
 <213> Homo sapiens

<400> 214  
 Met Gly Arg Val Ser Gly Leu Val Pro Ser Arg Phe Leu Thr Leu  
 1 5 10 15  
 Leu Ala His Leu Val Val Val Ile Thr Leu Phe Trp Ser Arg Asp  
 20 25 30  
 Ser Asn Ile Gln Ala Cys Leu Pro Leu Thr Phe Thr Pro Glu Glu  
 35 40 45  
 Tyr Asp Lys Gln Asp Ile Gln Leu Val Ala Ala Leu Ser Val Thr  
 50 55 60  
 Leu Gly Leu Phe Ala Val Glu Leu Ala Gly Phe Leu Ser Gly Val  
 65 70 75  
 Ser Met Phe Asn Ser Thr Gln Ser Leu Ile Ser Ile Gly Ala His  
 80 85 90  
 Cys Ser Ala Ser Val Ala Leu Ser Phe Phe Ile Phe Glu Arg Trp  
 95 100 105  
 Glu Cys Thr Thr Tyr Trp Tyr Ile Phe Val Phe Cys Ser Ala Leu  
 110 115 120  
 Pro Ala Val Thr Glu Met Ala Leu Phe Val Thr Val Phe Gly Leu  
 125 130 135  
 Lys Lys Lys Pro Phe  
 140

<210> 215  
 <211> 697  
 <212> DNA  
 <213> Homo sapiens

<400> 215  
 tcccgaccc tgccgcctg ccactatgtc ccgccgtct atgctgcttg 50



```

cctgggctct cccagcctc cttcgactcg gagcggtca ggagacagaa 100
gaccgcgcct gctgcagccc catagtgcc cggaacgagt ggaaggccct 150
ggcatcagag tgcgcccagc acctgagcct gcccttacgc tatgtggtgg 200
tatcgcacac ggcgggcagc agctgcaaca ccccgccctc gtgccagcag 250
cagggccgga atgtgcagca ctaccacatg aagacactgg gctggtgcga 300
cgtgggctac aacttcctga ttggagaaga cgggctcgta tacgagggcc 350
gtggctggaa cttcacgggt gccactcag gtcacttatg gaaccccatg 400
tccattggca tcagcttcat gggcaactac atggatcggg tgcccacacc 450
ccaggccatc cgggcagccc agggctctact ggctgcgggt gtggctcagg 500
gagccctgag gtccaactat gtgctcaaag gacaccggga tgtgcagcgt 550
acactctctc caggcaacca gctctaccac ctcatccaga attggccaca 600
ctaccgctcc ccctgaggcc ctgctgatcc gcacccatt cctccctcc 650
catggccaaa aacccactg tctccttctc caataaagat gtagctc 697

```

<210> 216

<211> 196

<212> PRT

<213> Homo sapiens

<400> 216

```

Met Ser Arg Arg Ser Met Leu Leu Ala Trp Ala Leu Pro Ser Leu
  1                      5                      10                      15

Leu Arg Leu Gly Ala Ala Gln Glu Thr Glu Asp Pro Ala Cys Cys
                      20                      25                      30

Ser Pro Ile Val Pro Arg Asn Glu Trp Lys Ala Leu Ala Ser Glu
                      35                      40                      45

Cys Ala Gln His Leu Ser Leu Pro Leu Arg Tyr Val Val Val Ser
  50                      55                      60

His Thr Ala Gly Ser Ser Cys Asn Thr Pro Ala Ser Cys Gln Gln
  65                      70                      75

Gln Ala Arg Asn Val Gln His Tyr His Met Lys Thr Leu Gly Trp
  80                      85                      90

Cys Asp Val Gly Tyr Asn Phe Leu Ile Gly Glu Asp Gly Leu Val
  95                      100                     105

Tyr Glu Gly Arg Gly Trp Asn Phe Thr Gly Ala His Ser Gly His
  110                     115                     120

```

Leu	Trp	Asn	Pro	Met	Ser	Ile	Gly	Ile	Ser	Phe	Met	Gly	Asn	Tyr
				125					130					135
Met	Asp	Arg	Val	Pro	Thr	Pro	Gln	Ala	Ile	Arg	Ala	Ala	Gln	Gly
				140					145					150
Leu	Leu	Ala	Cys	Gly	Val	Ala	Gln	Gly	Ala	Leu	Arg	Ser	Asn	Tyr
				155					160					165
Val	Leu	Lys	Gly	His	Arg	Asp	Val	Gln	Arg	Thr	Leu	Ser	Pro	Gly
				170					175					180
Asn	Gln	Leu	Tyr	His	Leu	Ile	Gln	Asn	Trp	Pro	His	Tyr	Arg	Ser
				185					190					195

Pro

<210> 217  
 <211> 1871  
 <212> DNA  
 <213> Homo sapiens

<400> 217  
 ctgggacccc gaaaagagaa ggggagagcg aggggacgag agcggaggag 50  
 gaagatgcaa ctgactcgct gctgcttcgt gttcctggtg cagggtagcc 100  
 tctatctggt catctgtggc caggatgatg gtcctcccgg ctacagaggac 150  
 cctgagcgtg atgaccacga gggccagccc cggccccggg tgcctcggaa 200  
 gcggggccac atctcaccta agtcccgccc catggccaat tccactctcc 250  
 tagggctgct ggccccgcct ggggaggctt ggggcattct tgggcagccc 300  
 cccaaccgcc cgaaccacag cccccaccc tcagccaagg tgaagaaaat 350  
 ctttggtggt ggcgacttct actccaacat caagacggtg gccctgaacc 400  
 tgctcgtcac aggggaagatt gtggaccatg gcaatgggac cttcagcgtc 450  
 cacttccaac acaatgccac aggccagga aacatctcca tcagcctcgt 500  
 gccccccagt aaagctgtag agttccacca ggaacagcag atcttcatcg 550  
 aagccaaggc ctccaaaatc ttcaactgcc ggatggagtg ggagaaggta 600  
 gaacggggcc gccggacctc gctttgcacc cagcaccag ccaagatctg 650  
 ctcccagac cagctcaga gctcagccac ctggagctgc tcccagccct 700  
 tcaaagtcgt ctgtgtctac atcgcttct acagcacgga ctatcggctg 750  
 gtccagaagg tgtgccaga ttacaactac catagtata cccctacta 800  
 cccatctggg tgaccggggg caggccacag aggccaggcc agggctggaa 850

ggacaggcct gcccatgcag gagaccatct ggacaccggg caggaaggg 900  
 gttgggcctc aggcaggag gggggtggag acgaggagat gccaagtggg 950  
 gccagggccca agtctcaagt ggcagagaaa ggggcccaag tgctgggtccc 1000  
 aacctgaagc tgtggagtga ctagatcaca ggagcactgg aggaggagtg 1050  
 ggctctctgt gcagcctcac agggctttgc cacggagcca cagagagatg 1100  
 ctgggtcccc gaggcctgtg ggcaggccga tcagtgtggc cccagatcaa 1150  
 gtcattgggag gaagctaagc ccttggttct tgccatcctg aggaaagata 1200  
 gcaacaggga gggggagatt tcatcagtgt ggacagcctg tcaacttagg 1250  
 atggatggct gagagggctt cctaggagcc agtcagcagg gtgggggtggg 1300  
 gccagaggag ctctccagcc ctgcctagtg ggcgcctga gcccttgtc 1350  
 gtgtgctgag catggcatga ggctgaagtg gcaaccctgg ggtctttgat 1400  
 gtcttgacag attgaccatc tgtctccagc caggccaccc ctttccaaaa 1450  
 ttccctcttc tgccagtact cccctgtac caccattgc tgatggcaca 1500  
 cccatcctta agctaagaca ggacgattgt ggtcctcca cactaaggcc 1550  
 acagcccatc cgcgtgctgt gtgtccctct tccaccccaa cccctgctgg 1600  
 ctctcttggg agcatccatg tcccggagag gggccctca acagtcagcc 1650  
 tcacctgtca gaccgggggt ctcccggatc tggatggcgc cgccctctca 1700  
 gcagcgggca cgggtggggc ggggccgggc cgcagagcat gtgctggatc 1750  
 tgttctgtgt gtctgtctgt ggggtggggg aggggagggg agtcttgtga 1800  
 aaccgctgat tgctgacttt tgtgtgaaga atcgtgttct tggagcagga 1850  
 aataaagctt gccccggggc a 1871

<210> 218

<211> 252

<212> PRT

<213> Homo sapiens

<400> 218

Met	Gln	Leu	Thr	Arg	Cys	Cys	Phe	Val	Phe	Leu	Val	Gln	Gly	Ser
1				5					10					15

Leu	Tyr	Leu	Val	Ile	Cys	Gly	Gln	Asp	Asp	Gly	Pro	Pro	Gly	Ser
				20					25					30

Glu	Asp	Pro	Glu	Arg	Asp	Asp	His	Glu	Gly	Gln	Pro	Arg	Pro	Arg
				35					40					45

Val	Pro	Arg	Lys	Arg	Gly	His	Ile	Ser	Pro	Lys	Ser	Arg	Pro	Met	
				50					55					60	
Ala	Asn	Ser	Thr	Leu	Leu	Gly	Leu	Leu	Ala	Pro	Pro	Gly	Glu	Ala	
				65					70					75	
Trp	Gly	Ile	Leu	Gly	Gln	Pro	Pro	Asn	Arg	Pro	Asn	His	Ser	Pro	
				80					85					90	
Pro	Pro	Ser	Ala	Lys	Val	Lys	Lys	Ile	Phe	Gly	Trp	Gly	Asp	Phe	
				95					100					105	
Tyr	Ser	Asn	Ile	Lys	Thr	Val	Ala	Leu	Asn	Leu	Leu	Val	Thr	Gly	
				110					115					120	
Lys	Ile	Val	Asp	His	Gly	Asn	Gly	Thr	Phe	Ser	Val	His	Phe	Gln	
				125					130					135	
His	Asn	Ala	Thr	Gly	Gln	Gly	Asn	Ile	Ser	Ile	Ser	Leu	Val	Pro	
				140					145					150	
Pro	Ser	Lys	Ala	Val	Glu	Phe	His	Gln	Glu	Gln	Gln	Ile	Phe	Ile	
				155					160					165	
Glu	Ala	Lys	Ala	Ser	Lys	Ile	Phe	Asn	Cys	Arg	Met	Glu	Trp	Glu	
				170					175					180	
Lys	Val	Glu	Arg	Gly	Arg	Arg	Thr	Ser	Leu	Cys	Thr	His	Asp	Pro	
				185					190					195	
Ala	Lys	Ile	Cys	Ser	Arg	Asp	His	Ala	Gln	Ser	Ser	Ala	Thr	Trp	
				200					205					210	
Ser	Cys	Ser	Gln	Pro	Phe	Lys	Val	Val	Cys	Val	Tyr	Ile	Ala	Phe	
				215					220					225	
Tyr	Ser	Thr	Asp	Tyr	Arg	Leu	Val	Gln	Lys	Val	Cys	Pro	Asp	Tyr	
				230					235					240	
Asn	Tyr	His	Ser	Asp	Thr	Pro	Tyr	Tyr	Pro	Ser	Gly				
				245					250						

<210> 219

<211> 2065

<212> DNA

<213> Homo sapiens

<400> 219

gtgaatgtga gggtttgatg acttttcagat gtctaggaac cagagtgggt 50

gcagggggccc caggcagggc tgattcttgg gcggaggaga gtagggtaaa 100

gggttctgca tgagctcctt aaaggacaaa ggtaacagag ccagcgagag 150

agctcgaggg gagactttga cttcaagcca cagaattggg ggaagtgtgc 200

gcgcccgcgc cgccgtcgct cctgcagcgc tgtcgacctc gccgctagca 250  
tcttccccgag caccgggata ccggggtagg aggcgacgcg ggcgagcacc 300  
agcgccagcc ggctgcggct gcccacacgg ctcaccatgg gctccggggc 350  
ccgggcgctg tccgcgggtg cggccgtgct gctggctctc acgctgccgg 400  
ggctgccgtg ctgggcacag aacgacacgg agcccatcgt gctggagggc 450  
aagtgtctgg tgggtgtgca ctcgaacccg gccacggact ccaagggctc 500  
ctcttctctc ccgctgggga tatcggtccg ggccggccaac tccaaggctc 550  
ccttctcggc ggtgcggagc accaaccacg agccatccga gatgagcaac 600  
aagacgcgca tcatttactt cgatcagatc ctggtgaatg tgggtaattt 650  
tttcacattg gagtctgtct ttgtagcacc aagaaaagga atttacagtt 700  
tcagttttca cgtgattaaa gtctaccaga gccaaactat ccaggttaac 750  
ttgatgttaa atggaaaacc agtaatatct gcctttgcgg gggacaaaga 800  
tgttactcgt gaagctgcca cgaatggtgt cctgctctac ctagataaag 850  
aggataaggt ttacctaaaa ctggagaaaag gtaatttggg tggaggctgg 900  
cagtattcca cgttttctgg ctttctgggtg ttccccctat aggattcaat 950  
ttctccatga tgttcatcca ggtgagggat gaccactcc tgagttattg 1000  
gaagatcatt ttttcatcat tggattgatg tcttttattg gtttctcatg 1050  
gggtggatatg gattctaagg attctagcct gtctgaacca atacaaaatt 1100  
tcacagatta tttgtgtgtg tctgtttcag tatatttgga ttgggactct 1150  
aagcagataa tacctatgct taaatgtaac agtcaaaagc tgtctgcaag 1200  
acttattctg aatttcattt cctgggatta ctgaattagt tacagatgtg 1250  
gaattttatt tgtttagttt taaaagactg gcaaccaggc ctaaggatta 1300  
gaaaactcta aagttctgac ttcaatcaac ggtagtgtg atactgcaa 1350  
agaactgtat actgtgttaa tatattgatt atatttgttt ttattccttt 1400  
ggaattagtt tgtttggttc ttgtaaaaaa cttggatttt ttttttcagt 1450  
aactgggtatt atgttttctc ttaaaataag gtaatgaatg gcttgccac 1500  
aaatttacct tgactacgat atcatcgaca tgacttctct caaaaaaaaa 1550  
gaatgcttca tagttgtatt ttaattgtat atgtgaaaga gtcataattt 1600  
ccaagttata ttttctaaga agaagaatag atcataaatc tgacaaggaa 1650

aaagttgctt acccaaaatc taagtgtc atccctgagc ctcagcaaaa 1700  
 cagctcccct ccgagggaaa tcttatactt tattgctcaa ctttaattaa 1750  
 aatgattgat aataaccact ttattaaaaa cctaagggtt ttttttttc 1800  
 cgtagacatg accactttat taactggtgg tgggatgctg ttgtttctaa 1850  
 ttatacctat ttttcaaggc ttctgttgta tttgaagtat catctggttt 1900  
 tgccttaact ctttaaattg tatatattta tctgttttagc taatattaaa 1950  
 ttcaaatatc ccatatctaa atttagtgc atatcttgtc ttttgtatag 2000  
 gtcatatgaa ttcataaaat tatttatgtc tgttatagaa taaagattaa 2050  
 tatatgttaa aaaaa 2065

<210> 220

<211> 201

<212> PRT

<213> Homo sapiens

<400> 220

Met	Gly	Ser	Gly	Arg	Arg	Ala	Leu	Ser	Ala	Val	Pro	Ala	Val	Leu
1				5				10						15

Leu	Val	Leu	Thr	Leu	Pro	Gly	Leu	Pro	Val	Trp	Ala	Gln	Asn	Asp
				20				25						30

Thr	Glu	Pro	Ile	Val	Leu	Glu	Gly	Lys	Cys	Leu	Val	Val	Cys	Asp
				35				40						45

Ser	Asn	Pro	Ala	Thr	Asp	Ser	Lys	Gly	Ser	Ser	Ser	Ser	Pro	Leu
				50				55						60

Gly	Ile	Ser	Val	Arg	Ala	Ala	Asn	Ser	Lys	Val	Ala	Phe	Ser	Ala
				65				70						75

Val	Arg	Ser	Thr	Asn	His	Glu	Pro	Ser	Glu	Met	Ser	Asn	Lys	Thr
				80				85						90

Arg	Ile	Ile	Tyr	Phe	Asp	Gln	Ile	Leu	Val	Asn	Val	Gly	Asn	Phe
				95				100						105

Phe	Thr	Leu	Glu	Ser	Val	Phe	Val	Ala	Pro	Arg	Lys	Gly	Ile	Tyr
				110				115						120

Ser	Phe	Ser	Phe	His	Val	Ile	Lys	Val	Tyr	Gln	Ser	Gln	Thr	Ile
				125				130						135

Gln	Val	Asn	Leu	Met	Leu	Asn	Gly	Lys	Pro	Val	Ile	Ser	Ala	Phe
				140				145						150

Ala	Gly	Asp	Lys	Asp	Val	Thr	Arg	Glu	Ala	Ala	Thr	Asn	Gly	Val
				155				160						165

Leu Leu Tyr Leu Asp Lys Glu Asp Lys Val Tyr Leu Lys Leu Glu  
170 175 180

Lys Gly Asn Leu Val Gly Gly Trp Gln Tyr Ser Thr Phe Ser Gly  
185 190 195

Phe Leu Val Phe Pro Leu  
200

<210> 221

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 221

acggctcacc atgggctccg 20

<210> 222

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 222

aggaagagga gcccttggag tccg 24

<210> 223

<211> 40

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 223

cgtgctggag ggcaagtgtc tgggtggtgtg cgactcgaac 40

<210> 224

<211> 902

<212> DNA

<213> Homo sapiens

<400> 224

cggtggccat gactgcggcc gtgttcttcg gctgcgcctt cattgccttc 50

gggcctgcgc tcgcccttta tgtcttcacc atcgccatcg agccgttgcg 100

tatcatcttc ctcacgcgcg gagctttctt ctggttggtg tctctactga 150

tttcgtccct tgtttggttc atggcaagag tcattattga caacaaagat 200

ggaccaacac agaaatatct gctgatcttt ggagcgtttg tctctgtcta 250  
 tatccaagaa atgttccgat ttgcatatta taaactotta aaaaaagcca 300  
 gtgaagggtt gaagagtata aaccaggtg agacagcacc ctctatgcga 350  
 ctgctggcct atgtttctgg cttgggcttt ggaatcatga gtggagtatt 400  
 ttcctttgtg aataccctat ctgactcctt ggggccaggc acagtgggca 450  
 ttcattggaga ttctcctcaa ttcttccttt attcagcttt catgacgctg 500  
 gtcattatct tgctgcatgt attctggggc attgtatatt ttgatggctg 550  
 tgagaagaaa aagtggggca tcctccttat cgttctcctg acccacctgc 600  
 tgggtgacgc ccagaccttc ataagttctt attatggaat aaacctggcg 650  
 tcagcattta taatcctggt gctcatgggc acctgggcat tcttagctgc 700  
 gggaggcagc tgccgaagcc tgaaactctg cctgctctgc caagacaaga 750  
 actttcttct ttacaaccag cgctccagat aacctcaggg aaccagcact 800  
 tcccaaaccg cagactacat ctttagagga agcacaactg tgcccttttc 850  
 tgaaaatccc tttttctggt ggaattgaga aagaaataaa actatgcaga 900  
 ta 902

<210> 225

<211> 257

<212> PRT

<213> Homo sapiens

<400> 225

Met	Thr	Ala	Ala	Val	Phe	Phe	Gly	Cys	Ala	Phe	Ile	Ala	Phe	Gly
1				5					10					15
Pro	Ala	Leu	Ala	Leu	Tyr	Val	Phe	Thr	Ile	Ala	Ile	Glu	Pro	Leu
				20					25					30
Arg	Ile	Ile	Phe	Leu	Ile	Ala	Gly	Ala	Phe	Phe	Trp	Leu	Val	Ser
				35					40					45
Leu	Leu	Ile	Ser	Ser	Leu	Val	Trp	Phe	Met	Ala	Arg	Val	Ile	Ile
				50					55					60
Asp	Asn	Lys	Asp	Gly	Pro	Thr	Gln	Lys	Tyr	Leu	Leu	Ile	Phe	Gly
				65					70					75
Ala	Phe	Val	Ser	Val	Tyr	Ile	Gln	Glu	Met	Phe	Arg	Phe	Ala	Tyr
				80					85					90
Tyr	Lys	Leu	Leu	Lys	Lys	Ala	Ser	Glu	Gly	Leu	Lys	Ser	Ile	Asn
				95					100					105



Pro Gly Glu Thr	Ala	Pro Ser Met Arg	Leu Leu Ala Tyr Val	Ser
	110		115	120
Gly Leu Gly Phe	Gly Ile Met Ser Gly	Val Phe Ser Phe	Val Asn	
	125		130	135
Thr Leu Ser Asp	Ser Leu Gly Pro Gly	Thr Val Gly Ile His	Gly	
	140		145	150
Asp Ser Pro Gln	Phe Phe Leu Tyr Ser	Ala Phe Met Thr Leu	Val	
	155		160	165
Ile Ile Leu Leu	His Val Phe Trp Gly	Ile Val Phe Phe Asp	Gly	
	170		175	180
Cys Glu Lys Lys	Lys Trp Gly Ile Leu	Leu Ile Val Leu Leu	Thr	
	185		190	195
His Leu Leu Val	Ser Ala Gln Thr Phe	Ile Ser Ser Tyr Tyr	Gly	
	200		205	210
Ile Asn Leu Ala	Ser Ala Phe Ile Ile	Leu Val Leu Met Gly	Thr	
	215		220	225
Trp Ala Phe Leu	Ala Ala Gly Gly Ser	Cys Arg Ser Leu Lys	Leu	
	230		235	240
Cys Leu Leu Cys	Gln Asp Lys Asn Phe	Leu Leu Tyr Asn Gln	Arg	
	245		250	255

Ser Arg

<210> 226  
 <211> 3939  
 <212> DNA  
 <213> Homo sapiens

<400> 226  
 cggcaaccag cgcgcgccac caccgctgcc actgccgcc tgcgggggcc 50  
 atgttcgctc tgggcttgcc cttcttggtg ctcttggtgg cctcggtcga 100  
 gagccatctg ggggttctg ggcccaagaa cgtctcgag aaagacgccg 150  
 agtttgagcg cacctacgtg gacgaggtca acagcgagct ggtaacatc 200  
 tacaccttca accatactgt gacccgcaac aggacagagg gcgtgcgtgt 250  
 gtctgtgaac gtctgaaca agcagaaggg ggcgccgttg ctgtttgtgg 300  
 tccgccagaa ggaggctgtg gtgtccttcc aggtgccct aatcctgcga 350  
 gggatgtttc agcgcaagta cctctaccaa aaagtggaac gaaccctgtg 400  
 tcagccccc accaagaatg agtcggagat tcagttcttc tacgtggatg 450

tgtccaccct gtcaccagtc aacaccacat accagctccg ggtcagccgc 500  
atggacgatt ttgtgctcag gactggggag cagttcagct tcaataccac 550  
agcagcacag cccagctact tcaagtatga gttccctgaa ggcgtggact 600  
cggtaattgt caaggtgacc tccaacaagg ccttccctg ctacgtcatc 650  
tccattcagg atgtgctgtg tctgtctat gacctggaca acaacgtagc 700  
cttcatcggc atgtaccaga cgatgaccaa gaaggcggcc atcacgtac 750  
agcgcaaaga cttccccagc aacagctttt atgtggtggt ggtggtgaag 800  
accgaagacc aagcctgcgg gggctccctg cctttctacc ccttcgcaga 850  
agatgaaccg gtcgatcaag ggcaccgcca gaaaaccctg tcagtgtctg 900  
tgtctcaagc agtcacgtct gaggcatacg tcagtgggat gctcttttgc 950  
ctgggtatat ttctctcctt ttacctgctg accgtcctcc tggcctgctg 1000  
ggagaactgg aggcagaaga agaagaccct gctggtggcc attgaccgag 1050  
cctgcccaag aagcggtcac cctcgagtcc tggctgattc ttttcctggc 1100  
agttccccct atgaggggta caactatggc tcctttgaga atgtttctgg 1150  
atctaccgat ggtctgggtg acagcgtgg cactggggac ctctcttacg 1200  
gttaccaggg ccgctccttt gaacctgtag gtactcggcc ccgagtggac 1250  
tccatgagct ctgtggagga ggatgactac gacacattga ccgacatcga 1300  
ttccgacaag aatgtcattc gcaccaagca atacctctat gtggctgacc 1350  
tggcacggaa ggacaagcgt gttctgcgga aaaagtaacca gatctacttc 1400  
tggaacattg ccaccattgc tgtcttctat gcccttctg tgggtgcagct 1450  
ggtgatcacc taccagacgg tggatgaatgt cacagggaat caggacatct 1500  
gctactacaa cttcctctgc gccacccac tgggcaatct cagcgccttc 1550  
aacaacatcc tcagcaacct ggggtacatc ctgctggggc tgcttttcct 1600  
gctcatcatc ctgcaacggg agatcaacca caaccgggccc ctgctgcgca 1650  
atgacctctg tgccctggaa tgtgggatcc ccaaactt tgggcttttc 1700  
tacgccatgg gcacagccct gatgatggag gggctgctca gtgcttgcta 1750  
tcatgtgtgc cccaactata ccaatttcca gtttgacaca tcgttcatgt 1800  
acatgatcgc cggactctgc atgctgaagc tctaccagaa gcggcacccg 1850  
gacatcaacg ccagcgcta cagtgcctac gcctgcctgg ccattgtcat 1900

cttcttctct gtgctgggcg tggcttttgg caaagggaac acggcgttct 1950  
ggatcgtctt ctccatcatt cacatcatcg ccacctgct cctcagcacg 2000  
cagctctatt acatggggcg gtggaaactg gactcgggga tcttccgccg 2050  
catcctccac gtgctctaca cagactgcat ccggcagtgc agcggggcgc 2100  
tctacgtgga ccgcatggtg ctgctggtca tgggcaacgt catcaactgg 2150  
tcgctggctg cctatgggct tatcatgcgc cccaatgatt tcgcttctta 2200  
cttgttggcc attggcatct gcaacctgct cctttacttc gccttctaca 2250  
tcatcatgaa gctccggagt ggggagagga tcaagctcat cccctgctc 2300  
tgcacgtttt gcacctcgt ggtctggggo ttcgcgtctt tcttcttctt 2350  
ccagggactc agcacctggc agaaaacccc tgcagagtcg agggagcaca 2400  
accgggactg catcctctc gacttctttg acgaccacga catctggcac 2450  
ttcctctcct ccacgccat gttcgggtcc ttctggtgt tgctgacact 2500  
ggatgacgac ctggatactg tgcagcggga caagatctat gtcttctagc 2550  
aggagctggg cccttcgctt cacctcaagg ggccctgagc tcctttgtgt 2600  
catagaccgg tcaactctgc gtgctgtggg gatgagtccc agcaccgctg 2650  
cccagcactg gatggcagca ggacagccag gtctagctta ggcttggcct 2700  
gggacagcca tgggggtggca tggaaacctg cagctgccct ctgccagga 2750  
gcaggcctgc tcccctggaa ccccagatg ttggccaaat tgctgcttct 2800  
ttctcagtgt tggggccttc catgggcccc tgtcctttgg ctctccattt 2850  
gtccctttgc aagaggaagg atggaaggga caccctcccc atttcatgcc 2900  
ttgcattttg ccgctcctcc tcccacaaat gcccagcct gggacctaa 2950  
gcctcttttt cctcccatc tcccactcca gggcctagtc tggggcctga 3000  
atctctgtcc tgtatcaggg cccagttct ctttgggctg tcctggctg 3050  
ccatcactgc ccattccagt cagccaggat ggatgggggt atgagatttt 3100  
gggggttggc cagctggtgc cagacttttg gtgctaaggc ctgcaagggg 3150  
cctggggcag tgcgtattct cttccctctg acctgtgctc agggctggct 3200  
ctttagcaat gcgctcagcc caatttgaga accgccttct gattcaagag 3250  
gctgaattca gaggtcacct cttcatccca tcagctccca gactgatgcc 3300

agcaccagga ctggagggag aagcgctca ccccttcct tccttcttc 3350  
 caggccctta gtcttgccaa accccagctg gtggccttc agtgccattg 3400  
 aactgcccaga aatgtcca ggggcaaagg agggatgata cagagttcag 3450  
 cccgttctgc ctccacagct gtgggcaccc cagtgcctac cttagaaagg 3500  
 ggcttcagga agggatgtgc tgtttccctc tacgtgcca gtcctagcct 3550  
 cgctctagga cccagggctg gcttctaagt ttccgtccag tcttcaggca 3600  
 agttctgtgt tagtcatgca cacacatacc tatgaaacct tggagtttac 3650  
 aaagaattgc cccagctctg ggcaccctgg ccaccctggg ccttgatcc 3700  
 ccttcgtccc acctggtcca cccagatgc tgaggatggg ggagctcagg 3750  
 cggggcctct gctttgggga tgggaatgtg tttttctccc aaacttgttt 3800  
 ttatagctct gcttgaaggg ctgggagatg aggtgggtct ggatcttttc 3850  
 tcagagcgtc tccatgctat gggtgcattt ccgttttcta tgaatgaatt 3900  
 tgcattcaat aaacaaccag actcaaaaaa aaaaaaaaaa 3939

<210> 227

<211> 832

<212> PRT

<213> Homo sapiens

<400> 227

Met	Phe	Ala	Leu	Gly	Leu	Pro	Phe	Leu	Val	Leu	Leu	Val	Ala	Ser
1				5					10					15
Val	Glu	Ser	His	Leu	Gly	Val	Leu	Gly	Pro	Lys	Asn	Val	Ser	Gln
				20					25					30
Lys	Asp	Ala	Glu	Phe	Glu	Arg	Thr	Tyr	Val	Asp	Glu	Val	Asn	Ser
				35					40					45
Glu	Leu	Val	Asn	Ile	Tyr	Thr	Phe	Asn	His	Thr	Val	Thr	Arg	Asn
				50					55					60
Arg	Thr	Glu	Gly	Val	Arg	Val	Ser	Val	Asn	Val	Leu	Asn	Lys	Gln
				65					70					75
Lys	Gly	Ala	Pro	Leu	Leu	Phe	Val	Val	Arg	Gln	Lys	Glu	Ala	Val
				80					85					90
Val	Ser	Phe	Gln	Val	Pro	Leu	Ile	Leu	Arg	Gly	Met	Phe	Gln	Arg
				95					100					105
Lys	Tyr	Leu	Tyr	Gln	Lys	Val	Glu	Arg	Thr	Leu	Cys	Gln	Pro	Pro
				110					115					120
Thr	Lys	Asn	Glu	Ser	Glu	Ile	Gln	Phe	Phe	Tyr	Val	Asp	Val	Ser

	125		130		135
Thr Leu Ser Pro	Val Asn Thr Thr Tyr	Gln Leu Arg Val Ser Arg			
	140	145			150
Met Asp Asp Phe	Val Leu Arg Thr Gly	Glu Gln Phe Ser Phe Asn			
	155	160			165
Thr Thr Ala Ala	Gln Pro Gln Tyr Phe	Lys Tyr Glu Phe Pro Glu			
	170	175			180
Gly Val Asp Ser	Val Ile Val Lys Val	Thr Ser Asn Lys Ala Phe			
	185	190			195
Pro Cys Ser Val	Ile Ser Ile Gln Asp	Val Leu Cys Pro Val Tyr			
	200	205			210
Asp Leu Asp Asn	Asn Val Ala Phe Ile	Gly Met Tyr Gln Thr Met			
	215	220			225
Thr Lys Lys Ala	Ala Ile Thr Val Gln	Arg Lys Asp Phe Pro Ser			
	230	235			240
Asn Ser Phe Tyr	Val Val Val Val Val	Lys Thr Glu Asp Gln Ala			
	245	250			255
Cys Gly Gly Ser	Leu Pro Phe Tyr Pro	Phe Ala Glu Asp Glu Pro			
	260	265			270
Val Asp Gln Gly	His Arg Gln Lys Thr	Leu Ser Val Leu Val Ser			
	275	280			285
Gln Ala Val Thr	Ser Glu Ala Tyr Val	Ser Gly Met Leu Phe Cys			
	290	295			300
Leu Gly Ile Phe	Leu Ser Phe Tyr Leu	Leu Thr Val Leu Leu Ala			
	305	310			315
Cys Trp Glu Asn	Trp Arg Gln Lys Lys	Lys Thr Leu Leu Val Ala			
	320	325			330
Ile Asp Arg Ala	Cys Pro Glu Ser Gly	His Pro Arg Val Leu Ala			
	335	340			345
Asp Ser Phe Pro	Gly Ser Ser Pro Tyr	Glu Gly Tyr Asn Tyr Gly			
	350	355			360
Ser Phe Glu Asn	Val Ser Gly Ser Thr	Asp Gly Leu Val Asp Ser			
	365	370			375
Ala Gly Thr Gly	Asp Leu Ser Tyr Gly	Tyr Gln Gly Arg Ser Phe			
	380	385			390
Glu Pro Val Gly	Thr Arg Pro Arg Val	Asp Ser Met Ser Ser Val			
	395	400			405
Glu Glu Asp Asp	Tyr Asp Thr Leu Thr	Asp Ile Asp Ser Asp Lys			

410					415					420				
Asn	Val	Ile	Arg	Thr	Lys	Gln	Tyr	Leu	Tyr	Val	Ala	Asp	Leu	Ala
				425										435
Arg	Lys	Asp	Lys	Arg	Val	Leu	Arg	Lys	Lys	Tyr	Gln	Ile	Tyr	Phe
				440										450
Trp	Asn	Ile	Ala	Thr	Ile	Ala	Val	Phe	Tyr	Ala	Leu	Pro	Val	Val
				455										465
Gln	Leu	Val	Ile	Thr	Tyr	Gln	Thr	Val	Val	Asn	Val	Thr	Gly	Asn
				470										480
Gln	Asp	Ile	Cys	Tyr	Tyr	Asn	Phe	Leu	Cys	Ala	His	Pro	Leu	Gly
				485										495
Asn	Leu	Ser	Ala	Phe	Asn	Asn	Ile	Leu	Ser	Asn	Leu	Gly	Tyr	Ile
				500										510
Leu	Leu	Gly	Leu	Leu	Phe	Leu	Leu	Ile	Ile	Leu	Gln	Arg	Glu	Ile
				515										525
Asn	His	Asn	Arg	Ala	Leu	Leu	Arg	Asn	Asp	Leu	Cys	Ala	Leu	Glu
				530										540
Cys	Gly	Ile	Pro	Lys	His	Phe	Gly	Leu	Phe	Tyr	Ala	Met	Gly	Thr
				545										555
Ala	Leu	Met	Met	Glu	Gly	Leu	Leu	Ser	Ala	Cys	Tyr	His	Val	Cys
				560										570
Pro	Asn	Tyr	Thr	Asn	Phe	Gln	Phe	Asp	Thr	Ser	Phe	Met	Tyr	Met
				575										585
Ile	Ala	Gly	Leu	Cys	Met	Leu	Lys	Leu	Tyr	Gln	Lys	Arg	His	Pro
				590										600
Asp	Ile	Asn	Ala	Ser	Ala	Tyr	Ser	Ala	Tyr	Ala	Cys	Leu	Ala	Ile
				605										615
Val	Ile	Phe	Phe	Ser	Val	Leu	Gly	Val	Val	Phe	Gly	Lys	Gly	Asn
				620										630
Thr	Ala	Phe	Trp	Ile	Val	Phe	Ser	Ile	Ile	His	Ile	Ile	Ala	Thr
				635										645
Leu	Leu	Leu	Ser	Thr	Gln	Leu	Tyr	Tyr	Met	Gly	Arg	Trp	Lys	Leu
				650										660
Asp	Ser	Gly	Ile	Phe	Arg	Arg	Ile	Leu	His	Val	Leu	Tyr	Thr	Asp
				665										675
Cys	Ile	Arg	Gln	Cys	Ser	Gly	Pro	Leu	Tyr	Val	Asp	Arg	Met	Val
				680										690
Leu	Leu	Val	Met	Gly	Asn	Val	Ile	Asn	Trp	Ser	Leu	Ala	Ala	Tyr



ggcatcccct tcctcttctt tgaggcttca gaccgggatg agccaggcac 600  
agccaactcg gatcttcgat tccacatcct gagccaggct ccagcccagc 650  
cttccccaga catgttccag ctggagcctc ggctgggggc tctggccctc 700  
agccccaagg ggagcaccag ccttgaccac gccctggaga ggacctacca 750  
gctgttggtg caggtcaagg acatgggtga ccaggcctca ggccaccagg 800  
ccactgccac cgtggaagtc tccatcatag agagcacctg ggtgtcccta 850  
gagcctatcc acctggcaga gaatctcaaa gtcctatacc cgcaccacat 900  
ggcccaggta cactggagtg ggggtgatgt gcactatcac ctggagagcc 950  
atcccccgga accctttgaa gtgaatgcag agggaaacct ctacgtgacc 1000  
agagagctgg acagagaagc ccaggctgag tacctgctcc aggtgcgggc 1050  
tcagaattcc catggcgagg actatgcggc ccctctggag ctgcacgtgc 1100  
tggtgatgga tgagaatgac aacgtgccta tctgccctcc cctgaccccc 1150  
acagtcagca tccctgagct cagtccacca ggtactgaag tgactagact 1200  
gtcagcagag gatgcagatg cccccggctc cccaattcc cacgttgtgt 1250  
atcagctcct gagccctgag cctgaggatg gggtagaggg gagagccttc 1300  
caggtggacc ccacttcagg cagtgtgacg ctgggggtgc tcccactccg 1350  
agcaggccag aacatcctgc ttctgggtgt ggccatggac ctggcaggcg 1400  
cagaggggtg cttcagcagc acgtgtgaag tcgaagtcgc agtcacagat 1450  
atcaatgatc acgcccctga gttcatcact tcccagattg ggcctataag 1500  
cctccctgag gatgtggagc ccgggactct ggtggccatg ctaacagcca 1550  
ttgatgtga cctcgagccc gccttcgcgc tcatggattt tgccattgag 1600  
aggggagaca cagaaggga ttttggcctg gattgggagc cagactctgg 1650  
gcatgttaga ctcagactct gcaagaacct cagttatgag gcagctcaa 1700  
gtcatgaggt ggtgggtggtg gtgcagagtg tggcgaagct ggtggggcca 1750  
ggcccaggcc ctggagccac cgccacgggtg actgtgctag tggagagagt 1800  
gatgccaccc cccaagttgg accaggagag ctacgaggcc agtgtcccca 1850  
tcagtgcctc agccggctct ttctgtctga ccatccagcc ctccgacccc 1900  
atcagccgaa ccctcaggtt ctccctagtc aatgactcag agggctggct 1950  
ctgcattgag aaattctccg gggaggtgca caccgccag tccctgcagg 2000



gcgcccagcc tggggacacc tacacggtgc ttgtggaggc ccaggataca 2050  
 gccctgactc ttgccctgt gccctccaa tacctctgca cccccgcca 2100  
 agaccatggc ttgatcgtga gtggacccag caaggacccc gatctggcca 2150  
 gtgggcacgg tccctacagc ttcacccttg gtcccaaccc cacggtgcaa 2200  
 cgggattggc gcctccagac tctcaatggt tcccatgcct acctcacctt 2250  
 ggccctgcat tgggtggagc cacgtgaaca cataatcccc gtggtggtca 2300  
 gccacaatgc ccagatgtgg cagctcctgg ttcgagtgat cgtgtgtcgc 2350  
 tgcaacgtgg aggggcagt catgcgcaag gtgggcccga tgaaggcat 2400  
 gccacgaag ctgtcggcag tgggcatcct ttaggcacc ctggtagcaa 2450  
 taggaatctt cctcatcctc attttcaccc actggaccat gtcaaggaag 2500  
 aaggacccgg atcaaccagc agacagcgtg cccctgaagg cgactgtctg 2550  
 aatggcccag gcagctctag ctgggagctt ggccctctggc tccatctgag 2600  
 tcccctggga gagagcccag cacccaagat ccagcagggg acaggacaga 2650  
 gtagaagccc ctccatctgc cctgggggtgg aggcaccatc accatcacca 2700  
 ggcatgtctg cagagcctgg acaccaactt tatggactgc ccatgggagt 2750  
 gctccaaatg tcagggtgtt tgcccaataa taaagcccca gagaactggg 2800  
 ctgggcccta tgggaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaag 2848

<210> 229

<211> 807

<212> PRT

<213> Homo sapiens

<400> 229

Met	Val	Pro	Ala	Trp	Leu	Trp	Leu	Leu	Cys	Val	Ser	Val	Pro	Gln
1				5					10					15

Ala	Leu	Pro	Lys	Ala	Gln	Pro	Ala	Glu	Leu	Ser	Val	Glu	Val	Pro
				20					25					30

Glu	Asn	Tyr	Gly	Gly	Asn	Phe	Pro	Leu	Tyr	Leu	Thr	Lys	Leu	Pro
				35					40					45

Leu	Pro	Arg	Glu	Gly	Ala	Glu	Gly	Gln	Ile	Val	Leu	Ser	Gly	Asp
				50					55					60

Ser	Gly	Lys	Ala	Thr	Glu	Gly	Pro	Phe	Ala	Met	Asp	Pro	Asp	Ser
				65					70					75

Gly	Phe	Leu	Leu	Val	Thr	Arg	Ala	Leu	Asp	Arg	Glu	Glu	Gln	Ala
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

80										85					90				
Glu	Tyr	Gln	Leu	Gln	Val	Thr	Leu	Glu	Met	Gln	Asp	Gly	His	Val					
				95					100					105					
Leu	Trp	Gly	Pro	Gln	Pro	Val	Leu	Val	His	Val	Lys	Asp	Glu	Asn					
				110					115					120					
Asp	Gln	Val	Pro	His	Phe	Ser	Gln	Ala	Ile	Tyr	Arg	Ala	Arg	Leu					
				125					130					135					
Ser	Arg	Gly	Thr	Arg	Pro	Gly	Ile	Pro	Phe	Leu	Phe	Leu	Glu	Ala					
				140					145					150					
Ser	Asp	Arg	Asp	Glu	Pro	Gly	Thr	Ala	Asn	Ser	Asp	Leu	Arg	Phe					
				155					160					165					
His	Ile	Leu	Ser	Gln	Ala	Pro	Ala	Gln	Pro	Ser	Pro	Asp	Met	Phe					
				170					175					180					
Gln	Leu	Glu	Pro	Arg	Leu	Gly	Ala	Leu	Ala	Leu	Ser	Pro	Lys	Gly					
				185					190					195					
Ser	Thr	Ser	Leu	Asp	His	Ala	Leu	Glu	Arg	Thr	Tyr	Gln	Leu	Leu					
				200					205					210					
Val	Gln	Val	Lys	Asp	Met	Gly	Asp	Gln	Ala	Ser	Gly	His	Gln	Ala					
				215					220					225					
Thr	Ala	Thr	Val	Glu	Val	Ser	Ile	Ile	Glu	Ser	Thr	Trp	Val	Ser					
				230					235					240					
Leu	Glu	Pro	Ile	His	Leu	Ala	Glu	Asn	Leu	Lys	Val	Leu	Tyr	Pro					
				245					250					255					
His	His	Met	Ala	Gln	Val	His	Trp	Ser	Gly	Gly	Asp	Val	His	Tyr					
				260					265					270					
His	Leu	Glu	Ser	His	Pro	Pro	Gly	Pro	Phe	Glu	Val	Asn	Ala	Glu					
				275					280					285					
Gly	Asn	Leu	Tyr	Val	Thr	Arg	Glu	Leu	Asp	Arg	Glu	Ala	Gln	Ala					
				290					295					300					
Glu	Tyr	Leu	Leu	Gln	Val	Arg	Ala	Gln	Asn	Ser	His	Gly	Glu	Asp					
				305					310					315					
Tyr	Ala	Ala	Pro	Leu	Glu	Leu	His	Val	Leu	Val	Met	Asp	Glu	Asn					
				320					325					330					
Asp	Asn	Val	Pro	Ile	Cys	Pro	Pro	Arg	Asp	Pro	Thr	Val	Ser	Ile					
				335					340					345					
Pro	Glu	Leu	Ser	Pro	Pro	Gly	Thr	Glu	Val	Thr	Arg	Leu	Ser	Ala					
				350					355					360					
Glu	Asp	Ala	Asp	Ala	Pro	Gly	Ser	Pro	Asn	Ser	His	Val	Val	Tyr					

365										370					375				
Gln	Leu	Leu	Ser	Pro	Glu	Pro	Glu	Asp	Gly	Val	Glu	Gly	Arg	Ala					
				380					385					390					
Phe	Gln	Val	Asp	Pro	Thr	Ser	Gly	Ser	Val	Thr	Leu	Gly	Val	Leu					
				395					400					405					
Pro	Leu	Arg	Ala	Gly	Gln	Asn	Ile	Leu	Leu	Leu	Val	Leu	Ala	Met					
				410					415					420					
Asp	Leu	Ala	Gly	Ala	Glu	Gly	Gly	Phe	Ser	Ser	Thr	Cys	Glu	Val					
				425					430					435					
Glu	Val	Ala	Val	Thr	Asp	Ile	Asn	Asp	His	Ala	Pro	Glu	Phe	Ile					
				440					445					450					
Thr	Ser	Gln	Ile	Gly	Pro	Ile	Ser	Leu	Pro	Glu	Asp	Val	Glu	Pro					
				455					460					465					
Gly	Thr	Leu	Val	Ala	Met	Leu	Thr	Ala	Ile	Asp	Ala	Asp	Leu	Glu					
				470					475					480					
Pro	Ala	Phe	Arg	Leu	Met	Asp	Phe	Ala	Ile	Glu	Arg	Gly	Asp	Thr					
				485					490					495					
Glu	Gly	Thr	Phe	Gly	Leu	Asp	Trp	Glu	Pro	Asp	Ser	Gly	His	Val					
				500					505					510					
Arg	Leu	Arg	Leu	Cys	Lys	Asn	Leu	Ser	Tyr	Glu	Ala	Ala	Pro	Ser					
				515					520					525					
His	Glu	Val	Val	Val	Val	Val	Gln	Ser	Val	Ala	Lys	Leu	Val	Gly					
				530					535					540					
Pro	Gly	Pro	Gly	Pro	Gly	Ala	Thr	Ala	Thr	Val	Thr	Val	Leu	Val					
				545					550					555					
Glu	Arg	Val	Met	Pro	Pro	Pro	Lys	Leu	Asp	Gln	Glu	Ser	Tyr	Glu					
				560					565					570					
Ala	Ser	Val	Pro	Ile	Ser	Ala	Pro	Ala	Gly	Ser	Phe	Leu	Leu	Thr					
				575					580					585					
Ile	Gln	Pro	Ser	Asp	Pro	Ile	Ser	Arg	Thr	Leu	Arg	Phe	Ser	Leu					
				590					595					600					
Val	Asn	Asp	Ser	Glu	Gly	Trp	Leu	Cys	Ile	Glu	Lys	Phe	Ser	Gly					
				605					610					615					
Glu	Val	His	Thr	Ala	Gln	Ser	Leu	Gln	Gly	Ala	Gln	Pro	Gly	Asp					
				620					625					630					
Thr	Tyr	Thr	Val	Leu	Val	Glu	Ala	Gln	Asp	Thr	Ala	Leu	Thr	Leu					
				635					640					645					
Ala	Pro	Val	Pro	Ser	Gln	Tyr	Leu	Cys	Thr	Pro	Arg	Gln	Asp	His					

650					655					660				
Gly	Leu	Ile	Val	Ser	Gly	Pro	Ser	Lys	Asp	Pro	Asp	Leu	Ala	Ser
				665					670					675
Gly	His	Gly	Pro	Tyr	Ser	Phe	Thr	Leu	Gly	Pro	Asn	Pro	Thr	Val
				680					685					690
Gln	Arg	Asp	Trp	Arg	Leu	Gln	Thr	Leu	Asn	Gly	Ser	His	Ala	Tyr
				695					700					705
Leu	Thr	Leu	Ala	Leu	His	Trp	Val	Glu	Pro	Arg	Glu	His	Ile	Ile
				710					715					720
Pro	Val	Val	Val	Ser	His	Asn	Ala	Gln	Met	Trp	Gln	Leu	Leu	Val
				725					730					735
Arg	Val	Ile	Val	Cys	Arg	Cys	Asn	Val	Glu	Gly	Gln	Cys	Met	Arg
				740					745					750
Lys	Val	Gly	Arg	Met	Lys	Gly	Met	Pro	Thr	Lys	Leu	Ser	Ala	Val
				755					760					765
Gly	Ile	Leu	Val	Gly	Thr	Leu	Val	Ala	Ile	Gly	Ile	Phe	Leu	Ile
				770					775					780
Leu	Ile	Phe	Thr	His	Trp	Thr	Met	Ser	Arg	Lys	Lys	Asp	Pro	Asp
				785					790					795
Gln	Pro	Ala	Asp	Ser	Val	Pro	Leu	Lys	Ala	Thr	Val			
				800					805					

<210> 230

<211> 50

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 230

cgcccttaccg cgcagcccgga agattcacta tgggtgaaaat cgccttcaat 50

<210> 231

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 231

cctgagctgt aacccactc cagg 24

<210> 232

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 232

agagtctgtc ccagctatct tgt 23

<210> 233

<211> 2786

<212> DNA

<213> Homo sapiens

<400> 233

ccggggacat gaggtggata ctgttcattg gggcccttat tgggtccagc 50  
atctgtggcc aagaaaaatt ttttggggac caagttttga ggattaatgt 100  
cagaaatgga gacgagatca gcaaattgag tcaactagtg aattcaaaca 150  
acttgaagct caatttctgg aaatctccct cctccttcaa tcggcctgtg 200  
gatgtcctgg tcccatctgt cagtctgcag gcatttaaata ccttcctgag 250  
atcccagggc ttagagtacg cagtgcacaat tgaggacctg caggcccttt 300  
tagacaatga agatgatgaa atgcaacaca atgaagggca agaacggagc 350  
agtaataact tcaactacgg ggcttaccat tccctggaag ctatttacca 400  
cgagatggac aacattgccg cagactttcc tgacctggcg aggaggggtga 450  
agattggaca ttcgtttgaa aaccggccga tgtatgtact gaagttcagc 500  
actgggaaag gcgtgaggcg gccggccgtt tggctgaatg caggcatcca 550  
ttcccagagag tggatctccc aggccactgc aatctggacg gcaaggaaga 600  
ttgtatctga ttaccagagg gatccagcta tcacctccat cttggagaaa 650  
atggatatatt tcttgttgcc tgtggccaat cctgatggat atgtgtatac 700  
tcaaactcaa aaccgattat ggaggaagac gcggtcccga aatcctggaa 750  
gctcctgcat tgggtgctgac ccaaatagaa actggaacgc tagttttgca 800  
ggaaagggag ccagcgacaa cccttgctcc gaagtgtacc atggacccca 850  
cgccaattcg gaagtggagg tgaaatcagt ggtagatttc atccaaaaac 900  
atgggaattt caagggttc atcgacctgc acagctactc gcagctgctg 950  
atgtatccat atgggtactc agtcaaaaag gcccagatg ccgaggaact 1000  
cgacaaggtg gcgaggcttg cggccaaagc tctggcttct gtgtcgggca 1050  
ctgagtacca agtgggtccc acctgcacca ctgtctatcc agctagcggg 1100

agcagcatcg actgggcgta tgacaacggc atcaaatttg cattcacatt 1150  
tgagttgaga gataccggga cctatggctt cctcctgcca gctaaccaga 1200  
tcatccccac tgcagaggag acgtggctgg ggctgaagac catcatggag 1250  
catgtgcggg acaacctcta ctaggcgatg gctctgctct gtctacattt 1300  
atttgtaccc acacgtgcac gcactgaggc cattgttaaa ggagctcttt 1350  
cctacctgtg tgagtcagag ccctctgggt ttgtggagca cacaggcctg 1400  
ccccctcca gccagctccc tggagtcgtg tgcctggcg gtgtccctgc 1450  
aagaactggg tctgccagcc tgctcaattt tggctcctgct gtttttgatg 1500  
agccttttgt ctgtttctcc ttccaccctg ctggctgggc ggctgcactc 1550  
agcatcacc cttcctgggt ggcatgtctc tctctacctc atttttagaa 1600  
ccaaagaaca tctgagatga ttctctaccc tcatccacat ctagccaagc 1650  
cagtgaacct gctctggtgg cactgtggga gacaccactt gtcttttaggt 1700  
gggtctcaaa gatgatgtag aatttccttt aatttctcgc agtcttctg 1750  
gaaaatattt tcctttgagc agcaaactct gtagggatat cagtgaaggt 1800  
ctctccctcc ctctctcct gttttttttt tttttgagac agagttttgc 1850  
tcttgttgcc caggctggag tgtgatggct cgatcttggc tcaccacaac 1900  
ctctgcctcc tgggttcaag caattctcct gcctcagcct cttgagtagc 1950  
ttggtttata ggcatgcc accatgcctg gctaattttg tgtttttagt 2000  
agagacaggg tttctccatg ttggtcaggc tggctctaaa ctcccaacct 2050  
caggatgatc gccctccttg gcctcccaga gtgctgggat tacagggtgtg 2100  
agccactgtg ccgggcccgt cccctccttt tttaggcctg aatacaaagt 2150  
agaagatcac tttccttcac tgtgctgaga atttctagat actacagttc 2200  
ttactcctct cttccctttg ttattcagtg tgaccaggat ggcgggaggg 2250  
gatctgtgtc actgtaggta ctgtgcccag gaaggctggg tgaagtgacc 2300  
atctaaattg caggatgggt aaattatccc catctgtcct aatgggctta 2350  
cctcctcttt gccttttgaa ctcaattcaa agatctaggc ctcatcttac 2400  
aggtcctaaa tcaactcatc ggctggata atctcactgc cctggcacat 2450  
tccatttgt gctgtggtgt atcctgtgtt tccttgcct ggtttgtgtg 2500

tgtgtgtgtg tgtgtgtgtg tgtgtgtgtt tgtgtgtgtg tgtctgtcta 2550  
 ttttgtatcc tggaccacaa gttcctaagt agagcaagaa ttcatcaacc 2600  
 agctgcctct tgtttcattt cacctcagca cgtaccatct gtccttttgt 2650  
 tgttgttgtt ttgtttttgt ttttttgctt ttaccaaaca tgtctgtaaa 2700  
 tcttaacctc ctgcctagga tttgtacagc atctggtgtg tgcttataag 2750  
 ccaataaata ttcaatgtga aaaaaaaaaa aaaaaa 2786

<210> 234  
 <211> 421  
 <212> PRT  
 <213> Homo sapiens

<400> 234

Met	Arg	Trp	Ile	Leu	Phe	Ile	Gly	Ala	Leu	Ile	Gly	Ser	Ser	Ile
1				5					10					15
Cys	Gly	Gln	Glu	Lys	Phe	Phe	Gly	Asp	Gln	Val	Leu	Arg	Ile	Asn
				20					25					30
Val	Arg	Asn	Gly	Asp	Glu	Ile	Ser	Lys	Leu	Ser	Gln	Leu	Val	Asn
				35					40					45
Ser	Asn	Asn	Leu	Lys	Leu	Asn	Phe	Trp	Lys	Ser	Pro	Ser	Ser	Phe
				50					55					60
Asn	Arg	Pro	Val	Asp	Val	Leu	Val	Pro	Ser	Val	Ser	Leu	Gln	Ala
				65					70					75
Phe	Lys	Ser	Phe	Leu	Arg	Ser	Gln	Gly	Leu	Glu	Tyr	Ala	Val	Thr
				80					85					90
Ile	Glu	Asp	Leu	Gln	Ala	Leu	Leu	Asp	Asn	Glu	Asp	Asp	Glu	Met
				95					100					105
Gln	His	Asn	Glu	Gly	Gln	Glu	Arg	Ser	Ser	Asn	Asn	Phe	Asn	Tyr
				110					115					120
Gly	Ala	Tyr	His	Ser	Leu	Glu	Ala	Ile	Tyr	His	Glu	Met	Asp	Asn
				125					130					135
Ile	Ala	Ala	Asp	Phe	Pro	Asp	Leu	Ala	Arg	Arg	Val	Lys	Ile	Gly
				140					145					150
His	Ser	Phe	Glu	Asn	Arg	Pro	Met	Tyr	Val	Leu	Lys	Phe	Ser	Thr
				155					160					165
Gly	Lys	Gly	Val	Arg	Arg	Pro	Ala	Val	Trp	Leu	Asn	Ala	Gly	Ile
				170					175					180
His	Ser	Arg	Glu	Trp	Ile	Ser	Gln	Ala	Thr	Ala	Ile	Trp	Thr	Ala
				185					190					195

Arg Lys Ile Val	Ser Asp Tyr Gln Arg Asp	Pro Ala Ile Thr Ser
200	205	210
Ile Leu Glu Lys	Met Asp Ile Phe Leu Leu Pro Val Ala Asn Pro	
215	220	225
Asp Gly Tyr Val	Tyr Thr Gln Thr Gln Asn Arg Leu Trp Arg Lys	
230	235	240
Thr Arg Ser Arg	Asn Pro Gly Ser Ser Cys Ile Gly Ala Asp Pro	
245	250	255
Asn Arg Asn Trp	Asn Ala Ser Phe Ala Gly Lys Gly Ala Ser Asp	
260	265	270
Asn Pro Cys Ser	Glu Val Tyr His Gly Pro His Ala Asn Ser Glu	
275	280	285
Val Glu Val Lys	Ser Val Val Asp Phe Ile Gln Lys His Gly Asn	
290	295	300
Phe Lys Gly Phe	Ile Asp Leu His Ser Tyr Ser Gln Leu Leu Met	
305	310	315
Tyr Pro Tyr Gly	Tyr Ser Val Lys Lys Ala Pro Asp Ala Glu Glu	
320	325	330
Leu Asp Lys Val	Ala Arg Leu Ala Ala Lys Ala Leu Ala Ser Val	
335	340	345
Ser Gly Thr Glu	Tyr Gln Val Gly Pro Thr Cys Thr Thr Val Tyr	
350	355	360
Pro Ala Ser Gly	Ser Ser Ile Asp Trp Ala Tyr Asp Asn Gly Ile	
365	370	375
Lys Phe Ala Phe	Thr Phe Glu Leu Arg Asp Thr Gly Thr Tyr Gly	
380	385	390
Phe Leu Leu Pro	Ala Asn Gln Ile Ile Pro Thr Ala Glu Glu Thr	
395	400	405
Trp Leu Gly Leu	Lys Thr Ile Met Glu His Val Arg Asp Asn Leu	
410	415	420

Tyr

<210> 235

<211> 1743

<212> DNA

<213> Homo sapiens

<400> 235

caaccatgca aggacagggc aggagaagag gaacctgcaa agacatattt 50

tgttccaaaa tggcatctta cctttatgga gtactctttg ctgttggcct 100



ctgtgctcca atctactgtg tgtccccggc caatgcccc agtgcatacc 150  
 cccgcccttc ctccacaaag agcacccttg cctcacaggt gtattccctc 200  
 aacaccgact ttgccttccg cctataccgc aggctggttt tggagacccc 250  
 gagtcagaac atcttcttct cccctgtgag tgtctccact tccctggcca 300  
 tgctctccct tggggcccac tcagtcacca agaccagat tctccagggc 350  
 ctgggcttca acctcacaca cacaccagag tctgccatcc accagggtt 400  
 ccagcacctg gttcactcac tgactgttcc cagcaaagac ctgacctga 450  
 agatgggaag tgccctcttc gtcaagaagg agctgcagct gcaggcaa 500  
 ttcttgggca atgtcaagag gctgtatgaa gcagaagtct tttctacaga 550  
 tttctccaac cctccattg cccaggcgag gatcaacagc catgtgaaaa 600  
 agaagacca aggaagggt gtagacataa tccaaggcct tgaccttctg 650  
 acggccatgg ttctggtgaa tcacattttc tttaaagcca agtgggagaa 700  
 gccctttcac cttgaatata caagaaagaa cttccattc ctgggtggcg 750  
 agcaggtcac tgtgcaagtc cccatgatgc accagaaaga gcagttcgct 800  
 tttggggtgg atacagagct gaactgcttt gtgctgcaga tggattacaa 850  
 gggagatgcc gtggccttct ttgtcctccc tagcaagggc aagatgaggc 900  
 aactggaaca ggccttgtca gccagaacac tgataaagtg gagccactca 950  
 ctccagaaaa ggtggataga ggtgttcac cccagatttt ccatttctgc 1000  
 ctctacaat ctggaaacca tcctcccgaa gatgggcac caaaatgcct 1050  
 ttgacaaaaa tgctgatttt tctggaattg caaagagaga ctccctgcag 1100  
 gtttctaaag caaccacaa ggctgtgctg gatgtcagtg aagagggcac 1150  
 tgaggccaca gcagctacca ccaccaagtt catagtccga tcgaaggatg 1200  
 gtccctctta cttcactgtc tccttcaata ggaccttct gatgatgatt 1250  
 acaaataaag ccacagacgg tattctcttt ctagggaag tggaatatcc 1300  
 cactaaatcc taggtgggaa atggcctgtt aactgatggc acattgctaa 1350  
 tgcacaagaa ataacaaacc acatccctct ttctgttctg aggggtgcatt 1400  
 tgacccagtg ggagctggat tcgctggcag ggatgccact tccaaggctc 1450  
 aatcaccaaa ccatcaacag ggacccagtg cacaagccaa caccattaa 1500

```

ccccagtcag tgcccttttc cacaaattct cccaggtaac tagcttcacg 1550
ggatgttgct gggttacat atttccattc cttggggctc ccaggaatgg 1600
aaatacgcca acccaggtta ggcacctcta ttgcagaatt acaataacac 1650
attcaataaa actaaaatat gaattcaaaa aaaaaaaaaa aaaaaaaaaa 1700
aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaa 1743

```

```

<210> 236
<211> 417
<212> PRT
<213> Homo sapiens

```

```

<400> 236

```

```

Met Ala Ser Tyr Leu Tyr Gly Val Leu Phe Ala Val Gly Leu Cys
 1             5             10             15
Ala Pro Ile Tyr Cys Val Ser Pro Ala Asn Ala Pro Ser Ala Tyr
             20             25             30
Pro Arg Pro Ser Ser Thr Lys Ser Thr Pro Ala Ser Gln Val Tyr
             35             40             45
Ser Leu Asn Thr Asp Phe Ala Phe Arg Leu Tyr Arg Arg Leu Val
             50             55             60
Leu Glu Thr Pro Ser Gln Asn Ile Phe Phe Ser Pro Val Ser Val
             65             70             75
Ser Thr Ser Leu Ala Met Leu Ser Leu Gly Ala His Ser Val Thr
             80             85             90
Lys Thr Gln Ile Leu Gln Gly Leu Gly Phe Asn Leu Thr His Thr
             95             100            105
Pro Glu Ser Ala Ile His Gln Gly Phe Gln His Leu Val His Ser
            110            115            120
Leu Thr Val Pro Ser Lys Asp Leu Thr Leu Lys Met Gly Ser Ala
            125            130            135
Leu Phe Val Lys Lys Glu Leu Gln Leu Gln Ala Asn Phe Leu Gly
            140            145            150
Asn Val Lys Arg Leu Tyr Glu Ala Glu Val Phe Ser Thr Asp Phe
            155            160            165
Ser Asn Pro Ser Ile Ala Gln Ala Arg Ile Asn Ser His Val Lys
            170            175            180
Lys Lys Thr Gln Gly Lys Val Val Asp Ile Ile Gln Gly Leu Asp
            185            190            195
Leu Leu Thr Ala Met Val Leu Val Asn His Ile Phe Phe Lys Ala
            200            205            210

```

Lys Trp Glu Lys	Pro Phe His Leu Glu	Tyr Thr Arg Lys Asn Phe	215	220	225
Pro Phe Leu Val	Gly Glu Gln Val Thr	Val Gln Val Pro Met Met	230	235	240
His Gln Lys Glu	Gln Phe Ala Phe Gly	Val Asp Thr Glu Leu Asn	245	250	255
Cys Phe Val Leu	Gln Met Asp Tyr Lys	Gly Asp Ala Val Ala Phe	260	265	270
Phe Val Leu Pro	Ser Lys Gly Lys Met	Arg Gln Leu Glu Gln Ala	275	280	285
Leu Ser Ala Arg	Thr Leu Ile Lys Trp	Ser His Ser Leu Gln Lys	290	295	300
Arg Trp Ile Glu	Val Phe Ile Pro Arg	Phe Ser Ile Ser Ala Ser	305	310	315
Tyr Asn Leu Glu	Thr Ile Leu Pro Lys	Met Gly Ile Gln Asn Ala	320	325	330
Phe Asp Lys Asn	Ala Asp Phe Ser Gly	Ile Ala Lys Arg Asp Ser	335	340	345
Leu Gln Val Ser	Lys Ala Thr His Lys	Ala Val Leu Asp Val Ser	350	355	360
Glu Glu Gly Thr	Glu Ala Thr Ala Ala	Thr Thr Thr Lys Phe Ile	365	370	375
Val Arg Ser Lys	Asp Gly Pro Ser Tyr	Phe Thr Val Ser Phe Asn	380	385	390
Arg Thr Phe Leu	Met Met Ile Thr Asn	Lys Ala Thr Asp Gly Ile	395	400	405
Leu Phe Leu Gly	Lys Val Glu Asn Pro	Thr Lys Ser	410	415	

<210> 237

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 237

caaccatgca aggacagggc agg 23

<210> 238

<211> 47

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 238

ctttgctgtt ggcctctgtg ctccaacca tgcaaggaca gggcagg 47

<210> 239

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 239

tgactcgggg tctccaaaac cagc 24

<210> 240

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 240

ggtataggcg gaaggcaaag tcgg 24

<210> 241

<211> 48

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 241

ggcatcttac ctttatggag tactctttgc tgttggcctc tgtgctcc 48

<210> 242

<211> 2436

<212> DNA

<213> Homo sapiens

<400> 242

ggctgaccgt gctacattgc ctggaggaag cctaaggaac ccaggcatcc 50

agctgccac gcctgagtcc aagattcttc ccaggaacac aaacgtagga 100

gaccacgct cctggaagca ccagccttta tctcttcacc ttcaagtccc 150

ctttctcaag aatcctctgt tctttgccct ctaaagtctt ggtacatcta 200

ggaccaggc atcttgcttt ccagccacaa agagacagat gaagatgcag 250

aaaggaaatg ttctccttat gtttgggtcta ctattgcatt tagaagctgc 300  
aacaaattcc aatgagacta gcacctctgc caaacttga tccagtgtga 350  
tctccagtgg agccagcaca gccaccaact ctgggtccag tgtgacctcc 400  
agtggggtca gcacagccac catctcaggg tccagcgtga cctccaatgg 450  
ggtcagcata gtcaccaact ctgagttcca tacaacctcc agtgggatca 500  
gcacagccac caactctgag ttcagcacag cgtccagtgg gatcagcata 550  
gccaccaact ctgagtccag cacaacctcc agtggggcca gcacagccac 600  
caactctgag tccagcacac cctccagtgg ggccagcaca gtcaccaact 650  
ctgggtccag tgtgacctcc agtggagcca gcaactgccac caactctgag 700  
tccagcacag tgtccagtag ggccagcact gccaccaact ctgagtctag 750  
cacactctcc agtggggcca gcacagccac caactctgac tccagcaca 800  
cctccagtgg ggctagcaca gccaccaact ctgagtccag cacaacctcc 850  
agtggggcca gcacagccac caactctgag tccagcacag tgtccagtag 900  
ggccagcact gccaccaact ctgagtccag cacaacctcc agtggggcca 950  
gcacagccac caactctgag tccagaacga cctccaatgg ggctggcaca 1000  
gccaccaact ctgagtccag cagacctcc agtggggcca gcacagccac 1050  
caactctgac tccagcacag tgtccagtgg ggccagcact gccaccaact 1100  
ctgagtccag cagacctcc agtggggcca gcacagccac caactctgag 1150  
tccagcacga cctccagtgg ggctagcaca gccaccaact ctgactccag 1200  
cacaacctcc agtggggccg gcacagccac caactctgag tccagcacag 1250  
tgtccagtgg gatcagcaca gtcaccaatt ctgagtccag cacacctcc 1300  
agtggggcca acacagccac caactctgag tccagtacga cctccagtgg 1350  
ggccaacaca gccaccaact ctgagtccag cacagtgtcc agtggggcca 1400  
gcaactgccac caactctgag tccagcaca cctccagtgg ggtcagcaca 1450  
gccaccaact ctgagtccag cacaacctcc agtggggcta gcacagccac 1500  
caactctgac tccagcaca cctccagtga ggccagcaca gccaccaact 1550  
ctgagtctag cacagtgtcc agtgggatca gcacagtcac caattctgag 1600  
tccagcaca cctccagtgg ggccaacaca gccaccaact ctgggtccag 1650  
tgtgacctct gcaggctctg gaacagcagc tctgactgga atgcacaca 1700

ctccccatag tgcattctact gcagtgagtg aggcaaagcc tgggtgggtcc 1750  
 ctgggtgccgt gggaaatctt cctcatcacc ctgggtctcgg ttgtggcggc 1800  
 cgtgggggctc tttgctgggc tcttcttctg tgtgagaaac agcctgtccc 1850  
 tgagaaacac cttaacaca gctgtctacc accctcatgg cctcaacat 1900  
 ggccttggtc caggccctgg agggaaatcat ggagcccccc acaggcccag 1950  
 gtggagtcct aactggttct ggaggagacc agtatcatcg atagccatgg 2000  
 agatgagcgg gaggaacagc gggccctgag cagccccgga agcaagtgcc 2050  
 gcattcttca ggaaggaaga gacctgggca cccaagacct ggtttccttt 2100  
 cattcatccc aggagacccc tcccagcttt gtttgagatc ctgaaaatct 2150  
 tgaagaaggt attcctcacc tttcttgctt ttaccagaca ctggaaagag 2200  
 aatactatct tgctcattta gctaagaaat aaatacatct catctaacac 2250  
 acacgacaaa gagaagctgt gcttgccccg ggggtgggtat ctagctctga 2300  
 gatgaactca gttataggag aaaacctcca tgctggactc catctggcat 2350  
 tcaaaatctc cacagtaaaa tccaaagacc tcaaaaaaaaa aaaaaaaaaa 2400  
 aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaa 2436

<210> 243  
 <211> 596  
 <212> PRT  
 <213> Homo sapiens

<400> 243  
 Met Lys Met Gln Lys Gly Asn Val Leu Leu Met Phe Gly Leu Leu  
 1 5 10 15  
 Leu His Leu Glu Ala Ala Thr Asn Ser Asn Glu Thr Ser Thr Ser  
 20 25 30  
 Ala Asn Thr Gly Ser Ser Val Ile Ser Ser Gly Ala Ser Thr Ala  
 35 40 45  
 Thr Asn Ser Gly Ser Ser Val Thr Ser Ser Gly Val Ser Thr Ala  
 50 55 60  
 Thr Ile Ser Gly Ser Ser Val Thr Ser Asn Gly Val Ser Ile Val  
 65 70 75  
 Thr Asn Ser Glu Phe His Thr Thr Ser Ser Gly Ile Ser Thr Ala  
 80 85 90  
 Thr Asn Ser Glu Phe Ser Thr Ala Ser Ser Gly Ile Ser Ile Ala  
 95 100 105

Thr	Asn	Ser	Glu	Ser	Ser	Thr	Thr	Ser	Ser	Gly	Ala	Ser	Thr	Ala	110	115	120
Thr	Asn	Ser	Glu	Ser	Ser	Thr	Pro	Ser	Ser	Gly	Ala	Ser	Thr	Val	125	130	135
Thr	Asn	Ser	Gly	Ser	Ser	Val	Thr	Ser	Ser	Gly	Ala	Ser	Thr	Ala	140	145	150
Thr	Asn	Ser	Glu	Ser	Ser	Thr	Val	Ser	Ser	Arg	Ala	Ser	Thr	Ala	155	160	165
Thr	Asn	Ser	Glu	Ser	Ser	Thr	Leu	Ser	Ser	Gly	Ala	Ser	Thr	Ala	170	175	180
Thr	Asn	Ser	Asp	Ser	Ser	Thr	Thr	Ser	Ser	Gly	Ala	Ser	Thr	Ala	185	190	195
Thr	Asn	Ser	Glu	Ser	Ser	Thr	Thr	Ser	Ser	Gly	Ala	Ser	Thr	Ala	200	205	210
Thr	Asn	Ser	Glu	Ser	Ser	Thr	Val	Ser	Ser	Arg	Ala	Ser	Thr	Ala	215	220	225
Thr	Asn	Ser	Glu	Ser	Ser	Thr	Thr	Ser	Ser	Gly	Ala	Ser	Thr	Ala	230	235	240
Thr	Asn	Ser	Glu	Ser	Arg	Thr	Thr	Ser	Asn	Gly	Ala	Gly	Thr	Ala	245	250	255
Thr	Asn	Ser	Glu	Ser	Ser	Thr	Thr	Ser	Ser	Gly	Ala	Ser	Thr	Ala	260	265	270
Thr	Asn	Ser	Asp	Ser	Ser	Thr	Val	Ser	Ser	Gly	Ala	Ser	Thr	Ala	275	280	285
Thr	Asn	Ser	Glu	Ser	Ser	Thr	Thr	Ser	Ser	Gly	Ala	Ser	Thr	Ala	290	295	300
Thr	Asn	Ser	Glu	Ser	Ser	Thr	Thr	Ser	Ser	Gly	Ala	Ser	Thr	Ala	305	310	315
Thr	Asn	Ser	Asp	Ser	Ser	Thr	Thr	Ser	Ser	Gly	Ala	Gly	Thr	Ala	320	325	330
Thr	Asn	Ser	Glu	Ser	Ser	Thr	Val	Ser	Ser	Gly	Ile	Ser	Thr	Val	335	340	345
Thr	Asn	Ser	Glu	Ser	Ser	Thr	Pro	Ser	Ser	Gly	Ala	Asn	Thr	Ala	350	355	360
Thr	Asn	Ser	Glu	Ser	Ser	Thr	Thr	Ser	Ser	Gly	Ala	Asn	Thr	Ala	365	370	375
Thr	Asn	Ser	Glu	Ser	Ser	Thr	Val	Ser	Ser	Gly	Ala	Ser	Thr	Ala	380	385	390

Thr Asn Ser Glu Ser Ser Thr Thr Ser Ser Gly Val Ser Thr Ala	395	400	405
Thr Asn Ser Glu Ser Ser Thr Thr Ser Ser Gly Ala Ser Thr Ala	410	415	420
Thr Asn Ser Asp Ser Ser Thr Thr Ser Ser Glu Ala Ser Thr Ala	425	430	435
Thr Asn Ser Glu Ser Ser Thr Val Ser Ser Gly Ile Ser Thr Val	440	445	450
Thr Asn Ser Glu Ser Ser Thr Thr Ser Ser Gly Ala Asn Thr Ala	455	460	465
Thr Asn Ser Gly Ser Ser Val Thr Ser Ala Gly Ser Gly Thr Ala	470	475	480
Ala Leu Thr Gly Met His Thr Thr Ser His Ser Ala Ser Thr Ala	485	490	495
Val Ser Glu Ala Lys Pro Gly Gly Ser Leu Val Pro Trp Glu Ile	500	505	510
Phe Leu Ile Thr Leu Val Ser Val Val Ala Ala Val Gly Leu Phe	515	520	525
Ala Gly Leu Phe Phe Cys Val Arg Asn Ser Leu Ser Leu Arg Asn	530	535	540
Thr Phe Asn Thr Ala Val Tyr His Pro His Gly Leu Asn His Gly	545	550	555
Leu Gly Pro Gly Pro Gly Gly Asn His Gly Ala Pro His Arg Pro	560	565	570
Arg Trp Ser Pro Asn Trp Phe Trp Arg Arg Pro Val Ser Ser Ile	575	580	585
Ala Met Glu Met Ser Gly Arg Asn Ser Gly Pro	590	595	

<210> 244

<211> 26

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 244

gaagcaccag cctttatctc ttcacc 26

<210> 245

<211> 24

<212> DNA



<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 245

gtcagagttg gtggctgtgc tagc 24

<210> 246

<211> 48

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 246

ggacccaggc atcttgcttt ccagccacaa agagacagat gaagatgc 48

<210> 247

<211> 957

<212> DNA

<213> Homo sapiens

<400> 247

gggagagagg ataaatagca gcgtggcttc cctggctcct ctctgcatcc 50  
ttcccgacct tcccagcaat atgcatcttg cacgtctggt cggctcctgc 100  
tccctccttc tgctactggg ggccctgtct ggatgggagg ccagcgatga 150  
ccccattgag aagggtcattg aagggatcaa ccgagggctg agcaatgcag 200  
agagagaggt gggcaaggcc ctggatggca tcaacagtgg aatcacgcat 250  
gccggaaggg aagtggagaa ggttttcaac ggacttagca acatggggag 300  
ccacaccggc aaggagttgg acaaaggcgt ccaggggctc aaccacggca 350  
tggaacaagg tgcccatgag atcaaccatg gtattggaca agcaggaaaag 400  
gaagcagaga agcttgcca tggggtaac aacgctgctg gacaggccgg 450  
gaaggaagca gacaaagcgg tccaagggtt ccacactggg gtccaccagg 500  
ctgggaagga agcagagaaa cttggccaag gggtaacca tgctgctgac 550  
caggctggaa aggaagtga gaagcttggc caaggtgccc accatgctgc 600  
tgccaggcc gggaaggagc tgcagaatgc tcataatggg gtcaaccaag 650  
ccagcaagga ggccaaccag ctgctgaatg gcaaccatca aagcggatct 700  
tccagccatc aaggaggggc cacaaccacg ccgttagcct ctggggcctc 750  
agtcaacacg cctttcatca accttccgc cctgtggagg agcgtcgcca 800

acatcatgcc ctaaactggc atccggcctt gctgggagaa taatgtcgcc 850  
 gttgtcacat cagctgacat gacctggagg gggtgggggt gggggacagg 900  
 tttctgaaat ccctgaaggg gggtgtactg ggatttgtga ataaacttga 950  
 tacacca 957

<210> 248

<211> 247

<212> PRT

<213> Homo sapiens

<400> 248

Met	His	Leu	Ala	Arg	Leu	Val	Gly	Ser	Cys	Ser	Leu	Leu	Leu	Leu	1	5	10	15
Leu	Gly	Ala	Leu	Ser	Gly	Trp	Ala	Ala	Ser	Asp	Asp	Pro	Ile	Glu	20	25	30	
Lys	Val	Ile	Glu	Gly	Ile	Asn	Arg	Gly	Leu	Ser	Asn	Ala	Glu	Arg	35	40	45	
Glu	Val	Gly	Lys	Ala	Leu	Asp	Gly	Ile	Asn	Ser	Gly	Ile	Thr	His	50	55	60	
Ala	Gly	Arg	Glu	Val	Glu	Lys	Val	Phe	Asn	Gly	Leu	Ser	Asn	Met	65	70	75	
Gly	Ser	His	Thr	Gly	Lys	Glu	Leu	Asp	Lys	Gly	Val	Gln	Gly	Leu	80	85	90	
Asn	His	Gly	Met	Asp	Lys	Val	Ala	His	Glu	Ile	Asn	His	Gly	Ile	95	100	105	
Gly	Gln	Ala	Gly	Lys	Glu	Ala	Glu	Lys	Leu	Gly	His	Gly	Val	Asn	110	115	120	
Asn	Ala	Ala	Gly	Gln	Ala	Gly	Lys	Glu	Ala	Asp	Lys	Ala	Val	Gln	125	130	135	
Gly	Phe	His	Thr	Gly	Val	His	Gln	Ala	Gly	Lys	Glu	Ala	Glu	Lys	140	145	150	
Leu	Gly	Gln	Gly	Val	Asn	His	Ala	Ala	Asp	Gln	Ala	Gly	Lys	Glu	155	160	165	
Val	Glu	Lys	Leu	Gly	Gln	Gly	Ala	His	His	Ala	Ala	Gly	Gln	Ala	170	175	180	
Gly	Lys	Glu	Leu	Gln	Asn	Ala	His	Asn	Gly	Val	Asn	Gln	Ala	Ser	185	190	195	
Lys	Glu	Ala	Asn	Gln	Leu	Leu	Asn	Gly	Asn	His	Gln	Ser	Gly	Ser	200	205	210	
Ser	Ser	His	Gln	Gly	Gly	Ala	Thr	Thr	Thr	Pro	Leu	Ala	Ser	Gly				

215	220	225
Ala Ser Val Asn Thr Pro Phe Ile Asn Leu Pro Ala Leu Trp Arg		
230	235	240

Ser Val Ala Asn Ile Met Pro  
245

<210> 249  
<211> 23  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 249  
caatatgcat cttgcacgtc tgg 23

<210> 250  
<211> 24  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 250  
aagcttctct gcttcctttc ctgc 24

<210> 251  
<211> 43  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 251  
tgacccatt gagaaggatc ttgaaggat caaccgagg ctg 43

<210> 252  
<211> 3781  
<212> DNA  
<213> Homo sapiens

<400> 252  
ctccgggtcc ccaggggctg cgccgggccg gcctggcaag ggggacgagt 50  
  
cagtggacac tccaggaaga gcgccccgc gggggcgat gaccgtgcgc 100  
  
tgaccctgac tcaactcagg tccggaggcg gggcccccg gggcgactcg 150  
  
ggggcgacc gcggggcgga gctgccgcc gtgagtccg ccgagccacc 200  
  
tgagcccag ccgcgggaca ccgtcgctcc tgctctccga atgctgcgca 250

ccgcgatggg cctgaggagc tggctcgccg ccccatgggg cgcgctgccg 300  
cctcggccac cgctgctgct gctcctgctg ctgctgctcc tgctgcagcc 350  
gcccgcctccg acctggggcg tcagcccccg gatcagcctg cctctgggct 400  
ctgaagagcg gccattcctc agattcgaag ctgaacacat ctccaactac 450  
acagcccttc tgctgagcag ggatggcagg accctgtacg tgggtgctcg 500  
agaggccctc tttgcaactca gtagcaacct cagcttcctg ccaggcgggg 550  
agtaccagga gctgcttttg ggtgcagacg cagagaagaa acagcagtgc 600  
agcttcaagg gcaaggacct acagcgcgac tgtcaaaact acatcaagat 650  
cctcctgccg ctacgcggca gtcacctgtt cacctgtggc acagcagcct 700  
tcagcccat gtgtacctac atcaacatgg agaacttcac cctggcaagg 750  
gacgagaagg ggaatgtcct cctggaagat ggcaagggcc gttgtccctt 800  
cgaccgaat ttcaagtcca ctgccctggg ggttgatggc gagctctaca 850  
ctggaacagt cagcagcttc caagggaatg acccggccat ctgcgagc 900  
caaagccttc gcccaccaa gaccgagagc tccctcaact ggctgcaaga 950  
cccagctttt gtggcctcag cctacattcc tgagagcctg ggcagcttgc 1000  
aaggcgatga tgacaagatc tactttttct tcagcgagac tggccaggaa 1050  
tttgagttct ttgagaacac cattgtgtcc cgcattgccg gcatctgcaa 1100  
gggcgatgag ggtggagagc ggtgctaca gcagcgctgg acctccttc 1150  
tcaaggccca gctgctgtgc tcacggcccg acgatggctt ccccttcaac 1200  
gtgctgcagg atgtcttcac gctgagcccc agccccagg actggcgtga 1250  
cacccttttc tatgggtct tcaactccca gtggcacagg ggaactacag 1300  
aaggctctgc cgtctgtgtc ttcacaatga aggatgtgca gagagtcttc 1350  
agcggcctct acaaggaggt gaaccgtgag acacagcagt ggtacaccgt 1400  
gaccacccg gtgcccacac cccggcctgg agcgtgcac accaacagtg 1450  
cccgggaaag gaagatcaac tcatccctgc agctcccaga ccgctgctg 1500  
aacttctca aggaccactt cctgatggac gggcaggctc gaagccgcat 1550  
gctgctgctg cagccccagg ctgcctacca gcgctggct gtacaccgcg 1600  
tccctggcct gcaccacacc tacgatgtcc tcttctggg cactggtgac 1650  
ggccggctcc acaaggcagt gagcgtgggc cccgggtgc acatcattga 1700

ggagctgcag atcttctcat cgggacagcc cgtgcagaat ctgctcctgg 1750  
acacccacag ggggctgctg tatgcggcct cacactcggg cgtagtccag 1800  
gtgcccattg ccaactgcag cctgtaccgg agctgtgggg actgcctcct 1850  
cgcccgggac ccctactgtg cttggagcgg ctccagctgc aagcacgtca 1900  
gcctctacca gcctcagctg gccaccaggc cgtggatcca ggacatcgag 1950  
ggagccagcg ccaaggacct ttgcagcgcg tcttcgggtt tgtccccgtc 2000  
ttttgtacca acaggggaga agccatgtga gcaagtccag ttccagccca 2050  
acacagtga cactttggcc tgcccgtccc tctccaacct ggcgacccga 2100  
ctctggctac gcaacggggc ccccgtaaat gcctcggcct cctgccacgt 2150  
gctaccact ggggacctgc tgctggtggg caccacaacag ctgggggagt 2200  
tccagtgtg gtcactagag gagggcttcc agcagctggt agccagctac 2250  
tgcccagagg tgggtggagga cggggtggca gaccaaacag atgagggtgg 2300  
cagtgtaccc gtcattatca gcacatcgcg tgtgagtga ccagctggtg 2350  
gcaaggccag ctggggtgca gacaggtcct actggaagga gttcctggtg 2400  
atgtgcacgc tttttgtgct ggccgtgctg ctcccagttt tattcttgc 2450  
ctaccggcac cggaacagca tgaaagtctt cctgaagcag ggggaatgtg 2500  
ccagcgtgca cccaagacc tgccctgtgg tgetgcccc tgagaccgc 2550  
ccactcaacg gcctagggcc ccctagcacc ccgctcgatc accgagggtg 2600  
ccagtccctg tcagacagcc ccccgggggc ccgagtcttc actgagtcag 2650  
agaagaggcc actcagcatc caagacagct tcgtggaggt atccccagt 2700  
tgccccggc cccgggtccg ccttggtcgc gagatccgtg actctgtggt 2750  
gtgagagctg acttccagag gacgctgccc tggtttcagg ggctgtgaat 2800  
gctcgagag ggtcaactgg acctcccctc cgctctgctc ttcgtggaac 2850  
acgaccgtgg tgcccggccc ttgggagcct tggagccagc tggcctgctg 2900  
ctctccagtc aagtagcgaa gctcctacca ccagacacc caaacagccg 2950  
tgccccaga ggtcctggcc aaatatgggg gcctgcctag gttggtggaa 3000  
cagtgtcct tatgtaaact gagccctttg tttaaaaaac aattccaaat 3050  
gtgaaactag aatgagaggg aagagatagc atggcatgca gcacacacgg 3100

ctgctccagt tcattggcctc ccaggggtgc tggggatgca tccaaagtgg 3150  
 ttgtctgaga cagagttgga aaccctcacc aactggcctc ttcaccttcc 3200  
 acattatccc gctgccaccg gctgccctgt ctactgcag attcaggacc 3250  
 agcttgggct gcgtgcgttc tgccttgcca gtcagccgag gatgtagttg 3300  
 ttgctgccgt cgtcccacca cctcaggac cagagggcta gggtggcact 3350  
 gcggccctca ccaggtcctg ggctcggacc caactcctgg acctttccag 3400  
 cctgtatcag gctgtggcca cacgagagga cagcgcgagc tcaggagaga 3450  
 tttcgtgaca atgtacgcct ttccctcaga attcagggaa gagactgtcg 3500  
 cctgccttcc tccgttggtg cgtgagaacc cgtgtgcccc ttcccacat 3550  
 atccaccctc gctccatctt tgaactcaaa cacgaggaac taactgcacc 3600  
 ctggtcctct cccagtccc cagttcacc tccatccctc accttccctc 3650  
 actctaaggg atatcaacac tgcccagcac aggggccctg aatttatgtg 3700  
 gtttttatac attttttaat aagatgcact ttatgtcatt ttttaataaa 3750  
 gtctgaagaa ttactgttta aaaaaaaaaa a 3781

<210> 253

<211> 837

<212> PRT

<213> Homo sapiens

<400> 253

Met	Leu	Arg	Thr	Ala	Met	Gly	Leu	Arg	Ser	Trp	Leu	Ala	Ala	Pro
1				5					10					15
Trp	Gly	Ala	Leu	Pro	Pro	Arg	Pro	Pro	Leu	Leu	Leu	Leu	Leu	Leu
				20					25					30
Leu	Leu	Leu	Leu	Leu	Gln	Pro	Pro	Pro	Pro	Thr	Trp	Ala	Leu	Ser
				35					40					45
Pro	Arg	Ile	Ser	Leu	Pro	Leu	Gly	Ser	Glu	Glu	Arg	Pro	Phe	Leu
				50					55					60
Arg	Phe	Glu	Ala	Glu	His	Ile	Ser	Asn	Tyr	Thr	Ala	Leu	Leu	Leu
				65					70					75
Ser	Arg	Asp	Gly	Arg	Thr	Leu	Tyr	Val	Gly	Ala	Arg	Glu	Ala	Leu
				80					85					90
Phe	Ala	Leu	Ser	Ser	Asn	Leu	Ser	Phe	Leu	Pro	Gly	Gly	Glu	Tyr
				95					100					105
Gln	Glu	Leu	Leu	Trp	Gly	Ala	Asp	Ala	Glu	Lys	Lys	Gln	Gln	Cys
				110					115					120

Ser	Phe	Lys	Gly	Lys	Asp	Pro	Gln	Arg	Asp	Cys	Gln	Asn	Tyr	Ile	125	130	135
Lys	Ile	Leu	Leu	Pro	Leu	Ser	Gly	Ser	His	Leu	Phe	Thr	Cys	Gly	140	145	150
Thr	Ala	Ala	Phe	Ser	Pro	Met	Cys	Thr	Tyr	Ile	Asn	Met	Glu	Asn	155	160	165
Phe	Thr	Leu	Ala	Arg	Asp	Glu	Lys	Gly	Asn	Val	Leu	Leu	Glu	Asp	170	175	180
Gly	Lys	Gly	Arg	Cys	Pro	Phe	Asp	Pro	Asn	Phe	Lys	Ser	Thr	Ala	185	190	195
Leu	Val	Val	Asp	Gly	Glu	Leu	Tyr	Thr	Gly	Thr	Val	Ser	Ser	Phe	200	205	210
Gln	Gly	Asn	Asp	Pro	Ala	Ile	Ser	Arg	Ser	Gln	Ser	Leu	Arg	Pro	215	220	225
Thr	Lys	Thr	Glu	Ser	Ser	Leu	Asn	Trp	Leu	Gln	Asp	Pro	Ala	Phe	230	235	240
Val	Ala	Ser	Ala	Tyr	Ile	Pro	Glu	Ser	Leu	Gly	Ser	Leu	Gln	Gly	245	250	255
Asp	Asp	Asp	Lys	Ile	Tyr	Phe	Phe	Phe	Ser	Glu	Thr	Gly	Gln	Glu	260	265	270
Phe	Glu	Phe	Phe	Glu	Asn	Thr	Ile	Val	Ser	Arg	Ile	Ala	Arg	Ile	275	280	285
Cys	Lys	Gly	Asp	Glu	Gly	Gly	Glu	Arg	Val	Leu	Gln	Gln	Arg	Trp	290	295	300
Thr	Ser	Phe	Leu	Lys	Ala	Gln	Leu	Leu	Cys	Ser	Arg	Pro	Asp	Asp	305	310	315
Gly	Phe	Pro	Phe	Asn	Val	Leu	Gln	Asp	Val	Phe	Thr	Leu	Ser	Pro	320	325	330
Ser	Pro	Gln	Asp	Trp	Arg	Asp	Thr	Leu	Phe	Tyr	Gly	Val	Phe	Thr	335	340	345
Ser	Gln	Trp	His	Arg	Gly	Thr	Thr	Glu	Gly	Ser	Ala	Val	Cys	Val	350	355	360
Phe	Thr	Met	Lys	Asp	Val	Gln	Arg	Val	Phe	Ser	Gly	Leu	Tyr	Lys	365	370	375
Glu	Val	Asn	Arg	Glu	Thr	Gln	Gln	Trp	Tyr	Thr	Val	Thr	His	Pro	380	385	390
Val	Pro	Thr	Pro	Arg	Pro	Gly	Ala	Cys	Ile	Thr	Asn	Ser	Ala	Arg	395	400	405

Glu Arg Lys Ile Asn Ser Ser Leu Gln Leu Pro Asp Arg Val Leu	410	415	420
Asn Phe Leu Lys Asp His Phe Leu Met Asp Gly Gln Val Arg Ser	425	430	435
Arg Met Leu Leu Leu Gln Pro Gln Ala Arg Tyr Gln Arg Val Ala	440	445	450
Val His Arg Val Pro Gly Leu His His Thr Tyr Asp Val Leu Phe	455	460	465
Leu Gly Thr Gly Asp Gly Arg Leu His Lys Ala Val Ser Val Gly	470	475	480
Pro Arg Val His Ile Ile Glu Glu Leu Gln Ile Phe Ser Ser Gly	485	490	495
Gln Pro Val Gln Asn Leu Leu Leu Asp Thr His Arg Gly Leu Leu	500	505	510
Tyr Ala Ala Ser His Ser Gly Val Val Gln Val Pro Met Ala Asn	515	520	525
Cys Ser Leu Tyr Arg Ser Cys Gly Asp Cys Leu Leu Ala Arg Asp	530	535	540
Pro Tyr Cys Ala Trp Ser Gly Ser Ser Cys Lys His Val Ser Leu	545	550	555
Tyr Gln Pro Gln Leu Ala Thr Arg Pro Trp Ile Gln Asp Ile Glu	560	565	570
Gly Ala Ser Ala Lys Asp Leu Cys Ser Ala Ser Ser Val Val Ser	575	580	585
Pro Ser Phe Val Pro Thr Gly Glu Lys Pro Cys Glu Gln Val Gln	590	595	600
Phe Gln Pro Asn Thr Val Asn Thr Leu Ala Cys Pro Leu Leu Ser	605	610	615
Asn Leu Ala Thr Arg Leu Trp Leu Arg Asn Gly Ala Pro Val Asn	620	625	630
Ala Ser Ala Ser Cys His Val Leu Pro Thr Gly Asp Leu Leu Leu	635	640	645
Val Gly Thr Gln Gln Leu Gly Glu Phe Gln Cys Trp Ser Leu Glu	650	655	660
Glu Gly Phe Gln Gln Leu Val Ala Ser Tyr Cys Pro Glu Val Val	665	670	675
Glu Asp Gly Val Ala Asp Gln Thr Asp Glu Gly Gly Ser Val Pro	680	685	690



Val	Ile	Ile	Ser	Thr	Ser	Arg	Val	Ser	Ala	Pro	Ala	Gly	Gly	Lys	
			695						700					705	
Ala	Ser	Trp	Gly	Ala	Asp	Arg	Ser	Tyr	Trp	Lys	Glu	Phe	Leu	Val	
			710						715					720	
Met	Cys	Thr	Leu	Phe	Val	Leu	Ala	Val	Leu	Leu	Pro	Val	Leu	Phe	
			725						730					735	
Leu	Leu	Tyr	Arg	His	Arg	Asn	Ser	Met	Lys	Val	Phe	Leu	Lys	Gln	
			740						745					750	
Gly	Glu	Cys	Ala	Ser	Val	His	Pro	Lys	Thr	Cys	Pro	Val	Val	Leu	
			755						760					765	
Pro	Pro	Glu	Thr	Arg	Pro	Leu	Asn	Gly	Leu	Gly	Pro	Pro	Ser	Thr	
			770						775					780	
Pro	Leu	Asp	His	Arg	Gly	Tyr	Gln	Ser	Leu	Ser	Asp	Ser	Pro	Pro	
			785						790					795	
Gly	Ala	Arg	Val	Phe	Thr	Glu	Ser	Glu	Lys	Arg	Pro	Leu	Ser	Ile	
			800						805					810	
Gln	Asp	Ser	Phe	Val	Glu	Val	Ser	Pro	Val	Cys	Pro	Arg	Pro	Arg	
			815						820					825	
Val	Arg	Leu	Gly	Ser	Glu	Ile	Arg	Asp	Ser	Val	Val				
			830						835						

<210> 254

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 254

agcccgtagca gaatctgctc ctgg 24

<210> 255

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 255

tgaagccagg gcagcgtcct ctgg 24

<210> 256

<211> 18

<212> DNA

<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 256  
gtacaggctg cagttggc 18

<210> 257  
<211> 41  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 257  
agaagccatg tgagcaagtc cagttccagc ccaacacagt g 41

<210> 258  
<211> 45  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 258  
gagctgcaga tcttctcatc gggacagccc gtgcagaatc tgctc 45

<210> 259  
<211> 4563  
<212> DNA  
<213> Homo sapiens

<220>  
<221> unsure  
<222> 3635  
<223> unknown base

<400> 259  
ctaagccgga ggatgtgcag ctgcggcggc ggcgccggct acgaagagga 50  
cggggacagg cgccgtgcga accgagccca gccagccgga ggacgcgggc 100  
agggcgggac gggagcccgg actcgtctgc cgccgccgtc gtcgccgtcg 150  
tgccggcccc gcgtccccgc gcgcgagcgg gaggagccgc cgccacctcg 200  
cgcccagagcc gccgctagcg cgcgccgggc atggtcccct cttaaaggcg 250  
caggccgcgg cggcgggggc ggggtgtcgg aacaaagcgc cggcgcgggg 300  
cctgcgggcg gctcgggggc cgcgatgggc gcggcgggcc cgcggcggcg 350  
gcggcgctgc ccgggccggg cctcgcgggc ctagggcggg ctggcctccg 400  
tgggcggggg cagcgggctg agggcgcgcg gagcctgcgg cggcgggcggc 450

ggcggcggcg gcggcccggc gggcggagcg gcgcgggcat ggccgcgcgc 500  
ggccggcgcg cctggctcag cgtgctgctc gggctcgtcc tgggcttcgt 550  
gctggcctcg cggetcgtec tgccccgggc ttccgagctg aagcgagcgg 600  
gcccacggcg ccgcgccagc cccgagggct gccgggtccg gcaggcggcg 650  
gcttcccagg ccggcggggc gcgcggcgat gcgcgcgggg cgcagctctg 700  
gccgcccggc tcggaccag atggcggccc gcgcgacagg aactttctct 750  
tcgtgggagt catgaccgcc cagaaatacc tgcagactcg ggccgtggcc 800  
gcctacagaa catggtccaa gacaattcct gggaaagttc agttcttctc 850  
aagtgagggg tctgacacat ctgtaccaat tccagtagtg ccaactacggg 900  
gtgtggacga ctctacccg cccagaaga agtccttcat gatgctcaag 950  
tacatgcacg accactactt ggacaagtat gaatggttta tgagagcaga 1000  
tgatgacgtg tacatcaaag gagaccgtct ggagaacttc ctgaggagtt 1050  
tgaacagcag cgagcccctc tttcttgggc agacaggcct gggcaccacg 1100  
gaagaaatgg gaaaactggc cctggagcct ggtgagaact tctgcatggg 1150  
ggggcctggc gtgatcatga gccgggaggt gcttcggaga atggtgccgc 1200  
acattggcaa gtgtctccgg gagatgtaca ccacccatga ggacgtggag 1250  
gtgggaaggt gtgtccggag gtttgcaggg gtgcagtgtg tctggtctta 1300  
tgagatgcgg cagctttttt atgagaatta cgagcagaac aaaaaggggt 1350  
acattagaga tctccataac agtaaaattc accaagctat cacattacac 1400  
cccaacaaaa acccacccta ccagtacagg ctccacagct acatgctgag 1450  
ccgcaagata tccgagctcc gccatcgac aatacagctg caccgcgaaa 1500  
ttgtcctgat gagcaaatac agcaacacag aaattcataa agaggacctc 1550  
cagctgggaa tccctccctc cttcatgagg ttccagcccc gccagcgaga 1600  
ggagattctg gaatgggagt ttctgactgg aaaatacttg tattcggcag 1650  
ttgacggcca gcccctcga agaggaatgg actccgcca gagggagacc 1700  
ttggacgaca ttgtcatgca ggtcatggag atgatcaatg ccaacgcaa 1750  
gaccagaggg cgcattctg acttcaaaga gatccagtac ggctaccgcc 1800  
gggtgaacc catgtatgg gctgagtaca tcctggacct gctgcttctg 1850

tacaaaaagc acaaagggaa gaaaatgacg gtccctgtga ggaggcacgc 1900  
gtatttacag cagactttca gcaaaatcca gtttgtggag catgaggagc 1950  
tggatgcaca agagttggcc aagagaatca atcaggaatc tggatccttg 2000  
tcctttctct caaactccct gaagaagctc gtcccctttc agctccctgg 2050  
gtcgaagagt gagcaciaag aacccaaaga taaaaagata aacatactga 2100  
ttcctttgtc tgggcgtttc gacatgtttg tgagatttat gggaaacttt 2150  
gagaagacgt gtcttatccc caatcagaac gtcaagctcg tggttctgct 2200  
tttcaattct gactccaacc ctgacaaggc caacaagtt gaactgatga 2250  
gagattaccg cattaagtac cctaaagccg acatgcagat tttgcctgtg 2300  
tctggagagt tttcaagagc cctggccctg gaagtaggat cctcccagtt 2350  
taacaatgaa tctttgctct tcttctgcga cgtcgacctc gtgtttacta 2400  
cagaattcct tcagcgatgt cgagcaaata cagttctggg ccaacaaata 2450  
tattttccaa tcactttcag ccagtatgac ccaaagattg tttatagtgg 2500  
gaaagttccc agtgacaacc attttgcctt tactcagaaa actggcttct 2550  
ggagaaaacta tgggtttggc atcacgtgta tttataaggg agatcttgtc 2600  
cgagtgggtg gctttgatgt ttccatccaa ggctgggggc tggaggatgt 2650  
ggaccttttc aacaaggttg tccaggcagg tttgaagacg tttaggagcc 2700  
aggaagtagg agtagtccac gtccaccatc ctgtcttttg tgatcccaat 2750  
cttgacccca aacagtacaa aatgtgcttg gggcccaaag catcgacctc 2800  
tgggtccacc cagcagctgg ctgagatgtg gctggaaaaa aatgatccaa 2850  
gttacagtaa aagcagcaat aataatggct cagtgaggac agcctaattg 2900  
ccagctttgc tggaaaagac gtttttaatt atctaattta tttttcaaaa 2950  
attttttgta tgatcagttt ttgaagtccg tatacaagga tatattttac 3000  
aagtggtttt cttacatagg actcctttaa gattgagctt tctgaacaag 3050  
aaggatgatca gtgtttgcct ttgaacacat cttcttgctg aacattatgt 3100  
agcagacctg cttaactttg acttgaaatg tacctgatga acaaaacttt 3150  
tttaaaaaaa tgttttcttt tgagaccctt tgctccagtc ctatggcaga 3200  
aaacgtgaac attcctgcaa agtattattg taacaaaaca ctgtaactct 3250  
ggtaaattgt ctgttgatg tgtaaacatt ccacagattc taccttttgt 3300

gttttgtttt ttttttttac aattgtttta aagccatttc atgttccagt 3350  
 tgtaagataa ggaaatgtga taatagctgt ttcattcattg tcttcaggag 3400  
 agctttccag agttgatcat ttcctctcat ggtactctgc tcagcatggc 3450  
 cacgtagggt ttttgtttgt tttgttttgt tctttttttg agacggagtc 3500  
 tcactctgtt acccaggctg gaatgcagtg gcgcaatctt ggctcacttt 3550  
 aacctccact tccctgggtc aagcaattcc cctgcctttg cctcccagag 3600  
 agctgggatt acaggcacac accaccacgc ccagntagtt tttttgtatt 3650  
 tttagtagag acgggggttc accatgcaag cccagctggc cacgtagggt 3700  
 ttaaagcaag gggcgtgaag aaggcacagt gaggtatgtg gctgttctcg 3750  
 tggtagttca ttcggcctaa atagacctgg cattaaattt caagaaggat 3800  
 ttggcatttt ctcttcttga cccttctctt taaagggtaa aatattaatg 3850  
 tttagaatga caaagatgaa ttattacaat aaatctgatg tacacagact 3900  
 gaaacataca cacatacacc ctaatcaaaa cgttggggaa aaatgtattt 3950  
 ggttttgttc ctttcatcct gtctgtgtta tgtgggtgga gatggttttc 4000  
 attctttcat tactgttttg ttttatcctt tgtatctgaa ataccttta 4050  
 tttatttaat atctgttggt cagagctctg ccatttcttg agtacctgtt 4100  
 agttagtatt atttatgtgt atcgggagtg tgtttagtct gttttatttg 4150  
 cagtaaaccg atctccaaag atttcctttt ggaaacgctt tttcccctcc 4200  
 ttaattttta tattccttac tgttttacta aatattaagt gttctttgac 4250  
 aattttggtg ctcatgtgtt ttggggacaa aagtgaaatg aatctgtcat 4300  
 tataccagaa agttaaattc tcagatcaaa tgtgccttaa taaatttggt 4350  
 ttcattttaga tttcaaacag tgatagactt gccattttta tacacgtcat 4400  
 tggagggctg cgtatttgta aatagcctga tgctcatttg gaaaaataaa 4450  
 ccagtgaaca atatttttct attgtacttt tcgaaccatt ttgtctcatt 4500  
 attcctgttt tagctgaaga attgtattac atttgagag taaaaaactt 4550  
 aaacacgaaa aaa 4563

<210> 260  
 <211> 802  
 <212> PRT  
 <213> Homo sapiens

<400> 260

Met	Ala	Ala	Arg	Gly	Arg	Arg	Ala	Trp	Leu	Ser	Val	Leu	Leu	Gly	
1				5					10					15	
Leu	Val	Leu	Gly	Phe	Val	Leu	Ala	Ser	Arg	Leu	Val	Leu	Pro	Arg	
				20					25					30	
Ala	Ser	Glu	Leu	Lys	Arg	Ala	Gly	Pro	Arg	Arg	Arg	Ala	Ser	Pro	
				35					40					45	
Glu	Gly	Cys	Arg	Ser	Gly	Gln	Ala	Ala	Ala	Ser	Gln	Ala	Gly	Gly	
				50					55					60	
Ala	Arg	Gly	Asp	Ala	Arg	Gly	Ala	Gln	Leu	Trp	Pro	Pro	Gly	Ser	
				65					70					75	
Asp	Pro	Asp	Gly	Gly	Pro	Arg	Asp	Arg	Asn	Phe	Leu	Phe	Val	Gly	
				80					85					90	
Val	Met	Thr	Ala	Gln	Lys	Tyr	Leu	Gln	Thr	Arg	Ala	Val	Ala	Ala	
				95					100					105	
Tyr	Arg	Thr	Trp	Ser	Lys	Thr	Ile	Pro	Gly	Lys	Val	Gln	Phe	Phe	
				110					115					120	
Ser	Ser	Glu	Gly	Ser	Asp	Thr	Ser	Val	Pro	Ile	Pro	Val	Val	Pro	
				125					130					135	
Leu	Arg	Gly	Val	Asp	Asp	Ser	Tyr	Pro	Pro	Gln	Lys	Lys	Ser	Phe	
				140					145					150	
Met	Met	Leu	Lys	Tyr	Met	His	Asp	His	Tyr	Leu	Asp	Lys	Tyr	Glu	
				155					160					165	
Trp	Phe	Met	Arg	Ala	Asp	Asp	Asp	Val	Tyr	Ile	Lys	Gly	Asp	Arg	
				170					175					180	
Leu	Glu	Asn	Phe	Leu	Arg	Ser	Leu	Asn	Ser	Ser	Glu	Pro	Leu	Phe	
				185					190					195	
Leu	Gly	Gln	Thr	Gly	Leu	Gly	Thr	Thr	Glu	Glu	Met	Gly	Lys	Leu	
				200					205					210	
Ala	Leu	Glu	Pro	Gly	Glu	Asn	Phe	Cys	Met	Gly	Gly	Pro	Gly	Val	
				215					220					225	
Ile	Met	Ser	Arg	Glu	Val	Leu	Arg	Arg	Met	Val	Pro	His	Ile	Gly	
				230					235					240	
Lys	Cys	Leu	Arg	Glu	Met	Tyr	Thr	Thr	His	Glu	Asp	Val	Glu	Val	
				245					250					255	
Gly	Arg	Cys	Val	Arg	Arg	Phe	Ala	Gly	Val	Gln	Cys	Val	Trp	Ser	
				260					265					270	
Tyr	Glu	Met	Arg	Gln	Leu	Phe	Tyr	Glu	Asn	Tyr	Glu	Gln	Asn	Lys	

275										280					285				
Lys	Gly	Tyr	Ile	Arg	Asp	Leu	His	Asn	Ser	Lys	Ile	His	Gln	Ala					
				290					295					300					
Ile	Thr	Leu	His	Pro	Asn	Lys	Asn	Pro	Pro	Tyr	Gln	Tyr	Arg	Leu					
				305					310					315					
His	Ser	Tyr	Met	Leu	Ser	Arg	Lys	Ile	Ser	Glu	Leu	Arg	His	Arg					
				320					325					330					
Thr	Ile	Gln	Leu	His	Arg	Glu	Ile	Val	Leu	Met	Ser	Lys	Tyr	Ser					
				335					340					345					
Asn	Thr	Glu	Ile	His	Lys	Glu	Asp	Leu	Gln	Leu	Gly	Ile	Pro	Pro					
				350					355					360					
Ser	Phe	Met	Arg	Phe	Gln	Pro	Arg	Gln	Arg	Glu	Glu	Ile	Leu	Glu					
				365					370					375					
Trp	Glu	Phe	Leu	Thr	Gly	Lys	Tyr	Leu	Tyr	Ser	Ala	Val	Asp	Gly					
				380					385					390					
Gln	Pro	Pro	Arg	Arg	Gly	Met	Asp	Ser	Ala	Gln	Arg	Glu	Ala	Leu					
				395					400					405					
Asp	Asp	Ile	Val	Met	Gln	Val	Met	Glu	Met	Ile	Asn	Ala	Asn	Ala					
				410					415					420					
Lys	Thr	Arg	Gly	Arg	Ile	Ile	Asp	Phe	Lys	Glu	Ile	Gln	Tyr	Gly					
				425					430					435					
Tyr	Arg	Arg	Val	Asn	Pro	Met	Tyr	Gly	Ala	Glu	Tyr	Ile	Leu	Asp					
				440					445					450					
Leu	Leu	Leu	Leu	Tyr	Lys	Lys	His	Lys	Gly	Lys	Lys	Met	Thr	Val					
				455					460					465					
Pro	Val	Arg	Arg	His	Ala	Tyr	Leu	Gln	Gln	Thr	Phe	Ser	Lys	Ile					
				470					475					480					
Gln	Phe	Val	Glu	His	Glu	Glu	Leu	Asp	Ala	Gln	Glu	Leu	Ala	Lys					
				485					490					495					
Arg	Ile	Asn	Gln	Glu	Ser	Gly	Ser	Leu	Ser	Phe	Leu	Ser	Asn	Ser					
				500					505					510					
Leu	Lys	Lys	Leu	Val	Pro	Phe	Gln	Leu	Pro	Gly	Ser	Lys	Ser	Glu					
				515					520					525					
His	Lys	Glu	Pro	Lys	Asp	Lys	Lys	Ile	Asn	Ile	Leu	Ile	Pro	Leu					
				530					535					540					
Ser	Gly	Arg	Phe	Asp	Met	Phe	Val	Arg	Phe	Met	Gly	Asn	Phe	Glu					
				545					550					555					
Lys	Thr	Cys	Leu	Ile	Pro	Asn	Gln	Asn	Val	Lys	Leu	Val	Val	Leu					

560										565					570				
Leu	Phe	Asn	Ser	Asp	Ser	Asn	Pro	Asp	Lys	Ala	Lys	Gln	Val	Glu					
				575					580					585					
Leu	Met	Arg	Asp	Tyr	Arg	Ile	Lys	Tyr	Pro	Lys	Ala	Asp	Met	Gln					
				590					595					600					
Ile	Leu	Pro	Val	Ser	Gly	Glu	Phe	Ser	Arg	Ala	Leu	Ala	Leu	Glu					
				605					610					615					
Val	Gly	Ser	Ser	Gln	Phe	Asn	Asn	Glu	Ser	Leu	Leu	Phe	Phe	Cys					
				620					625					630					
Asp	Val	Asp	Leu	Val	Phe	Thr	Thr	Glu	Phe	Leu	Gln	Arg	Cys	Arg					
				635					640					645					
Ala	Asn	Thr	Val	Leu	Gly	Gln	Gln	Ile	Tyr	Phe	Pro	Ile	Ile	Phe					
				650					655					660					
Ser	Gln	Tyr	Asp	Pro	Lys	Ile	Val	Tyr	Ser	Gly	Lys	Val	Pro	Ser					
				665					670					675					
Asp	Asn	His	Phe	Ala	Phe	Thr	Gln	Lys	Thr	Gly	Phe	Trp	Arg	Asn					
				680					685					690					
Tyr	Gly	Phe	Gly	Ile	Thr	Cys	Ile	Tyr	Lys	Gly	Asp	Leu	Val	Arg					
				695					700					705					
Val	Gly	Gly	Phe	Asp	Val	Ser	Ile	Gln	Gly	Trp	Gly	Leu	Glu	Asp					
				710					715					720					
Val	Asp	Leu	Phe	Asn	Lys	Val	Val	Gln	Ala	Gly	Leu	Lys	Thr	Phe					
				725					730					735					
Arg	Ser	Gln	Glu	Val	Gly	Val	Val	His	Val	His	His	Pro	Val	Phe					
				740					745					750					
Cys	Asp	Pro	Asn	Leu	Asp	Pro	Lys	Gln	Tyr	Lys	Met	Cys	Leu	Gly					
				755					760					765					
Ser	Lys	Ala	Ser	Thr	Tyr	Gly	Ser	Thr	Gln	Gln	Leu	Ala	Glu	Met					
				770					775					780					
Trp	Leu	Glu	Lys	Asn	Asp	Pro	Ser	Tyr	Ser	Lys	Ser	Ser	Asn	Asn					
				785					790					795					
Asn	Gly	Ser	Val	Arg	Thr	Ala													
				800															

<210> 261

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe



<400> 261  
gtgccactac ggggtgtgga cgac 24

<210> 262  
<211> 24  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 262  
tcccatttct tccgtggtgc ccag 24

<210> 263  
<211> 46  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 263  
ccagaagaag tccttcatga tgctcaagta catgcacgac cactac 46

<210> 264  
<211> 1419  
<212> DNA  
<213> Homo sapiens

<400> 264  
ggacaaccgt tgctgggtgt cccagggcct gaggcaggac ggtactcgc 50  
tgacaccttc ctttctggcc ttgaggttcc .cagcctggtg gccccaggac 100  
gttccggtcg catggcagag tgctacggac gacgcctatg aagcccttag 150  
tccttctagt tgcgcttttg ctatggcctt cgtctgtgcc ggcttatccg 200  
agcataactg tgacacctga tgaagagcaa aacttgaatc attatataca 250  
agtttttagag aacctagtac gaagtgttcc ctctggggag ccaggtcgtg 300  
agaaaaaatc taactctcca aaacatgttt attctatagc atcaaaggga 350  
tcaaaattta aggagctagt tacacatgga gacgcttcaa ctgagaatga 400  
tgttttaacc aatcctatca gtgaagaaac tacaactttc cctacaggag 450  
gcttcacacc ggaaatagga aagaaaaaac acacggaaag taccctattc 500  
tggtcgatca aaccaaaca tgtttccatt gttttgcatg cagaggaacc 550  
ttatattgaa aatgaagagc cagagccaga gccggagcca gctgcaaaac 600  
aaactgaggc accaagaatg ttgccagttg ttactgaatc atctacaagt 650

ccatatgtta cctcatacaa gtcacctgtc accacttttag ataagagcac 700  
 tggcattgag atctctacag aatcagaaga tgttctcag ctctcagggtg 750  
 aaactgcat agaaaaaccc gaagagtttg gaaagcacc agagagtttg 800  
 aataatgatg acattttgaa aaaaatttta gatattaatt cacaagtga 850  
 acaggcactt cttagtgaca ccagcaaccc agcatataga gaagatattg 900  
 aagcctctaa agatcaccta aaacgaagcc ttgctctagc agcagcagca 950  
 gaacataaat taaaaacaat gtataagtcc cagttattgc cagtaggacg 1000  
 aacaagtaat aaaattgatg acatcgaaac tgttattaac atgctgtgta 1050  
 attctagatc taaactctat gaatatttag atattaaatg tgttccacca 1100  
 gagatgagag aaaaagctgc tacagtattc aatacattaa aaaatatgtg 1150  
 tagatcaagg agagtcacag ccttattaaa agtttattaa acaataatat 1200  
 aaaaatttta aacctacttg atattccata acaaagctga ttaagcaaa 1250  
 ctgcattttt tcacaggaga aataatcata ttcgtaattt caaaagttgt 1300  
 ataaaaatat tttctattgt agttcaaatg tgccaacatc tttatgtgtc 1350  
 atgtgttatg aacaattttc atatgcacta aaaaccta ttaaaataaa 1400  
 attttggttc aggaaaaaa 1419

<210> 265

<211> 350

<212> PRT

<213> Homo sapiens

<400> 265

Met	Lys	Pro	Leu	Val	Leu	Leu	Val	Ala	Leu	Leu	Leu	Trp	Pro	Ser
1				5					10					15
Ser	Val	Pro	Ala	Tyr	Pro	Ser	Ile	Thr	Val	Thr	Pro	Asp	Glu	Glu
				20					25					30
Gln	Asn	Leu	Asn	His	Tyr	Ile	Gln	Val	Leu	Glu	Asn	Leu	Val	Arg
				35					40					45
Ser	Val	Pro	Ser	Gly	Glu	Pro	Gly	Arg	Glu	Lys	Lys	Ser	Asn	Ser
				50					55					60
Pro	Lys	His	Val	Tyr	Ser	Ile	Ala	Ser	Lys	Gly	Ser	Lys	Phe	Lys
				65					70					75
Glu	Leu	Val	Thr	His	Gly	Asp	Ala	Ser	Thr	Glu	Asn	Asp	Val	Leu
				80					85					90

Thr Asn Pro Ile Ser Glu Glu Thr Thr Thr Phe Pro Thr Gly Gly	95	100	105
Phe Thr Pro Glu Ile Gly Lys Lys Lys His Thr Glu Ser Thr Pro	110	115	120
Phe Trp Ser Ile Lys Pro Asn Asn Val Ser Ile Val Leu His Ala	125	130	135
Glu Glu Pro Tyr Ile Glu Asn Glu Glu Pro Glu Pro Glu Pro Glu	140	145	150
Pro Ala Ala Lys Gln Thr Glu Ala Pro Arg Met Leu Pro Val Val	155	160	165
Thr Glu Ser Ser Thr Ser Pro Tyr Val Thr Ser Tyr Lys Ser Pro	170	175	180
Val Thr Thr Leu Asp Lys Ser Thr Gly Ile Glu Ile Ser Thr Glu	185	190	195
Ser Glu Asp Val Pro Gln Leu Ser Gly Glu Thr Ala Ile Glu Lys	200	205	210
Pro Glu Glu Phe Gly Lys His Pro Glu Ser Trp Asn Asn Asp Asp	215	220	225
Ile Leu Lys Lys Ile Leu Asp Ile Asn Ser Gln Val Gln Gln Ala	230	235	240
Leu Leu Ser Asp Thr Ser Asn Pro Ala Tyr Arg Glu Asp Ile Glu	245	250	255
Ala Ser Lys Asp His Leu Lys Arg Ser Leu Ala Leu Ala Ala Ala	260	265	270
Ala Glu His Lys Leu Lys Thr Met Tyr Lys Ser Gln Leu Leu Pro	275	280	285
Val Gly Arg Thr Ser Asn Lys Ile Asp Asp Ile Glu Thr Val Ile	290	295	300
Asn Met Leu Cys Asn Ser Arg Ser Lys Leu Tyr Glu Tyr Leu Asp	305	310	315
Ile Lys Cys Val Pro Pro Glu Met Arg Glu Lys Ala Ala Thr Val	320	325	330
Phe Asn Thr Leu Lys Asn Met Cys Arg Ser Arg Arg Val Thr Ala	335	340	345
Leu Leu Lys Val Tyr	350		

<210> 266

<211> 2403

<212> DNA

<213> Homo sapiens

<400> 266

cggtctgagc ggctcgagtg aagagcctct ccacggctcc tgcgcctgag 50  
acagctggcc tgacctcaa atcatccatc caccctgct gtcattctgtt 100  
ttcatagtgt gagatcaacc cacaggaata tccatggctt ttgtgctcat 150  
tttggttctc agtttctacg agctgggtgc aggacagtgg caagtcactg 200  
gaccgggcaa gtttgtccag gccttgggtg gggaggacgc cgtgttctcc 250  
tgctccctct ttctgagac cagtgcagag gctatggaag tgcggttctt 300  
caggaatcag ttccatgctg tggccacct ctacagagat ggggaagact 350  
gggaatctaa gcagatgcc aagtatcgag ggagaactga gtttgtgaag 400  
gactccattg caggggggagc tgtctctcta aggctaaaaa acatcactcc 450  
ctcggacatc ggctgtatg ggtgctggtt cagttcccag atttacgatg 500  
aggaggccac ctgggagctg cgggtggcag cactgggctc acttctctc 550  
atttccatcg tgggatatgt tgacggaggt atccagttac tctgcctgtc 600  
ctcaggctgg ttccccagc ccacagccaa gtggaaaggt ccacaaggac 650  
aggatttgtc ttcagactcc agagcaaatg cagatgggta cagcctgtat 700  
gatgtggaga tctccattat agtcaggaa aatgctggga gcatattgtg 750  
ttccatccac cttgctgagc agagtcatga ggtggaatcc aaggtattga 800  
taggagagac gtttttccag cctcacctt ggcgctggc ttctatttta 850  
ctcgggttac tctgtggtgc cctgtgtggt gttgtcatgg ggatgataat 900  
tgttttcttc aaatccaaag ggaaaatcca ggcggaactg gactggagaa 950  
gaaagcacgg acaggcagaa ttgagagacg cccggaaaca cgcagtggag 1000  
gtgactctgg atccagagac ggctcaccgc aagctctgcg tttctgatct 1050  
gaaaactgta acccatagaa aagctcccca ggaggtgcct cactctgaga 1100  
agagatttac aaggaagagt gtggtggctt ctcagggtt ccaagcaggg 1150  
agacattact gggaggtgga cgtgggacaa aatgtagggt ggtatgtggg 1200  
agtgtgtcgg gatgacgtag acagggggaa gaacaatgtg actttgtctc 1250  
ccaacaatgg gtattgggtc ctcagactga caacagaaca tttgtatttc 1300  
acattcaatc cccattttat cagcctcccc cccagcacc ctcctacacg 1350

```

agtaggggtc ttcttgact atgaggggtg gaccatctcc ttcttcaata 1400
caaatgacca gtcccttatt tataccctgc tgacatgtca gtttgaaggc 1450
ttgttgagac cctatatcca gcatgcatg tatgacgagg aaaaggggac 1500
tcccatattc atatgtccag tgcctgggg atgagacaga gaagaccctg 1550
cttaaagggc cccacaccac agaccagac acagccaagg gagagtgtc 1600
ccgacaggtg gcccagctt cctctccga gcctgcgcac agagagtcac 1650
gccccccact ctctttagg gagctgaggt tcttctgcc tgagccctgc 1700
agcagcggca gtcacagctt ccagatgagg ggggattggc ctgaccctgt 1750
gggagtcaga agccatggct gccctgaagt ggggacggaa tagactcaca 1800
ttaggttttag tttgtgaaaa ctccatccag ctaagcgatc ttgaacaagt 1850
cacaacctcc caggctctc atttgctagt cacggacagt gattcctgcc 1900
tcacaggtga agattaaaga gacaacgaat gtgaatcatg cttgcagggt 1950
tgagggcaca gtgtttgcta atgatgtgtt tttatattat acattttccc 2000
accataaact ctgtttgctt attccacatt aatttacttt tctctatacc 2050
aaatcaccca tggaatagtt attgaacacc tgctttgtga ggctcaaaga 2100
ataaagagga ggtaggattt ttcactgatt ctataagccc agcattacct 2150
gataccaaaa ccaggcaaag aaaacagaag aagaggaagg aaaactacag 2200
gtccatatcc ctcatthaaca cagacacaaa aattctaaat aaaattttta 2250
caaattaaac taaacaatat atttaaagat gatataaac tactcagtgt 2300
ggtttgtccc acaaatgcag agttggttta atatttaa atcaaccagt 2350
gtaattcagc acattaataa agtaaaaaag aaaaccataa aaaaaaaaaa 2400
aaa 2403

```

<210> 267

<211> 466

<212> PRT

<213> Homo sapiens

<400> 267

Met	Ala	Phe	Val	Leu	Ile	Leu	Val	Leu	Ser	Phe	Tyr	Glu	Leu	Val
1				5					10					15

Ser	Gly	Gln	Trp	Gln	Val	Thr	Gly	Pro	Gly	Lys	Phe	Val	Gln	Ala
				20					25					30

Leu	Val	Gly	Glu	Asp	Ala	Val	Phe	Ser	Cys	Ser	Leu	Phe	Pro	Glu
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

35										40					45				
Thr	Ser	Ala	Glu	Ala	Met	Glu	Val	Arg	Phe	Phe	Arg	Asn	Gln	Phe					
				50					55					60					
His	Ala	Val	Val	His	Leu	Tyr	Arg	Asp	Gly	Glu	Asp	Trp	Glu	Ser					
				65					70					75					
Lys	Gln	Met	Pro	Gln	Tyr	Arg	Gly	Arg	Thr	Glu	Phe	Val	Lys	Asp					
				80					85					90					
Ser	Ile	Ala	Gly	Gly	Arg	Val	Ser	Leu	Arg	Leu	Lys	Asn	Ile	Thr					
				95					100					105					
Pro	Ser	Asp	Ile	Gly	Leu	Tyr	Gly	Cys	Trp	Phe	Ser	Ser	Gln	Ile					
				110					115					120					
Tyr	Asp	Glu	Glu	Ala	Thr	Trp	Glu	Leu	Arg	Val	Ala	Ala	Leu	Gly					
				125					130					135					
Ser	Leu	Pro	Leu	Ile	Ser	Ile	Val	Gly	Tyr	Val	Asp	Gly	Gly	Ile					
				140					145					150					
Gln	Leu	Leu	Cys	Leu	Ser	Ser	Gly	Trp	Phe	Pro	Gln	Pro	Thr	Ala					
				155					160					165					
Lys	Trp	Lys	Gly	Pro	Gln	Gly	Gln	Asp	Leu	Ser	Ser	Asp	Ser	Arg					
				170					175					180					
Ala	Asn	Ala	Asp	Gly	Tyr	Ser	Leu	Tyr	Asp	Val	Glu	Ile	Ser	Ile					
				185					190					195					
Ile	Val	Gln	Glu	Asn	Ala	Gly	Ser	Ile	Leu	Cys	Ser	Ile	His	Leu					
				200					205					210					
Ala	Glu	Gln	Ser	His	Glu	Val	Glu	Ser	Lys	Val	Leu	Ile	Gly	Glu					
				215					220					225					
Thr	Phe	Phe	Gln	Pro	Ser	Pro	Trp	Arg	Leu	Ala	Ser	Ile	Leu	Leu					
				230					235					240					
Gly	Leu	Leu	Cys	Gly	Ala	Leu	Cys	Gly	Val	Val	Met	Gly	Met	Ile					
				245					250					255					
Ile	Val	Phe	Phe	Lys	Ser	Lys	Gly	Lys	Ile	Gln	Ala	Glu	Leu	Asp					
				260					265					270					
Trp	Arg	Arg	Lys	His	Gly	Gln	Ala	Glu	Leu	Arg	Asp	Ala	Arg	Lys					
				275					280					285					
His	Ala	Val	Glu	Val	Thr	Leu	Asp	Pro	Glu	Thr	Ala	His	Pro	Lys					
				290					295					300					
Leu	Cys	Val	Ser	Asp	Leu	Lys	Thr	Val	Thr	His	Arg	Lys	Ala	Pro					
				305					310					315					
Gln	Glu	Val	Pro	His	Ser	Glu	Lys	Arg	Phe	Thr	Arg	Lys	Ser	Val					

320										325					330				
Val	Ala	Ser	Gln	Gly	Phe	Gln	Ala	Gly	Arg	His	Tyr	Trp	Glu	Val					
				335					340					345					
Asp	Val	Gly	Gln	Asn	Val	Gly	Trp	Tyr	Val	Gly	Val	Cys	Arg	Asp					
				350					355					360					
Asp	Val	Asp	Arg	Gly	Lys	Asn	Asn	Val	Thr	Leu	Ser	Pro	Asn	Asn					
				365					370					375					
Gly	Tyr	Trp	Val	Leu	Arg	Leu	Thr	Thr	Glu	His	Leu	Tyr	Phe	Thr					
				380					385					390					
Phe	Asn	Pro	His	Phe	Ile	Ser	Leu	Pro	Pro	Ser	Thr	Pro	Pro	Thr					
				395					400					405					
Arg	Val	Gly	Val	Phe	Leu	Asp	Tyr	Glu	Gly	Gly	Thr	Ile	Ser	Phe					
				410					415					420					
Phe	Asn	Thr	Asn	Asp	Gln	Ser	Leu	Ile	Tyr	Thr	Leu	Leu	Thr	Cys					
				425					430					435					
Gln	Phe	Glu	Gly	Leu	Leu	Arg	Pro	Tyr	Ile	Gln	His	Ala	Met	Tyr					
				440					445					450					
Asp	Glu	Glu	Lys	Gly	Thr	Pro	Ile	Phe	Ile	Cys	Pro	Val	Ser	Trp					
				455					460					465					

Gly

<210> 268  
 <211> 2103  
 <212> DNA  
 <213> Homo sapiens

<400> 268  
 ccttcacagg actcttcatt gctggttggc aatgatgtat cggccagatg 50  
 tgggtgagggc taggaaaaga gtttggtggg aaccctgggt tatcggcctc 100  
 gtcacatctca tatccctgat tgccttgga gtgtgcattg gactcactgt 150  
 tcattatgtg agatataatc aaaagaagac ctacaattac tatagcacat 200  
 tgtcattttac aactgacaaa ctatatgctg agtttggcag agaggcttct 250  
 aacaatttta cagaaatgag ccagagactt gaatcaatgg tgaaaaatgc 300  
 attttataaa tctccattaa gggaagaatt tgtcaagtct caggttatca 350  
 agttcagtca acagaagcat ggagtgttg ctcatatgct gttgatttgt 400  
 agatttcact ctactgagga tcctgaaact gtagataaaa ttgttcaact 450  
 tgttttacat gaaaagctgc aagatgctgt aggaccccct aaagtagatc 500

ctcactcagt taaaattaaa aaaatcaaca agacagaaac agacagctat 550  
ctaaaccatt gctgcggaac acgaagaagt aaaactctag gtcagagtct 600  
caggatcggt ggtgggacag aagtagaaga gggatgaatgg ccctggcagg 650  
ctagcctgca gtgggatggg agtcacgct gtggagcaac cttaattaat 700  
gccacatggc ttgtgagtgc tgctcactgt ttacaacat ataagaaccc 750  
tgccagatgg actgcttcct ttggagtaac aataaacct tcgaaatga 800  
aacggggtct ccggagaata attgtccatg aaaaatacaa acacccatca 850  
catgactatg atatttctct tgcagagctt tctagccctg tccctacac 900  
aatgcagta catagagttt gtctccctga tgcacctat gagtttcaac 950  
caggatgatg gatgtttgtg acaggatttg gagcactgaa aaatgatgg 1000  
tacagtcaaa atcatcttcg acaagcacag gtgactctca tagacgctac 1050  
aacttgcaat gaacctcaag cttacaatga cgccataact cctagaatgt 1100  
tatgtgctgg ctccctagaa ggaaaaacag atgcatgcca gggtgactct 1150  
ggaggaccac tggtagttc agatgctaga gatatctggg accttgctgg 1200  
aatagtgagc tggggagatg aatgtgcga acccaacaag cctgggtgtt 1250  
atactagagt tacggccttg cgggactgga ttacttcaaa aactggtatc 1300  
taagagacaa aagcctcatg gaacagataa cttttttttt tgttttttgg 1350  
gtgtggaggc cttttttaga gatacagaat tggagaagac ttgcaaaaca 1400  
gctagatttg actgatctca ataaactgtt tgcttgatgc atgtattttc 1450  
ttcccagctc tgttcgcac gtaagcatcc tgcttctgcc agatcaactc 1500  
tgtcatctgt gagcaatagt tgaaacttta tgtacataga gaaatagata 1550  
atacaatatt acattacagc ctgtattcat ttgttctcta gaagttttgt 1600  
cagaattttg acttggtgac ataaatttgt aatgcatata tacaatttga 1650  
agcactcctt ttcttcagtt cctcagctcc tctcatttca gcaaatatcc 1700  
attttcaagg tgcagaacaa ggagtgaag aaaatataag aagaaaaaaa 1750  
tccctacat ttattggca cagaaaagta ttaggtgttt ttcttagtgg 1800  
aatattagaa atgatcatat tcattatgaa aggtcaagca aagacagcag 1850  
aataccaatc acttcatcat ttaggaagta tgggaactaa gttaaggaag 1900



tccagaaaga agccaagata tatccttatt ttcatttcca aacaactact 1950  
 atgataaatg tgaagaagat tctgtttttt tgtgacctat aataattata 2000  
 caaacttcat gcaatgtact tgttctaagc aaattaaagc aaatatttat 2050  
 ttaacattgt tactgaggat gtcaacatat aacaataaaa tataaatcac 2100  
 cca 2103

<210> 269  
 <211> 423  
 <212> PRT  
 <213> Homo sapiens

<400> 269

Met	Met	Tyr	Arg	Pro	Asp	Val	Val	Arg	Ala	Arg	Lys	Arg	Val	Cys
1				5					10					15
Trp	Glu	Pro	Trp	Val	Ile	Gly	Leu	Val	Ile	Phe	Ile	Ser	Leu	Ile
				20					25					30
Val	Leu	Ala	Val	Cys	Ile	Gly	Leu	Thr	Val	His	Tyr	Val	Arg	Tyr
				35					40					45
Asn	Gln	Lys	Lys	Thr	Tyr	Asn	Tyr	Tyr	Ser	Thr	Leu	Ser	Phe	Thr
				50					55					60
Thr	Asp	Lys	Leu	Tyr	Ala	Glu	Phe	Gly	Arg	Glu	Ala	Ser	Asn	Asn
				65					70					75
Phe	Thr	Glu	Met	Ser	Gln	Arg	Leu	Glu	Ser	Met	Val	Lys	Asn	Ala
				80					85					90
Phe	Tyr	Lys	Ser	Pro	Leu	Arg	Glu	Glu	Phe	Val	Lys	Ser	Gln	Val
				95					100					105
Ile	Lys	Phe	Ser	Gln	Gln	Lys	His	Gly	Val	Leu	Ala	His	Met	Leu
				110					115					120
Leu	Ile	Cys	Arg	Phe	His	Ser	Thr	Glu	Asp	Pro	Glu	Thr	Val	Asp
				125					130					135
Lys	Ile	Val	Gln	Leu	Val	Leu	His	Glu	Lys	Leu	Gln	Asp	Ala	Val
				140					145					150
Gly	Pro	Pro	Lys	Val	Asp	Pro	His	Ser	Val	Lys	Ile	Lys	Lys	Ile
				155					160					165
Asn	Lys	Thr	Glu	Thr	Asp	Ser	Tyr	Leu	Asn	His	Cys	Cys	Gly	Thr
				170					175					180
Arg	Arg	Ser	Lys	Thr	Leu	Gly	Gln	Ser	Leu	Arg	Ile	Val	Gly	Gly
				185					190					195
Thr	Glu	Val	Glu	Glu	Gly	Glu	Trp	Pro	Trp	Gln	Ala	Ser	Leu	Gln
				200					205					210

Trp Asp Gly Ser	His Arg Cys Gly Ala	Thr Leu Ile Asn Ala	Thr
	215	220	225
Trp Leu Val Ser	Ala Ala His Cys Phe	Thr Thr Tyr Lys Asn	Pro
	230	235	240
Ala Arg Trp Thr	Ala Ser Phe Gly Val	Thr Ile Lys Pro Ser	Lys
	245	250	255
Met Lys Arg Gly	Leu Arg Arg Ile Ile	Val His Glu Lys Tyr	Lys
	260	265	270
His Pro Ser His	Asp Tyr Asp Ile Ser	Leu Ala Glu Leu Ser	Ser
	275	280	285
Pro Val Pro Tyr	Thr Asn Ala Val His	Arg Val Cys Leu Pro	Asp
	290	295	300
Ala Ser Tyr Glu	Phe Gln Pro Gly Asp	Val Met Phe Val Thr	Gly
	305	310	315
Phe Gly Ala Leu	Lys Asn Asp Gly Tyr	Ser Gln Asn His Leu	Arg
	320	325	330
Gln Ala Gln Val	Thr Leu Ile Asp Ala	Thr Thr Cys Asn Glu	Pro
	335	340	345
Gln Ala Tyr Asn	Asp Ala Ile Thr Pro	Arg Met Leu Cys Ala	Gly
	350	355	360
Ser Leu Glu Gly	Lys Thr Asp Ala Cys	Gln Gly Asp Ser Gly	Gly
	365	370	375
Pro Leu Val Ser	Ser Asp Ala Arg Asp	Ile Trp Tyr Leu Ala	Gly
	380	385	390
Ile Val Ser Trp	Gly Asp Glu Cys Ala	Lys Pro Asn Lys Pro	Gly
	395	400	405
Val Tyr Thr Arg	Val Thr Ala Leu Arg	Asp Trp Ile Thr Ser	Lys
	410	415	420

Thr Gly Ile

<210> 270

<211> 1170

<212> DNA

<213> Homo sapiens

<400> 270

gtcgaaggtt ataaaagctt ccagccaaac ggcattgaag ttgaagatac 50

aacctgacag cacagcctga gatcttgggg atccctcagc ctaacaccca 100

cagacgtcag ctggtggatt cccgctgcat caaggcctac ccactgtctc 150

catgctgggc tctccctgcc ttctgtggct cctggccgtg accttcttgg 200  
tccccagagc tcagcccttg gcccctcaag actttgaaga agaggaggca 250  
gatgagactg agacggcgtg gccgcctttg ccggctgtcc cctgcgacta 300  
cgaccactgc cgacacctgc aggtgccctg caaggagcta cagaggggtcg 350  
ggccggcggc ctgcctgtgc ccaggactct ccagccccgc ccagccgccc 400  
gacccgccgc gcatgggaga agtgcgcatc gcggccgaag agggccgcgc 450  
agtgggtccac tgggtgtgcc ccttctcccc ggtcctccac tactgggtgc 500  
tgctttggga cggcagcgag gctgcgcaga aggggcccc gctgaacgct 550  
acggtcgcga gagccgaact gaaggggctg aagccagggg gcatttatgt 600  
cgtttgcgta gtggccgcta acgaggccgg ggcaagccgc gtgccccagg 650  
ctggaggaga gggcctcgag ggggccgaca tccctgcctt cgggccttgc 700  
agccgccttg cggtgccgcc caacccccgc actctggtcc acgcggccgt 750  
cgggggtgggc acggcccttg ccttgctaag ctgtgccgcc ctggtgtggc 800  
acttctgcct gcgcgatcgc tggggctgcc cgcgccgagc cgccgcccg 850  
gccgcagggg cgctctgaaa ggggcctggg ggcatctcgg gcacagacag 900  
ccccaccttg ggcgctcagc ctggcccccg ggaaagagga aaacccgctg 950  
cctccaggga gggctggacg gcgagctggg agccagcccc aggtccagg 1000  
gccacggcgg agtcatggtt ctcaggactg agcgcttggt taggtccggt 1050  
acttggcgct ttgtttcctg gctgaggtct gggaaggaat agaaaggggc 1100  
ccccaatttt tttttaagcg gccagataat aaataatgta acctttgcgg 1150  
ttaaaaaaaaa aaaaaaaaaa 1170

<210> 271

<211> 238

<212> PRT

<213> Homo sapiens

<400> 271

Met	Leu	Gly	Ser	Pro	Cys	Leu	Leu	Trp	Leu	Leu	Ala	Val	Thr	Phe
1				5				10						15

Leu	Val	Pro	Arg	Ala	Gln	Pro	Leu	Ala	Pro	Gln	Asp	Phe	Glu	Glu
				20					25					30

Glu	Glu	Ala	Asp	Glu	Thr	Glu	Thr	Ala	Trp	Pro	Pro	Leu	Pro	Ala
				35					40					45

Val	Pro	Cys	Asp	Tyr	Asp	His	Cys	Arg	His	Leu	Gln	Val	Pro	Cys	
				50					55					60	
Lys	Glu	Leu	Gln	Arg	Val	Gly	Pro	Ala	Ala	Cys	Leu	Cys	Pro	Gly	
				65					70					75	
Leu	Ser	Ser	Pro	Ala	Gln	Pro	Pro	Asp	Pro	Pro	Arg	Met	Gly	Glu	
				80					85					90	
Val	Arg	Ile	Ala	Ala	Glu	Glu	Gly	Arg	Ala	Val	Val	His	Trp	Cys	
				95					100					105	
Ala	Pro	Phe	Ser	Pro	Val	Leu	His	Tyr	Trp	Leu	Leu	Leu	Trp	Asp	
				110					115					120	
Gly	Ser	Glu	Ala	Ala	Gln	Lys	Gly	Pro	Pro	Leu	Asn	Ala	Thr	Val	
				125					130					135	
Arg	Arg	Ala	Glu	Leu	Lys	Gly	Leu	Lys	Pro	Gly	Gly	Ile	Tyr	Val	
				140					145					150	
Val	Cys	Val	Val	Ala	Ala	Asn	Glu	Ala	Gly	Ala	Ser	Arg	Val	Pro	
				155					160					165	
Gln	Ala	Gly	Gly	Glu	Gly	Leu	Glu	Gly	Ala	Asp	Ile	Pro	Ala	Phe	
				170					175					180	
Gly	Pro	Cys	Ser	Arg	Leu	Ala	Val	Pro	Pro	Asn	Pro	Arg	Thr	Leu	
				185					190					195	
Val	His	Ala	Ala	Val	Gly	Val	Gly	Thr	Ala	Leu	Ala	Leu	Leu	Ser	
				200					205					210	
Cys	Ala	Ala	Leu	Val	Trp	His	Phe	Cys	Leu	Arg	Asp	Arg	Trp	Gly	
				215					220					225	
Cys	Pro	Arg	Arg	Ala	Ala	Ala	Arg	Ala	Ala	Gly	Ala	Leu			
				230					235						

<210> 272

<211> 2397

<212> DNA

<213> Homo sapiens

<400> 272

```

agagaaagaa gcgtctccag ctgaagccaa tgcagccctc cggtctccg 50
cgaagaagtt ccctgccccg atgagcccc gccgtgcgtc cccgactatc 100
cccaggcggg cgtggggcac cgggccagc gccgacgac gctgccgttt 150
tgcccttggg agtaggatgt ggtgaaagga tggggcttct cccttacggg 200
gctcacaatg gccagagaag attccgtgaa gtgtctgcgc tgcctgctct 250
acgccctcaa tctgctcttt tggttaatgt ccatcagtgt gttggcagtt 300

```

tctgcttgga tgagggacta cctaaataat gttctcactt taactgcaga 350  
aacgagggta gaggaagcag tcattttgac ttactttcct gtggttcac 400  
cggatcatgat tgctgtttgc tgtttcctta tcattgtggg gatgttagga 450  
tattgtggaa cggtgaaaag aaatctgttg cttcttgcac ggtactttgg 500  
aagtttgctt gtcattttct gtgtagaact ggcttgtggc gtttgacat 550  
atgaacagga acttatgggt ccagtacaat ggtagatat ggtcactttg 600  
aaagccagga tgacaaatta tggattacct agatatcggg ggcttactca 650  
tgcttggaat ttttttcaga gagagtttaa gtgctgtgga gtagtatatt 700  
tcactgactg gttggaaatg acagagatgg actggcccc agattcctgc 750  
tgtgttagag aattcccagg atgttccaaa caggcccacc aggaagatct 800  
cagtacactt tatcaagagg gttgtgggaa gaaaatgtat tcctttttga 850  
gaggaaccaa acaactgcag gtgctgaggt ttctgggaat ctccattggg 900  
gtgacacaaa tcctggccat gattctcacc attactctgc tctgggctct 950  
gtattatgat agaagggagc ctgggacaga ccaaatgatg tccttgaaga 1000  
atgacaactc tcagcacctg tcatgtccct cagtagaact gttgaaacca 1050  
agcctgtcaa gaatctttga acacacatcc atggcaaaca gctttaatac 1100  
acactttgag atggaggagt tataaaaaga aatgtcacag aagaaaacca 1150  
caaacttggt ttattggact tgtgaatfff tgagtacata ctatgtgttt 1200  
cagaaatatg tagaaataaa aatgttgcca taaaataaca cctaagcata 1250  
tactattcta tgctttaaaa tgaggatgga aaagtttcat gtcataagtc 1300  
accacctgga caataattga tgcccttaaa atgctgaaga cagatgtcat 1350  
accactgtg tagcctgtgt atgactttta ctgaacacag ttatgttttg 1400  
aggcagcatg gtttgattag catttcgcga tccatgcaaa cgagtcacat 1450  
atggtgggac tggagccata gtaaagggtg atttacttct accaactagt 1500  
atataaagta ctaattaaat gctaacatag gaagttagaa aatactaata 1550  
acttttatta ctacgcgac tattcttctg atgctaaata aattatatat 1600  
cagaaaactt tcaatattgg tgactaccta aatgtgattt ttgctgggta 1650  
ctaaaatatt ctaccactt aaaagagcaa gctaacacat tgtcttaagc 1700

tgcacaggga ttttttgtat ataagtctgt gttaaactctg tataattcag 1750  
 tcgatttcag ttctgataat gttaagaata accattatga aaaggaaaat 1800  
 ttgtcctgta tagcatcatt attttttagcc tttcctgtta ataaagcttt 1850  
 actattctgt cctgggctta tattacacat ataactgtta tttaaatact 1900  
 taaccactaa ttttgaaaat taccagtgtg atacatagga atcattattc 1950  
 agaatgtagt ctgggtcttta ggaagtatta ataagaaaat ttgcacataa 2000  
 cttagtgtat tcagaaagga cttgtatgct gtttttctcc caaatgaaga 2050  
 ctctttttga cactaaacac tttttaaaaa gcttatcttt gccttctcca 2100  
 aacaagaagc aatagtctcc aagtcaatat aaattctaca gaaaatagtg 2150  
 ttctttttct ccagaaaaat gcttgtgaga atcattaaaa catgtgacaa 2200  
 tttagagatt ctttgtttta tttcactgat taatatactg tggcaaatta 2250  
 cacagattat taaatttttt tacaagagta tagtatattt atttgaaatg 2300  
 ggaaaagtgc attttactgt attttgtgta ttttgtttat ttctcagaat 2350  
 atggaaagaa aattaaaatg tgtcaataaa tattttctag agagtaa 2397

<210> 273

<211> 305

<212> PRT

<213> Homo sapiens

<400> 273

Met	Ala	Arg	Glu	Asp	Ser	Val	Lys	Cys	Leu	Arg	Cys	Leu	Leu	Tyr
1				5					10					15
Ala	Leu	Asn	Leu	Leu	Phe	Trp	Leu	Met	Ser	Ile	Ser	Val	Leu	Ala
				20					25					30
Val	Ser	Ala	Trp	Met	Arg	Asp	Tyr	Leu	Asn	Asn	Val	Leu	Thr	Leu
				35					40					45
Thr	Ala	Glu	Thr	Arg	Val	Glu	Glu	Ala	Val	Ile	Leu	Thr	Tyr	Phe
				50					55					60
Pro	Val	Val	His	Pro	Val	Met	Ile	Ala	Val	Cys	Cys	Phe	Leu	Ile
				65					70					75
Ile	Val	Gly	Met	Leu	Gly	Tyr	Cys	Gly	Thr	Val	Lys	Arg	Asn	Leu
				80					85					90
Leu	Leu	Leu	Ala	Trp	Tyr	Phe	Gly	Ser	Leu	Leu	Val	Ile	Phe	Cys
				95					100					105
Val	Glu	Leu	Ala	Cys	Gly	Val	Trp	Thr	Tyr	Glu	Gln	Glu	Leu	Met
				110					115					120

Val	Pro	Val	Gln	Trp	Ser	Asp	Met	Val	Thr	Leu	Lys	Ala	Arg	Met	
				125					130					135	
Thr	Asn	Tyr	Gly	Leu	Pro	Arg	Tyr	Arg	Trp	Leu	Thr	His	Ala	Trp	
				140					145					150	
Asn	Phe	Phe	Gln	Arg	Glu	Phe	Lys	Cys	Cys	Gly	Val	Val	Tyr	Phe	
				155					160					165	
Thr	Asp	Trp	Leu	Glu	Met	Thr	Glu	Met	Asp	Trp	Pro	Pro	Asp	Ser	
				170					175					180	
Cys	Cys	Val	Arg	Glu	Phe	Pro	Gly	Cys	Ser	Lys	Gln	Ala	His	Gln	
				185					190					195	
Glu	Asp	Leu	Ser	Asp	Leu	Tyr	Gln	Glu	Gly	Cys	Gly	Lys	Lys	Met	
				200					205					210	
Tyr	Ser	Phe	Leu	Arg	Gly	Thr	Lys	Gln	Leu	Gln	Val	Leu	Arg	Phe	
				215					220					225	
Leu	Gly	Ile	Ser	Ile	Gly	Val	Thr	Gln	Ile	Leu	Ala	Met	Ile	Leu	
				230					235					240	
Thr	Ile	Thr	Leu	Leu	Trp	Ala	Leu	Tyr	Tyr	Asp	Arg	Arg	Glu	Pro	
				245					250					255	
Gly	Thr	Asp	Gln	Met	Met	Ser	Leu	Lys	Asn	Asp	Asn	Ser	Gln	His	
				260					265					270	
Leu	Ser	Cys	Pro	Ser	Val	Glu	Leu	Leu	Lys	Pro	Ser	Leu	Ser	Arg	
				275					280					285	
Ile	Phe	Glu	His	Thr	Ser	Met	Ala	Asn	Ser	Phe	Asn	Thr	His	Phe	
				290					295					300	
Glu	Met	Glu	Glu	Leu											
				305											

<210> 274

<211> 2063

<212> DNA

<213> Homo sapiens

<400> 274

gagagaggca gcagcttgct cagcggacaa ggatgctggg cgtgaggac 50

caaggcctgc cctgcactcg ggccctctcc agccagtgc gaccaggac 100

ttctgacctg ctggccagcc aggacctgtg tggggaggcc ctctgctgc 150

cttggggtga caatctcagc tccaggctac agggagaccg ggaggatcac 200

agagccagca tgttacagga tcctgacagt gatcaacctc tgaacagcct 250

cgatgtcaaa cccctgcgca aaccccgat ccccatggag accttcagaa 300

aggtggggat ccccatcatc atagcactac tgagcctggc gagtatcatc 350  
attgtggttg tccatcatcaa ggtgattctg gataaatact acttcctctg 400  
cgggcagcct ctccacttca tcccaggaa gcagctgtgt gacggagagc 450  
tggaactgtcc cttgggggag gacgaggagc actgtgtcaa gagcttcccc 500  
gaagggcctg cagtggcagt ccgcctctcc aaggaccgat ccacactgca 550  
ggtgctggac tcggccacag ggaactggtt ctctgcctgt ttcgacaact 600  
tcacagaagc tctcgctgag acagcctgta ggcagatggg ctacagcaga 650  
gctgtggaga ttggcccaga ccaggatctg gatgttgttg aaatcacaga 700  
aaacagccag gagcttcgca tgcggaactc aagtgggccc tgtctctcag 750  
gtccctggt ctccctgcac tgtcttgctt gtgggaagag cctgaagacc 800  
ccccgtgtgg tgggtgggga ggaggcctct gtggattctt ggccttggca 850  
ggtcagcatc cagtacgaca aacagcacgt ctgtggaggg agcatcctgg 900  
acccccactg ggtcctcacg gcagccact gcttcaggaa acataccgat 950  
gtgttcaact ggaaggtgcg ggcaggctca gacaaactgg gcagcttccc 1000  
atccctggct gtggccaaga tcatcatcat tgaattcaac cccatgtacc 1050  
ccaaagacaa tgacatcgcc ctcatgaagc tgcagttccc actcactttc 1100  
tcaggcacag tcaggcccat ctgtctgccc ttctttgatg aggagctcac 1150  
tccagccacc cactctgga tcattggatg gggctttacg aagcagaatg 1200  
gaggggaagat gtctgacata ctgctgcagg cgtcagtcca ggtcattgac 1250  
agcacacggt gcaatgcaga cgatgcgtac cagggggaag tcaccgagaa 1300  
gatgatgtgt gcaggcatcc cggaaggggg tgtggacacc tgccagggtg 1350  
acagtgggtg gccctgatg taccaatctg accagtggca tgtggtgggc 1400  
atcgtagct ggggctatgg ctgcgggggc ccgagcacc caggagtata 1450  
caccaaggtc tcagcctatc tcaactggat ctacaatgtc tggaaggctg 1500  
agctgtaatg ctgctgcccc tttgcagtgc tgggagccgc ttccttcctg 1550  
ccctgcccac ctggggatcc cccaaagtca gacacagagc aagagtcccc 1600  
ttgggtacac ccctctgccc acagcctcag catttcttgg agcagcaaag 1650  
ggcctcaatt cctgtaagag accctcgag cccagaggcg cccagaggaa 1700



gtcagcagcc ctagctcggc cacacttggt gctcccagca tcccagggag 1750  
 agacacagcc cactgaacaa ggtctcaggg gtattgctaa gccaagaagg 1800  
 aactttccca cactactgaa tggaagcagg ctgtcttgta aaagcccaga 1850  
 tcaactgtggg ctggagagga gaaggaaagg gtctgcgcca gccctgtccg 1900  
 tcttcaccca tcccgaagcc tactagagca agaaaccagt tgtaatataa 1950  
 aatgcactgc cctactgttg gtatgactac cgttacctac tgttgtcatt 2000  
 gttattacag ctatggccac tattattaaa gagctgtgta acatctctgg 2050  
 caaaaaaaaaaaa aaa 2063

<210> 275

<211> 432

<212> PRT

<213> Homo sapiens

<400> 275

Met	Leu	Gln	Asp	Pro	Asp	Ser	Asp	Gln	Pro	Leu	Asn	Ser	Leu	Asp	1	5	10	15
Val	Lys	Pro	Leu	Arg	Lys	Pro	Arg	Ile	Pro	Met	Glu	Thr	Phe	Arg	20	25	30	
Lys	Val	Gly	Ile	Pro	Ile	Ile	Ile	Ala	Leu	Leu	Ser	Leu	Ala	Ser	35	40	45	
Ile	Ile	Ile	Val	Val	Val	Leu	Ile	Lys	Val	Ile	Leu	Asp	Lys	Tyr	50	55	60	
Tyr	Phe	Leu	Cys	Gly	Gln	Pro	Leu	His	Phe	Ile	Pro	Arg	Lys	Gln	65	70	75	
Leu	Cys	Asp	Gly	Glu	Leu	Asp	Cys	Pro	Leu	Gly	Glu	Asp	Glu	Glu	80	85	90	
His	Cys	Val	Lys	Ser	Phe	Pro	Glu	Gly	Pro	Ala	Val	Ala	Val	Arg	95	100	105	
Leu	Ser	Lys	Asp	Arg	Ser	Thr	Leu	Gln	Val	Leu	Asp	Ser	Ala	Thr	110	115	120	
Gly	Asn	Trp	Phe	Ser	Ala	Cys	Phe	Asp	Asn	Phe	Thr	Glu	Ala	Leu	125	130	135	
Ala	Glu	Thr	Ala	Cys	Arg	Gln	Met	Gly	Tyr	Ser	Arg	Ala	Val	Glu	140	145	150	
Ile	Gly	Pro	Asp	Gln	Asp	Leu	Asp	Val	Val	Glu	Ile	Thr	Glu	Asn	155	160	165	
Ser	Gln	Glu	Leu	Arg	Met	Arg	Asn	Ser	Ser	Gly	Pro	Cys	Leu	Ser	170	175	180	

Gly Ser Leu Val	Ser Leu His Cys Leu	Ala Cys Gly Lys Ser	Leu
185	190		195
Lys Thr Pro Arg	Val Val Gly Gly Glu	Glu Ala Ser Val Asp	Ser
200	205		210
Trp Pro Trp Gln	Val Ser Ile Gln Tyr	Asp Lys Gln His Val	Cys
215	220		225
Gly Gly Ser Ile	Leu Asp Pro His Trp	Val Leu Thr Ala Ala	His
230	235		240
Cys Phe Arg Lys	His Thr Asp Val Phe	Asn Trp Lys Val Arg	Ala
245	250		255
Gly Ser Asp Lys	Leu Gly Ser Phe Pro	Ser Leu Ala Val Ala	Lys
260	265		270
Ile Ile Ile Ile	Glu Phe Asn Pro Met	Tyr Pro Lys Asp Asn	Asp
275	280		285
Ile Ala Leu Met	Lys Leu Gln Phe Pro	Leu Thr Phe Ser Gly	Thr
290	295		300
Val Arg Pro Ile	Cys Leu Pro Phe Phe	Asp Glu Glu Leu Thr	Pro
305	310		315
Ala Thr Pro Leu	Trp Ile Ile Gly Trp	Gly Phe Thr Lys Gln	Asn
320	325		330
Gly Gly Lys Met	Ser Asp Ile Leu Leu	Gln Ala Ser Val Gln	Val
335	340		345
Ile Asp Ser Thr	Arg Cys Asn Ala Asp	Asp Ala Tyr Gln Gly	Glu
350	355		360
Val Thr Glu Lys	Met Met Cys Ala Gly	Ile Pro Glu Gly Gly	Val
365	370		375
Asp Thr Cys Gln	Gly Asp Ser Gly Gly	Pro Leu Met Tyr Gln	Ser
380	385		390
Asp Gln Trp His	Val Val Gly Ile Val	Ser Trp Gly Tyr Gly	Cys
395	400		405
Gly Gly Pro Ser	Thr Pro Gly Val Tyr	Thr Lys Val Ser Ala	Tyr
410	415		420
Leu Asn Trp Ile	Tyr Asn Val Trp Lys	Ala Glu Leu	
425	430		

<210> 276

<211> 3143

<212> DNA

<213> Homo sapiens

<400> 276

gggctgaggc actgagagac cggaaaagcct ggcattccag agggagggaa 50  
acgcagcggc atccccaggc tccagagctc cctggtgaca gtctgtggct 100  
gagcatggcc ctcccagccc tgggcctgga cccctggagc ctctggggc 150  
ttttcctctt ccaactgctt cagctgctgc tgccgacgac gaccgcgggg 200  
ggaggcgggc agggggcccat gcccagggtc agatactatg caggggatga 250  
acgtagggca cttagcttct tccaccagaa gggcctccag gattttgaca 300  
ctctgctcct gagtggatg ggaatactc tctacgtggg ggctcgagaa 350  
gccattctgg ctttgatat ccaggatcca ggggtcccca ggctaaagaa 400  
catgataccg tggccagcca gtgacagaaa aaagagtga tgtgccttta 450  
agaagaagag caatgagaca cagtgtttca acttcatccg tgtcctggtt 500  
tcttacaatg tcacccatct ctacacctgc ggcacctcg ccttcagccc 550  
tgcttgtagc ttcatgaac ttcaagattc ctacctgttg cccatctcgg 600  
aggacaaggt catggaggga aaaggccaaa gccctttga ccccgctcac 650  
aagcatacgg ctgtcttggt ggatgggatg ctctattctg gtactatgaa 700  
caacttctg ggcagtgagc ccacctgat gcgcacactg ggatcccagc 750  
ctgtcctcaa gaccgacaac ttcctccgct ggctgcatca tgacgcctcc 800  
tttgtggcag ccatcccttc gaccaggtc gtctacttct tcttcgagga 850  
gacagccagc gagtttgact tctttgagag gctccacaca tcgcggttg 900  
ctagagtctg caagaatgac gtgggcggcg aaaagctgct gcagaagaag 950  
tggaaccact tcctgaaggc ccagctgctc tgcaccagc cggggcagct 1000  
gcccttcaac gtcacccgcc acgcggctct gctccccgcc gattctcca 1050  
cagctcccca catctacgca gtcttcacct cccagtggca ggttggcggg 1100  
accaggagct ctgcggtttg tgcttctct ctcttgaca ttgaacgtgt 1150  
ctttaagggg aaatacaaag agttgaacaa agaaacttca cgctggacta 1200  
cttatagggg ccctgagacc aacccccggc caggcagttg ctcagtggc 1250  
ccctcctctg ataaggccct gaccttcag aaggaccatt tcctgatgga 1300  
tgagcaagtg gtggggacgc ccctgctggt gaaatctggc gtggagtata 1350  
cacggcttgc agtggagaca gcccagggcc ttgatgggca cagccatctt 1400

gtcatgtacc tgggaaccac cacagggtcg ctccacaagg ctgtggtaag 1450  
tggggacagc agtgctcatc tgggtggaaga gattcagctg ttccctgacc 1500  
ctgaacctgt tcgcaacctg cagctggccc ccacccaggg tgcagtgttt 1550  
gtaggcttct caggaggtgt ctggaggggtg ccccgagcca actgtagtgt 1600  
ctatgagagc tgtgtggact gtgtccttgc ccgggacccc cactgtgcct 1650  
gggaccctga gtcccgaacc tgttgccctcc tgtctgcccc caacctgaac 1700  
tcctggaagc aggacatgga gcgggggaac ccagagtggg catgtgccag 1750  
tggcccatg agcaggagcc ttcggcctca gagccgcccg caaatcatta 1800  
aagaagtcct ggctgtcccc aactccatcc tggagctccc ctgccccac 1850  
ctgtcagcct tggcctctta ttattggagt catggcccag cagcagtcct 1900  
agaagcctct tccactgtct acaatggctc cctcttgctg atagtgcagg 1950  
atggagttgg gggctcttac cagtgtctgg caactgagaa tggcttttca 2000  
taccctgtga tctctactg ggtggacagc caggaccaga ccctggccct 2050  
ggatcctgaa ctggcaggca tccccggga gcatgtgaag gtcccgttga 2100  
ccagggtcag tgggtggggc gccctggctg ccagcagtc ctactggccc 2150  
cactttgtca ctgtcactgt cctctttgcc ttagtgcttt caggagccct 2200  
catcatcctc gtggcctccc cattgagagc actccgggct cggggcaagg 2250  
ttcagggtctg tgagaccctg cgccctgggg agaaggcccc gttaagcaga 2300  
gagcaacacc tccagtctcc caaggaatgc aggacctctg ccagtgatgt 2350  
ggacgctgac aacaactgcc taggcactga ggtagcttaa actctaggca 2400  
caggccgggg ctgcggtgca ggcacctggc catgctggct gggcggccca 2450  
agcacagccc tgactaggat gacagcagca caaaagacca cttttctccc 2500  
ctgagaggag cttctgctac tctgcatcac tgatgacact cagcaggggtg 2550  
atgcacagca gtctgcctcc cctatgggac tcccttctac caagcacatg 2600  
agctctctaa cagggtgggg gctaccccca gacctgctcc tacactgata 2650  
ttgaagaacc tggagaggat ccttcagttc tggccattcc agggaccctc 2700  
cagaaacaca gtgtttcaag agaccctaaa aaacctgcct gtcccaggac 2750  
cctatggtaa tgaacaccaa acatctaaac aatcatatgc taacatgcca 2800  
ctcctggaaa ctccactctg aagctgccgc tttggacacc aacactccct 2850

tctcccaggg tcatgcaggg atctgctccc tctgcttcc cttaccagtc 2900  
 gtgcaccgct gactcccagg aagtctttcc tgaagtctga ccacctttct 2950  
 tcttgcttca gttggggcag actctgatcc cttctgccct ggcagaatgg 3000  
 caggggtaat ctgagccttc ttcactcctt taccctagct gacccttca 3050  
 cctctcccc tcccttttcc ttgttttgg gattcagaaa actgcttgtc 3100  
 agagactggt tattttttat taaaaatata aggcttaaaa aaa 3143

<210> 277

<211> 761

<212> PRT

<213> Homo sapiens

<400> 277

Met	Ala	Leu	Pro	Ala	Leu	Gly	Leu	Asp	Pro	Trp	Ser	Leu	Leu	Gly	1	5	10	15
Leu	Phe	Leu	Phe	Gln	Leu	Leu	Gln	Leu	Leu	Leu	Pro	Thr	Thr	Thr	20	25	30	
Ala	Gly	Gly	Gly	Gly	Gln	Gly	Pro	Met	Pro	Arg	Val	Arg	Tyr	Tyr	35	40	45	
Ala	Gly	Asp	Glu	Arg	Arg	Ala	Leu	Ser	Phe	Phe	His	Gln	Lys	Gly	50	55	60	
Leu	Gln	Asp	Phe	Asp	Thr	Leu	Leu	Leu	Ser	Gly	Asp	Gly	Asn	Thr	65	70	75	
Leu	Tyr	Val	Gly	Ala	Arg	Glu	Ala	Ile	Leu	Ala	Leu	Asp	Ile	Gln	80	85	90	
Asp	Pro	Gly	Val	Pro	Arg	Leu	Lys	Asn	Met	Ile	Pro	Trp	Pro	Ala	95	100	105	
Ser	Asp	Arg	Lys	Lys	Ser	Glu	Cys	Ala	Phe	Lys	Lys	Lys	Ser	Asn	110	115	120	
Glu	Thr	Gln	Cys	Phe	Asn	Phe	Ile	Arg	Val	Leu	Val	Ser	Tyr	Asn	125	130	135	
Val	Thr	His	Leu	Tyr	Thr	Cys	Gly	Thr	Phe	Ala	Phe	Ser	Pro	Ala	140	145	150	
Cys	Thr	Phe	Ile	Glu	Leu	Gln	Asp	Ser	Tyr	Leu	Leu	Pro	Ile	Ser	155	160	165	
Glu	Asp	Lys	Val	Met	Glu	Gly	Lys	Gly	Gln	Ser	Pro	Phe	Asp	Pro	170	175	180	
Ala	His	Lys	His	Thr	Ala	Val	Leu	Val	Asp	Gly	Met	Leu	Tyr	Ser	185	190	195	

Gly Thr Met Asn	Asn Phe Leu Gly Ser	Glu Pro Ile Leu Met Arg
200		205 210
Thr Leu Gly Ser	Gln Pro Val Leu Lys	Thr Asp Asn Phe Leu Arg
215		220 225
Trp Leu His His	Asp Ala Ser Phe Val	Ala Ala Ile Pro Ser Thr
230		235 240
Gln Val Val Tyr	Phe Phe Phe Glu Glu	Thr Ala Ser Glu Phe Asp
245		250 255
Phe Phe Glu Arg	Leu His Thr Ser Arg	Val Ala Arg Val Cys Lys
260		265 270
Asn Asp Val Gly	Gly Glu Lys Leu Leu	Gln Lys Lys Trp Thr Thr
275		280 285
Phe Leu Lys Ala	Gln Leu Leu Cys Thr	Gln Pro Gly Gln Leu Pro
290		295 300
Phe Asn Val Ile	Arg His Ala Val Leu	Leu Pro Ala Asp Ser Pro
305		310 315
Thr Ala Pro His	Ile Tyr Ala Val Phe	Thr Ser Gln Trp Gln Val
320		325 330
Gly Gly Thr Arg	Ser Ser Ala Val Cys	Ala Phe Ser Leu Leu Asp
335		340 345
Ile Glu Arg Val	Phe Lys Gly Lys Tyr	Lys Glu Leu Asn Lys Glu
350		355 360
Thr Ser Arg Trp	Thr Thr Tyr Arg Gly	Pro Glu Thr Asn Pro Arg
365		370 375
Pro Gly Ser Cys	Ser Val Gly Pro Ser	Ser Asp Lys Ala Leu Thr
380		385 390
Phe Met Lys Asp	His Phe Leu Met Asp	Glu Gln Val Val Gly Thr
395		400 405
Pro Leu Leu Val	Lys Ser Gly Val Glu	Tyr Thr Arg Leu Ala Val
410		415 420
Glu Thr Ala Gln	Gly Leu Asp Gly His	Ser His Leu Val Met Tyr
425		430 435
Leu Gly Thr Thr	Thr Gly Ser Leu His	Lys Ala Val Val Ser Gly
440		445 450
Asp Ser Ser Ala	His Leu Val Glu Glu	Ile Gln Leu Phe Pro Asp
455		460 465
Pro Glu Pro Val	Arg Asn Leu Gln Leu	Ala Pro Thr Gln Gly Ala
470		475 480

Val Phe Val Gly	Phe Ser Gly Gly Val	Trp Arg Val Pro Arg	Ala
	485	490	495
Asn Cys Ser Val	Tyr Glu Ser Cys Val	Asp Cys Val Leu Ala	Arg
	500	505	510
Asp Pro His Cys	Ala Trp Asp Pro Glu	Ser Arg Thr Cys Cys	Leu
	515	520	525
Leu Ser Ala Pro	Asn Leu Asn Ser Trp	Lys Gln Asp Met Glu	Arg
	530	535	540
Gly Asn Pro Glu	Trp Ala Cys Ala Ser	Gly Pro Met Ser Arg	Ser
	545	550	555
Leu Arg Pro Gln	Ser Arg Pro Gln Ile	Ile Lys Glu Val Leu	Ala
	560	565	570
Val Pro Asn Ser	Ile Leu Glu Leu Pro	Cys Pro His Leu Ser	Ala
	575	580	585
Leu Ala Ser Tyr	Tyr Trp Ser His Gly	Pro Ala Ala Val Pro	Glu
	590	595	600
Ala Ser Ser Thr	Val Tyr Asn Gly Ser	Leu Leu Leu Ile Val	Gln
	605	610	615
Asp Gly Val Gly	Gly Leu Tyr Gln Cys	Trp Ala Thr Glu Asn	Gly
	620	625	630
Phe Ser Tyr Pro	Val Ile Ser Tyr Trp	Val Asp Ser Gln Asp	Gln
	635	640	645
Thr Leu Ala Leu	Asp Pro Glu Leu Ala	Gly Ile Pro Arg Glu	His
	650	655	660
Val Lys Val Pro	Leu Thr Arg Val Ser	Gly Gly Ala Ala Leu	Ala
	665	670	675
Ala Gln Gln Ser	Tyr Trp Pro His Phe	Val Thr Val Thr Val	Leu
	680	685	690
Phe Ala Leu Val	Leu Ser Gly Ala Leu	Ile Ile Leu Val Ala	Ser
	695	700	705
Pro Leu Arg Ala	Leu Arg Ala Arg Gly	Lys Val Gln Gly Cys	Glu
	710	715	720
Thr Leu Arg Pro	Gly Glu Lys Ala Pro	Leu Ser Arg Glu Gln	His
	725	730	735
Leu Gln Ser Pro	Lys Glu Cys Arg Thr	Ser Ala Ser Asp Val	Asp
	740	745	750
Ala Asp Asn Asn	Cys Leu Gly Thr Glu	Val Ala	
	755	760	

<210> 278  
<211> 24  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 278  
ctgctggtga aatctggcgt ggag 24

<210> 279  
<211> 24  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 279  
gtctggtcct ggctgtccac ccag 24

<210> 280  
<211> 45  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 280  
catcttgtca tgtacctggg aaccaccaca gggtcgctcc acaag 45

<210> 281  
<211> 2320  
<212> DNA  
<213> Homo sapiens

<400> 281  
aggggtccctt agccggggcgc agggcgcgca gccaggctg agatccgcg 50  
cttcgtaga agtgagcatg gctgggcagc gagtgttct tctagtgggc 100  
ttccttctcc ctggggctct gctctcagag gctgccaaaa tcctgacaat 150  
atctacagta ggtggaagcc attatctact gatggaccgg gtttctcaga 200  
ttcttcaaga tcacgggtcat aatgtcacca tgcttaacca caaaagaggt 250  
ccttttatgc cagattttaa aaaggaagaa aaatcatatc aagttatcag 300  
ttggcttgca cctgaagatc atcaaagaga atttaaaaag agttttgatt 350  
tctttctgga agaaacttta ggtggcagag gaaaatttga aaacttatta 400  
aatgttctag aatacttggc gttgcagtc agtcattttt taaatagaaa 450



ggatatcatg gattccttaa agaatgagaa ctctgacatg gtgatagttg 500  
aaacttttga ctactgtcct ttcctgattg ctgagaagct tgggaagcca 550  
tttgtggcca ttctttccac ttcatctggc tctttggaat ttgggctacc 600  
aatccccttg tcttatgttc cagtattccg ttccttgctg actgatcaca 650  
tggacttctg gggccgagtg aagaattttc tgatgttctt tagtttctgc 700  
aggaggcaac agcacatgca gtctacattt gacaacacca tcaaggaaca 750  
tttcacagaa ggctctaggc cagttttgtc tcactcttcta ctgaaagcag 800  
agttgtgggt cattaactct gactttgcct ttgattttgc tcgacctctg 850  
cttcccaaca ctgtttatgt tggaggcttg atggaaaaac ctattaaacc 900  
agtaccacaa gacttgagga acttcattgc caagtttggg gactctggtt 950  
ttgtccttgt gacctggggc tccatggtga acacctgtca gaatccggaa 1000  
atcttcaagg agatgaacaa tgcctttgct cacctacccc aaggggtgat 1050  
atggaagtgt cagtgttctc attggcccaa agatgtccac ctggctgcaa 1100  
atgtgaaaat tgtggactgg ctctctcaga gtgacctcct ggctcaccca 1150  
agcatccgtc tgtttgtcac ccacggcggg cagaatagca taatggaggc 1200  
catccagcat ggtgtgcccc tgggtggggat ccctctcttt ggagaccagc 1250  
ctgaaaacat ggtccgagta gaagccaaaa agtttgggtg ttctattcag 1300  
ttaaagaagc tcaaggcaga gacattggct cttaagatga aacaaatcat 1350  
ggaagacaag agatacaagt ccgcggcagt ggctgccagt gtcactcctg 1400  
gtccccccc gctcagcccc acacagcggc tgggtgggctg gattgaccac 1450  
gtcctccaga cagggggcgc gacgcacctc aagccctatg tctttcagca 1500  
gccctggcat gagcagtacc tgttcgacgt ttttgtgttt ctgctggggc 1550  
tcactctggg gactctatgg ctttgtggga agctgctggg catggctgtc 1600  
tgggtggctgc gtggggccag aaaggtgaag gagacataag gccagggtgca 1650  
gccttggcgg ggtctgtttg gtgggcgatg tcaccatttc tagggagctt 1700  
cccactagtt ctggcagccc cattctctag tccttctagt tatctcctgt 1750  
tttcttgaag aacaggaaaa atggccaaaa atcatccttt ccacttgcta 1800  
attttgtac aaattcatcc ttaactagctc ctgcctgcta gcagaaatct 1850

ttccagtcct cttgtcctcc tttgtttgcc atcagcaagg gctatgctgt 1900  
 gattctgtct ctgagtgact tggaccactg accctcagat ttccagcctt 1950  
 aaaatccacc ttctttctca tgcgcctctc cgaatcacac cctgactctt 2000  
 ccagcctcca tgtccagacc tagtcagcct ctctcactcc tgcccctact 2050  
 atctatcatg gaataacatc caagaaagac accttgcata ttctttcagt 2100  
 ttctgttttg ttctcccaca tattctcttc aatgctcagg aagcctgccc 2150  
 tgtgcttgag agttcagggc cggacacagg ctcacaggtc tccacattgg 2200  
 gtccctgtct ctggtgccc cagtgaagctc cttcttggtt gagcagggcat 2250  
 ggagactgta ggtttccaga tttcctgaaa aataaaagtt tacagcgta 2300  
 tctctcccca acctcactaa 2320

<210> 282

<211> 523

<212> PRT

<213> Homo sapiens

<400> 282

Met	Ala	Gly	Gln	Arg	Val	Leu	Leu	Leu	Val	Gly	Phe	Leu	Leu	Pro
1					5				10					15
Gly	Val	Leu	Leu	Ser	Glu	Ala	Ala	Lys	Ile	Leu	Thr	Ile	Ser	Thr
				20					25					30
Val	Gly	Gly	Ser	His	Tyr	Leu	Leu	Met	Asp	Arg	Val	Ser	Gln	Ile
				35					40					45
Leu	Gln	Asp	His	Gly	His	Asn	Val	Thr	Met	Leu	Asn	His	Lys	Arg
				50					55					60
Gly	Pro	Phe	Met	Pro	Asp	Phe	Lys	Lys	Glu	Glu	Lys	Ser	Tyr	Gln
				65					70					75
Val	Ile	Ser	Trp	Leu	Ala	Pro	Glu	Asp	His	Gln	Arg	Glu	Phe	Lys
				80					85					90
Lys	Ser	Phe	Asp	Phe	Phe	Leu	Glu	Glu	Thr	Leu	Gly	Gly	Arg	Gly
				95					100					105
Lys	Phe	Glu	Asn	Leu	Leu	Asn	Val	Leu	Glu	Tyr	Leu	Ala	Leu	Gln
				110					115					120
Cys	Ser	His	Phe	Leu	Asn	Arg	Lys	Asp	Ile	Met	Asp	Ser	Leu	Lys
				125					130					135
Asn	Glu	Asn	Phe	Asp	Met	Val	Ile	Val	Glu	Thr	Phe	Asp	Tyr	Cys
				140					145					150
Pro	Phe	Leu	Ile	Ala	Glu	Lys	Leu	Gly	Lys	Pro	Phe	Val	Ala	Ile

155										160					165				
Leu	Ser	Thr	Ser	Phe	Gly	Ser	Leu	Glu	Phe	Gly	Leu	Pro	Ile	Pro					
				170					175					180					
Leu	Ser	Tyr	Val	Pro	Val	Phe	Arg	Ser	Leu	Leu	Thr	Asp	His	Met					
				185					190					195					
Asp	Phe	Trp	Gly	Arg	Val	Lys	Asn	Phe	Leu	Met	Phe	Phe	Ser	Phe					
				200					205					210					
Cys	Arg	Arg	Gln	Gln	His	Met	Gln	Ser	Thr	Phe	Asp	Asn	Thr	Ile					
				215					220					225					
Lys	Glu	His	Phe	Thr	Glu	Gly	Ser	Arg	Pro	Val	Leu	Ser	His	Leu					
				230					235					240					
Leu	Leu	Lys	Ala	Glu	Leu	Trp	Phe	Ile	Asn	Ser	Asp	Phe	Ala	Phe					
				245					250					255					
Asp	Phe	Ala	Arg	Pro	Leu	Leu	Pro	Asn	Thr	Val	Tyr	Val	Gly	Gly					
				260					265					270					
Leu	Met	Glu	Lys	Pro	Ile	Lys	Pro	Val	Pro	Gln	Asp	Leu	Glu	Asn					
				275					280					285					
Phe	Ile	Ala	Lys	Phe	Gly	Asp	Ser	Gly	Phe	Val	Leu	Val	Thr	Leu					
				290					295					300					
Gly	Ser	Met	Val	Asn	Thr	Cys	Gln	Asn	Pro	Glu	Ile	Phe	Lys	Glu					
				305					310					315					
Met	Asn	Asn	Ala	Phe	Ala	His	Leu	Pro	Gln	Gly	Val	Ile	Trp	Lys					
				320					325					330					
Cys	Gln	Cys	Ser	His	Trp	Pro	Lys	Asp	Val	His	Leu	Ala	Ala	Asn					
				335					340					345					
Val	Lys	Ile	Val	Asp	Trp	Leu	Pro	Gln	Ser	Asp	Leu	Leu	Ala	His					
				350					355					360					
Pro	Ser	Ile	Arg	Leu	Phe	Val	Thr	His	Gly	Gly	Gln	Asn	Ser	Ile					
				365					370					375					
Met	Glu	Ala	Ile	Gln	His	Gly	Val	Pro	Met	Val	Gly	Ile	Pro	Leu					
				380					385					390					
Phe	Gly	Asp	Gln	Pro	Glu	Asn	Met	Val	Arg	Val	Glu	Ala	Lys	Lys					
				395					400					405					
Phe	Gly	Val	Ser	Ile	Gln	Leu	Lys	Lys	Leu	Lys	Ala	Glu	Thr	Leu					
				410					415					420					
Ala	Leu	Lys	Met	Lys	Gln	Ile	Met	Glu	Asp	Lys	Arg	Tyr	Lys	Ser					
				425					430					435					
Ala	Ala	Val	Ala	Ala	Ser	Val	Ile	Leu	Arg	Ser	His	Pro	Leu	Ser					

	440		445		450
Pro Thr Gln Arg	Leu Val Gly Trp Ile Asp His Val Leu Gln Thr				
	455		460		465
Gly Gly Ala Thr	His Leu Lys Pro Tyr Val Phe Gln Gln Pro Trp				
	470		475		480
His Glu Gln Tyr	Leu Phe Asp Val Phe Val Phe Leu Leu Gly Leu				
	485		490		495
Thr Leu Gly Thr	Leu Trp Leu Cys Gly Lys Leu Leu Gly Met Ala				
	500		505		510
Val Trp Trp Leu	Arg Gly Ala Arg Lys Val Lys Glu Thr				
	515		520		

<210> 283  
 <211> 24  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 283  
 tgcctttgct cacctacccc aagg 24

<210> 284  
 <211> 24  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 284  
 tcaggctggt ctccaaagag aggg 24

<210> 285  
 <211> 45  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 285  
 cccaagatg tccacctggc tgcaaatgtg aaaattgtgg actgg 45

<210> 286  
 <211> 2340  
 <212> DNA  
 <213> Homo sapiens

<400> 286  
 gggctgttga tttgtggggg attttgaaga gaggaggaat aggaggaagg 50

ggttgagggg ctgcctctgg catatgcaca cactcacaca ttctgtcaca 100  
cccgtcacac acacatacca tggtctccat cccccaggt ccagccctca 150  
gtgctgtccc atccagcagg gctaccctga agctctggct gcagccctcc 200  
cgtccagtgg gcaggcggct tcatccctcc tttctctccc aaagcccaac 250  
tgctgtcact gcatgctctg ccaaggagga gggaaactgca gtgacagcag 300  
gagtaagagt gggaggcagg acagagctgg gacacaggta tggagagggg 350  
gttcagcgag cctagagagg gcagactatc agggtgccgg cggtgagaat 400  
ccaggagag gagcggaaac agaagagggg cagaagaccg gggcacttgt 450  
gggttgaga gccctcagc catgttgga gccaaagccac actggctacc 500  
aggtccccta cacagtcccg ggctgccctt gggtctgggtg cttctggccc 550  
tgggggcccgg gtgggcccag gaggggtcag agcccgtcct gctggagggg 600  
gagtgcctgg tgggtctgtga gcctggccga gctgctgcag gggggcccgg 650  
gggagcagcc ctgggagagg cccccctgg gcgagtggca tttgctgcgg 700  
tccgaagcca ccaccatgag ccagcagggg aaaccggcaa tggcaccagt 750  
ggggccatct acttcgacca ggtcctgggtg aacgagggcg gtggctttga 800  
ccgggcctct ggctccttcg tagccctgt ccgggggtgtc tacagcttcc 850  
ggttccatgt ggtgaagggtg tacaaccgcc aaactgtcca ggtgagcctg 900  
atgctgaaca cgtggcctgt catctcagcc tttgccaatg atcctgacgt 950  
gaccggggag gcagccacca gctctgtgt actgcccttg gaccctgggg 1000  
accgagtgtc tctgcgctg cgtcggggga atctactggg tggttggaaa 1050  
tactcaagtt tctctggctt cctcatcttc cctctctgag gaccaagtc 1100  
tttcaagcac aagaatccag cccctgacaa ctttcttctg ccctctcttg 1150  
ccccagaaac agcagaggca ggagagagac tccctctggc tcctatccca 1200  
cctctttgca tgggaccctg tgccaaacac ccaagtttaa gagaagagta 1250  
gagctgtggc atctccagac caggcctttc caccaccca cccccagtta 1300  
ccctcccagc cacctgctgc atctgttcct gcctgcagcc ctaggatcag 1350  
ggcaaggttt ggcaagaagg aagatctgca ctactttgcg gcctctgctc 1400  
ctccggttcc cccaccccag cttcctgctc aatgctgatc agggacaggt 1450

ggcgaggtg agcctgacag gccccacag gagcccagat ggacaagcct 1500  
 cagcgtaccc tgcaggcttc ttcctgtgag gaaagccagc atcacggatc 1550  
 tcagccagca ccgtcagaag ctgagccagc accgtatggg ctagggtggg 1600  
 aggctcagcc acaggcagaa ggggtgggaag ggcctggagt ctgtggctgg 1650  
 tgaggaagga aggaggggtgt attgtctaga ctgaacatgg tacacattct 1700  
 gcatgtatag cagagcagcc agcaggtagc aatcctggct gtccttctat 1750  
 gctggatccc agatggactc tggcccttac ctccccacct gagattaggg 1800  
 tgagtgtgtt tgctctggct gagagcagag ctgagagcag gtatacagag 1850  
 ctggaagtgg accatggaaa acatcgataa ccatgcatcc tcttgcttgg 1900  
 ccacctcctg aaactgctcc acctttgaag tttgaacttt agtccctcca 1950  
 cactctgact gctgcctcct tcctcccagc tctctcactg agttatcttc 2000  
 actgtacctg ttccagcata tccccactat ctctctttct cctgatctgt 2050  
 gctgtcttat tctcctcctt aggcttccta ttacctggga ttccatgatt 2100  
 cattccttca gacctctcc tgccagtatg ctaaaccctc cctctctctt 2150  
 tcttatcccg ctgtcccatt ggcccagcct ggatgaatct atcaataaaa 2200  
 caactagaga atggtgggtca gtgagacact atagaattac taaggagaag 2250  
 atgcctctgg agtttggatc ggggtgttaca ggtacaagta ggtatgttgc 2300  
 agaggaaaat aaatatcaaa ctgtatacta aaattaaaaa 2340

<210> 287

<211> 205

<212> PRT

<213> Homo sapiens

<400> 287

Met	Leu	Gly	Ala	Lys	Pro	His	Trp	Leu	Pro	Gly	Pro	Leu	His	Ser
1				5					10					15
Pro	Gly	Leu	Pro	Leu	Val	Leu	Val	Leu	Leu	Ala	Leu	Gly	Ala	Gly
			20						25					30
Trp	Ala	Gln	Glu	Gly	Ser	Glu	Pro	Val	Leu	Leu	Glu	Gly	Glu	Cys
				35					40					45
Leu	Val	Val	Cys	Glu	Pro	Gly	Arg	Ala	Ala	Ala	Gly	Gly	Pro	Gly
				50					55					60
Gly	Ala	Ala	Leu	Gly	Glu	Ala	Pro	Pro	Gly	Arg	Val	Ala	Phe	Ala
				65					70					75

Ala	Val	Arg	Ser	His	His	His	Glu	Pro	Ala	Gly	Glu	Thr	Gly	Asn	
				80					85					90	
Gly	Thr	Ser	Gly	Ala	Ile	Tyr	Phe	Asp	Gln	Val	Leu	Val	Asn	Glu	
				95					100					105	
Gly	Gly	Gly	Phe	Asp	Arg	Ala	Ser	Gly	Ser	Phe	Val	Ala	Pro	Val	
				110					115					120	
Arg	Gly	Val	Tyr	Ser	Phe	Arg	Phe	His	Val	Val	Lys	Val	Tyr	Asn	
				125					130					135	
Arg	Gln	Thr	Val	Gln	Val	Ser	Leu	Met	Leu	Asn	Thr	Trp	Pro	Val	
				140					145					150	
Ile	Ser	Ala	Phe	Ala	Asn	Asp	Pro	Asp	Val	Thr	Arg	Glu	Ala	Ala	
				155					160					165	
Thr	Ser	Ser	Val	Leu	Leu	Pro	Leu	Asp	Pro	Gly	Asp	Arg	Val	Ser	
				170					175					180	
Leu	Arg	Leu	Arg	Arg	Gly	Asn	Leu	Leu	Gly	Gly	Trp	Lys	Tyr	Ser	
				185					190					195	
Ser	Phe	Ser	Gly	Phe	Leu	Ile	Phe	Pro	Leu						
				200					205						

<210> 288

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 288

aggcagccac cagctctgtg ctac 24

<210> 289

<211> 27

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 289

cagagaggga agatgaggaa gccagag 27

<210> 290

<211> 42

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 290  
ctgtgtctact gcccttggac cctggggacc gagtgtctct gc 42

<210> 291

<211> 1570

<212> DNA

<213> Homo sapiens

<400> 291

gctgtttctc tcgcgccacc actggccgcc ggccgcagct ccagggtgtcc 50  
tagccgcca gccctgacgc cgtcccggga cccctgtgct ctgcgcgaag 100  
ccctggcccc gggggccggg gcatgggcca ggggcgcggg gtgaagcggc 150  
ttcccgcggg gccgtgactg ggccgggcttc agccatgaag accctcatag 200  
ccgcctactc cggggctctg cgcggcgagc gtcaggccga ggctgaccgg 250  
agccagcgct ctcacggagg acctgcgctg tcgcgcgagg ggtctgggag 300  
atggggcact ggatccagca tcctctccgc cctccaggac ctcttctctg 350  
tcacctggct caatagggtcc aagggtgaaa agcagctaca ggtcatctca 400  
gtgtctccagt gggctctgtc cttccttgta ctgggagtgg cctgcagtgc 450  
catcctcatg tacatattct gactgattg ctggctcatc gctgtgtct 500  
acttcacttg gctggtgttt gactggaaca cacccaagaa aggtggcagg 550  
aggtcacagt ggggtccgaaa ctgggctgtg tggcgctact ttcgagacta 600  
ctttcccatc cagctggtga agacacacaa cctgctgacc accaggaact 650  
atatctttgg ataccacccc catggtatca tgggcctggg tgccttctgc 700  
aacttcagca cagaggccac agaagtgagc aagaagttcc caggcatacg 750  
gccttacctg gctacactgg caggcaactt ccgaatgcct gtgttgaggg 800  
agtacctgat gtctggaggt atctgccctg tcagccggga caccatagac 850  
tatttgcttt caaagaatgg gagtggcaat gctatcatca tcgtgggtcgg 900  
gggtgctgct gagtctctga gctccatgcc tggcaagaat gcagtcaccc 950  
tgcggaaccg caagggtttt gtgaaactgg ccttgcgtca tggagctgac 1000  
ctggttccca tctactcctt tggagagaat gaagtgtaca agcagggtgat 1050  
cttcgaggag ggctcctggg gccgatgggt ccagaagaag ttccagaaat 1100  
acattggttt cgccccatgc atcttccatg gtcgaggcct cttctcctcc 1150  
gacacctggg ggctggtgcc ctactccaag cccatcacca ctgttggtggg 1200



agagcccatc accatcccca agctggagca cccaaccag caagacatcg 1250  
 acctgtacca caccatgtac atggaggccc tggatgaagct cttcgacaag 1300  
 cacaagacca agttcggcct cccggagact gaggtcctgg aggtgaactg 1350  
 agccagcctt cggggccaat tccctggagg aaccagctgc aaatcacttt 1400  
 tttgctctgt aaatttggaa gtgtcatggg tgtctgtggg ttatttataa 1450  
 gaaattataa caattttgct aaaccaaaaa aaaaaaaaaa aaaaaaaaaa 1500  
 aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 1550  
 aaaaaaaaaa aaaaaaaaaa 1570

<210> 292

<211> 388

<212> PRT

<213> Homo sapiens

<400> 292

Met	Lys	Thr	Leu	Ile	Ala	Ala	Tyr	Ser	Gly	Val	Leu	Arg	Gly	Glu	1	5	10	15
Arg	Gln	Ala	Glu	Ala	Asp	Arg	Ser	Gln	Arg	Ser	His	Gly	Gly	Pro	20	25	30	
Ala	Leu	Ser	Arg	Glu	Gly	Ser	Gly	Arg	Trp	Gly	Thr	Gly	Ser	Ser	35	40	45	
Ile	Leu	Ser	Ala	Leu	Gln	Asp	Leu	Phe	Ser	Val	Thr	Trp	Leu	Asn	50	55	60	
Arg	Ser	Lys	Val	Glu	Lys	Gln	Leu	Gln	Val	Ile	Ser	Val	Leu	Gln	65	70	75	
Trp	Val	Leu	Ser	Phe	Leu	Val	Leu	Gly	Val	Ala	Cys	Ser	Ala	Ile	80	85	90	
Leu	Met	Tyr	Ile	Phe	Cys	Thr	Asp	Cys	Trp	Leu	Ile	Ala	Val	Leu	95	100	105	
Tyr	Phe	Thr	Trp	Leu	Val	Phe	Asp	Trp	Asn	Thr	Pro	Lys	Lys	Gly	110	115	120	
Gly	Arg	Arg	Ser	Gln	Trp	Val	Arg	Asn	Trp	Ala	Val	Trp	Arg	Tyr	125	130	135	
Phe	Arg	Asp	Tyr	Phe	Pro	Ile	Gln	Leu	Val	Lys	Thr	His	Asn	Leu	140	145	150	
Leu	Thr	Thr	Arg	Asn	Tyr	Ile	Phe	Gly	Tyr	His	Pro	His	Gly	Ile	155	160	165	
Met	Gly	Leu	Gly	Ala	Phe	Cys	Asn	Phe	Ser	Thr	Glu	Ala	Thr	Glu	170	175	180	

Val Ser Lys Lys Phe Pro Gly Ile Arg	Pro Tyr Leu Ala Thr Leu
185	190 195
Ala Gly Asn Phe Arg Met Pro Val Leu	Arg Glu Tyr Leu Met Ser
200	205 210
Gly Gly Ile Cys Pro Val Ser Arg Asp	Thr Ile Asp Tyr Leu Leu
215	220 225
Ser Lys Asn Gly Ser Gly Asn Ala Ile	Ile Ile Val Val Gly Gly
230	235 240
Ala Ala Glu Ser Leu Ser Ser Met Pro	Gly Lys Asn Ala Val Thr
245	250 255
Leu Arg Asn Arg Lys Gly Phe Val Lys	Leu Ala Leu Arg His Gly
260	265 270
Ala Asp Leu Val Pro Ile Tyr Ser Phe	Gly Glu Asn Glu Val Tyr
275	280 285
Lys Gln Val Ile Phe Glu Glu Gly Ser	Trp Gly Arg Trp Val Gln
290	295 300
Lys Lys Phe Gln Lys Tyr Ile Gly Phe	Ala Pro Cys Ile Phe His
305	310 315
Gly Arg Gly Leu Phe Ser Ser Asp Thr	Trp Gly Leu Val Pro Tyr
320	325 330
Ser Lys Pro Ile Thr Thr Val Val Gly	Glu Pro Ile Thr Ile Pro
335	340 345
Lys Leu Glu His Pro Thr Gln Gln Asp	Ile Asp Leu Tyr His Thr
350	355 360
Met Tyr Met Glu Ala Leu Val Lys Leu	Phe Asp Lys His Lys Thr
365	370 375
Lys Phe Gly Leu Pro Glu Thr Glu Val	Leu Glu Val Asn
380	385

<210> 293

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 293

gctgacctgg ttcccatcta ctcc 24

<210> 294

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 294

cccacagaca cccatgacac ttcc 24

<210> 295

<211> 50

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 295

aagaatgaat tgtacaaagc aggtgatcctt cgaggagggc tcctggggcc 50

<210> 296

<211> 3060

<212> DNA

<213> Homo sapiens

<400> 296

gggcgggcggg atggggggcgg gggcgggcgg gcgcgcgact cgctgaggcc 50  
ccgacgcagg gccggggcgg gcccagggcc gaggagcgcg gcggccagag 100  
cgggggcgcg gaggcgacgc cggggacgcc cgcgcgacga gcaggtggcg 150  
gcggctgcag gcttgtccag ccggaagccc tgagggcagc tgttcccact 200  
ggctctgctg accttgtgcc ttggacggct gtcctcagcg agggggccgtg 250  
caccgcctcc tgagcagcgc catgggcctg ctggccttcc tgaagacca 300  
gttcgtgctg cacctgctgg tcggctttgt cttcgtggtg agtggctctg 350  
tcatcaactt cgtccagctg tgcacgctgg cgctctggcc ggtcagcaag 400  
cagctctacc gccgcctcaa ctgccgcctc gcctactcac tctggagcca 450  
actggtcatg ctgctggagt ggtggtcctg cacggagtgt aactgttca 500  
cggaccaggc cacggtagag cgctttggga aggagcacgc agtcatcatc 550  
ctcaaccaca acttcgagat cgacttcctc tgtgggtgga ccatgtgtga 600  
gcgcttcgga gtgctgggga gctccaaggt cctcgctaag aaggagctgc 650  
tctacgtgcc cctcatcggc tggacgtggt actttctgga gattgtgttc 700  
tgcaagcgga agtgggagga ggaccgggac accgtggtcg aagggtgag 750  
gcgcctgtcg gactaccccg agtacatgtg gtttctcctg tactgcgagg 800

ggacgcgctt cacggagacc aagcaccgcg ttagcatgga ggtggcggct 850  
gctaaggggc ttcctgtcct caagtaccac ctgctgccgc ggaccaaggg 900  
cttcaccacc gcagtcaagt gcctccgggg gacagtcgca gctgtctatg 950  
atgtaaccct gaacttcaga ggaaacaaga acccgtcctt gctggggatc 1000  
ctctacggga agaagtacga ggcggacatg tgcgtgagga gatttcctct 1050  
ggaagacatc ccgctggatg aaaaggaagc agctcagtgg cttcataaac 1100  
tgtaccagga gaaggacgcg ctccaggaga tatataatca gaagggcatg 1150  
tttcagggg agcagtttaa gcctgcccgg aggccgtgga ccctcctgaa 1200  
cttcctgtcc tgggccacca ttctcctgtc tcccctcttc agttttgtct 1250  
tgggcgtctt tgccagcggg tcacctctcc tgatcctgac tttcttgggg 1300  
tttgtgggag cagcttcctt tggagtctgc agactgatag gagaatcgct 1350  
tgaacctggg aggtggagat tgcagtgagc tgagatggca tcaactgtact 1400  
ccagcctagg caacagagca agactcagtc tcaaaaaaaaa aaaaaaaca 1450  
aaaaacccca gaaattctgg agttgaactg tgtagttact gacatgaaaa 1500  
attcactaga ggctgaacag cagatttgag caggcagaaa aaaatcagca 1550  
agcttgaaga tggtaacctg agatttttca ggctaataa aaaagaatga 1600  
aggaaaatta acagcctcag agacccatgg tgcaccgtca cacaaatcaa 1650  
catatgcatg atgagagtcc cagaaggaga ggagagaaag ggtcagaaag 1700  
aatggccaca agctgatgaa aaacagtaac ctaccactc aggaagctca 1750  
gtgaactcca atgaggatga atatcagaga tccacaccta gatatttcat 1800  
aatcaaagtg tcaaatagca aagaatcttg aaagcagcaa gagatgagca 1850  
acttatcttg ttcaaaggat ctttgatcag attaacagct catttctcct 1900  
cagaaatcat gggagccagg agatagtggg atgaacactg ttgaaggcaa 1950  
aaccttcaac tgtaattatt ggacttttga gtcttagatg gtcttgacct 2000  
ctttgtcttc agggacagtt tttcaattta atccctaata acaattagtc 2050  
aagcttcctt gacctgtagg aaggcctgtc tttaggccgg gcacagtggc 2100  
ttacacctgt aatcccagca ctttgggagg ccagacggg tggatcattt 2150  
ggggtcaggc tgatctcaaa ctctgagtt caggtgatct gcccgcctca 2200  
gcctcccaaa gtgttgtgat tgcaggcgtg agccactgcg cctggccgga 2250

atttcttttt aaggctgaat gatgggggcc aggcacgatg gctcacgcct 2300  
 gtgatcccaa gtagcttga ttgtaaacaat gcaccaccaa gcctggctaa 2350  
 tttttgtatt tttagtagag acgtgttagc caggctgggc tcgatctcct 2400  
 gacctcaagt gaccacctgc ctcagcctcc caaagtactg ggattacagg 2450  
 cgtgagccac tgtgcctggc cttgagcatc ttgtgatgtg cttattggcc 2500  
 atttgtatat cttctatctt ctttggggaa atgtctgttc aagtcctttg 2550  
 cctttttaaa tttttattat ttatttattt atttattttg agacagggtc 2600  
 ttgttctgtt gccaggctg gactacagtg gcacagtctt ggctcactgc 2650  
 agcctcgacc tcttgggctg cagtgatcct cccacctcag cctcccttgt 2700  
 agctgtattt ttttgtattt tgtattttgt agctgtagtt tttgtatttt 2750  
 ttgtggagac agcatttcac catgatgcc aggctgggtc tgaactcctg 2800  
 agctcaagtg atctgcctgc ttcagcctcc caaagtgtg ggattacaga 2850  
 catgagccac tgcacctggc aaactcccaa aattcaacac acacacacaa 2900  
 aaaaccacct gattcaaaat gggcagagg ggcgggtgtg gcccacta 2950  
 ccaggagac tgaagtggga ggatcgcttg ggcagagaa gtcgaggctg 3000  
 cagtgagtcg aggttgtgcg actgcattcc agcctggaca acagagtgag 3050  
 accctgtctc 3060

<210> 297

<211> 368

<212> PRT

<213> Homo sapiens

<400> 297

Met	Gly	Leu	Leu	Ala	Phe	Leu	Lys	Thr	Gln	Phe	Val	Leu	His	Leu
1				5					10					15

Leu	Val	Gly	Phe	Val	Phe	Val	Val	Ser	Gly	Leu	Val	Ile	Asn	Phe
				20					25					30

Val	Gln	Leu	Cys	Thr	Leu	Ala	Leu	Trp	Pro	Val	Ser	Lys	Gln	Leu
				35					40					45

Tyr	Arg	Arg	Leu	Asn	Cys	Arg	Leu	Ala	Tyr	Ser	Leu	Trp	Ser	Gln
				50					55					60

Leu	Val	Met	Leu	Leu	Glu	Trp	Trp	Ser	Cys	Thr	Glu	Cys	Thr	Leu
				65					70					75

Phe Thr Asp Gln Ala Thr Val Glu Arg Phe Gly Lys Glu His Ala

80										85					90				
Val	Ile	Ile	Leu	Asn	His	Asn	Phe	Glu	Ile	Asp	Phe	Leu	Cys	Gly					
				95					100					105					
Trp	Thr	Met	Cys	Glu	Arg	Phe	Gly	Val	Leu	Gly	Ser	Ser	Lys	Val					
				110					115					120					
Leu	Ala	Lys	Lys	Glu	Leu	Leu	Tyr	Val	Pro	Leu	Ile	Gly	Trp	Thr					
				125					130					135					
Trp	Tyr	Phe	Leu	Glu	Ile	Val	Phe	Cys	Lys	Arg	Lys	Trp	Glu	Glu					
				140					145					150					
Asp	Arg	Asp	Thr	Val	Val	Glu	Gly	Leu	Arg	Arg	Leu	Ser	Asp	Tyr					
				155					160					165					
Pro	Glu	Tyr	Met	Trp	Phe	Leu	Leu	Tyr	Cys	Glu	Gly	Thr	Arg	Phe					
				170					175					180					
Thr	Glu	Thr	Lys	His	Arg	Val	Ser	Met	Glu	Val	Ala	Ala	Ala	Lys					
				185					190					195					
Gly	Leu	Pro	Val	Leu	Lys	Tyr	His	Leu	Leu	Pro	Arg	Thr	Lys	Gly					
				200					205					210					
Phe	Thr	Thr	Ala	Val	Lys	Cys	Leu	Arg	Gly	Thr	Val	Ala	Ala	Val					
				215					220					225					
Tyr	Asp	Val	Thr	Leu	Asn	Phe	Arg	Gly	Asn	Lys	Asn	Pro	Ser	Leu					
				230					235					240					
Leu	Gly	Ile	Leu	Tyr	Gly	Lys	Lys	Tyr	Glu	Ala	Asp	Met	Cys	Val					
				245					250					255					
Arg	Arg	Phe	Pro	Leu	Glu	Asp	Ile	Pro	Leu	Asp	Glu	Lys	Glu	Ala					
				260					265					270					
Ala	Gln	Trp	Leu	His	Lys	Leu	Tyr	Gln	Glu	Lys	Asp	Ala	Leu	Gln					
				275					280					285					
Glu	Ile	Tyr	Asn	Gln	Lys	Gly	Met	Phe	Pro	Gly	Glu	Gln	Phe	Lys					
				290					295					300					
Pro	Ala	Arg	Arg	Pro	Trp	Thr	Leu	Leu	Asn	Phe	Leu	Ser	Trp	Ala					
				305					310					315					
Thr	Ile	Leu	Leu	Ser	Pro	Leu	Phe	Ser	Phe	Val	Leu	Gly	Val	Phe					
				320					325					330					
Ala	Ser	Gly	Ser	Pro	Leu	Leu	Ile	Leu	Thr	Phe	Leu	Gly	Phe	Val					
				335					340					345					
Gly	Ala	Ala	Ser	Phe	Gly	Val	Arg	Arg	Leu	Ile	Gly	Glu	Ser	Leu					
				350					355					360					
Glu	Pro	Gly	Arg	Trp	Arg	Leu	Gln												

<210> 298  
<211> 24  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 298  
cttcctctgt gggtaggacca tgtg 24

<210> 299  
<211> 21  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 299  
gccacctcca tgctaacgcg g 21

<210> 300  
<211> 45  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 300  
ccaaggtcct cgctaagaag gagctgctct acgtgccct catcg 45

<210> 301  
<211> 1334  
<212> DNA  
<213> Homo sapiens

<400> 301  
gatattcttt atttttaaga atctgaagta ctatgcatca ctccctccaa 50  
tgtcctgggg cagccaccag gcatattcat ctttgtgtgt gtttttcttt 100  
tgcttttagca ctggggcact tcttgcttat ttctttggta ggaaaggggc 150  
tcagtttgtc ttgtgggggtt ggtggcaggc aggccggctt acgcctgata 200  
cggccctggg ttagaaggga agggaagata aacttttata caaatgggga 250  
tagctggggg ctgagacctg cttcctcagt aaaattcctg ggatctgcct 300  
ataccttctt ttctctaacc tggcataccc tgcttaaagc ctctcagggc 350  
ttctctctgt tcttaggatc aaagtattta gagctacaag agccctcatg 400

gtctggcccc tgccccctg gccagcttca ttgtacatgt ggtgttctct 450  
 tgtcggttcct gtaatgtggt atgcatggg gtctttgcac aagcctttcc 500  
 tctttggctg gacactgttc cctgcccccc ccatactctt cctacttaat 550  
 atgtagtcat cctgcagatt tcaattctaa catcattttc tccagggatc 600  
 ctggcctgac agaattctcat cttgtttaat gctctcataa gaccacttgt 650  
 ttcccttttg cagcacttgc cactcagttg tatctttatg tgcgtttgtg 700  
 gttgtatggg ttgtgtctgt tccccagaat gccagctct gagctgcgtg 750  
 agggtaagg gcattgctgt gcctgccagg tatagtgcct acatgtggtg 800  
 ggtgctcatg ttttagagac taaatggagg aggagatgag gaaaagattg 850  
 aaatctctca gttcaccaga tgggttaggg ccagcattg taaattcaca 900  
 cgttgactgt gcttgtgaat tatctgggga tgcaggtcct gattcagtag 950  
 gccaggttg ggcattctta acaaaactccc acgtgatgct gatgctgggc 1000  
 ctatgaacta tactaaatag taagaatcta tggagccagg ctgggcatgg 1050  
 tggctcacac ctatgatccc agcactttgg gaggctgagg caggctgac 1100  
 acctggagtc aggatttcaa gactagcctg gccaacatgg tggaacccca 1150  
 tctgtactaa aaatacacia attagctggg catggtggca catgcctgta 1200  
 gtcccagcta cttgggaggg tgaagcaaga gaatcgcttg aacctgggag 1250  
 gcggagggtg cagtgagccg agatcaggcc actgtattcc aaccagggtg 1300  
 acagagtgag actctatgtc caaaaaaaaa aaaa 1334

<210> 302

<211> 143

<212> PRT

<213> Homo sapiens

<400> 302

Met	His	His	Ser	Leu	Gln	Cys	Pro	Gly	Ala	Ala	Thr	Arg	His	Ile
1				5					10					15

His	Leu	Cys	Val	Cys	Phe	Ser	Phe	Ala	Leu	Ala	Leu	Gly	His	Phe
			20						25					30

Leu	Leu	Ile	Ser	Leu	Val	Gly	Lys	Gly	Leu	Ser	Leu	Ser	Cys	Gly
			35						40					45

Val	Gly	Gly	Arg	Gln	Ala	Gly	Leu	Arg	Leu	Ile	Arg	Pro	Trp	Val
			50						55					60

Arg	Arg	Glu	Gly	Lys	Ile	Asn	Phe	Tyr	Thr	Asn	Gly	Asp	Ser	Trp
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----



	65		70		75
Gly Leu Arg Pro Ala Ser Ser Val Lys Phe Leu Gly Ser Ala Tyr					
	80		85		90
Thr Phe Phe Ser Leu Thr Trp His Thr Leu Leu Lys Ala Ser Gln					
	95		100		105
Gly Phe Ser Leu Phe Leu Gly Ser Lys Tyr Leu Glu Leu Gln Glu					
	110		115		120
Pro Ser Trp Ser Gly Pro Cys Pro Pro Gly Gln Leu His Cys Thr					
	125		130		135
Cys Gly Val Leu Leu Ser Phe Leu					
	140				

<210> 303

<211> 1768

<212> DNA

<213> Homo sapiens

<400> 303

```

ggctggactg gaactcctgg tcccaagtga tccaccgcc tcagcctccc 50
aaggtgctgt gattataggt gtaagccacc gtgtctggcc tctgaacaac 100
tttttcagca actaaaaaag ccacaggagt tgaactgcta ggattctgac 150
tatgctgtgg tggctagtgc tcctactcct acctacatta aaatctgttt 200
tttgttctct tgtaactagc ctttaccttc ctaacacaga ggatctgtca 250
ctgtggctct ggcccaaacc tgaccttcac tctggaacga gaacagaggt 300
ttctaccac accgtcccct cgaagccggg gacagcctca ccttgctggc 350
ctctcgctgg agcagtgcc tcaccaactg tctcacgtct ggaggcactg 400
actcgggcag tgcaggtagc tgagcctctt ggtagctgcg gctttcaagg 450
tgggccttgc cctggccgta gaagggattg acaagccga agatttcata 500
ggcgatggct cccactgccc aggcatcagc cttgctgtag tcaatcactg 550
ccctggggcc aggacgggcc gtggacacct gctcagaagc agtgggtgag 600
acatcacgct gcccgcccat ctaacctttt catgtcctgc acatcacctg 650
atccatgggc taatctgaac tctgtcccaa ggaaccaga gcttgagtga 700
gctgtggctc agaccagaa ggggtctgct tagaccacct ggtttatgtg 750
acaggacttg cattctcctg gaacatgagg gaacgccgga ggaaagcaaa 800
gtggcagggg aggaacttgt gccaaattat gggtcagaaa agatggaggt 850

```

gttgggttat cacaaggcat cgagtctcct gcattcagtg gacatgtggg 900  
 ggaagggctg ccgatggcgc atgacacact cgggactcac ctctggggcc 950  
 atcagacagc cgtttccgcc ccgatccacg taccagctgc tgaagggcaa 1000  
 ctgcaggccg atgtctctcat cagccaggca gcagccaaaa tctgcgatca 1050  
 ccagccaggg gcagccgtct gggaaggagc aagcaaagtg accatttctc 1100  
 ctcccctcct tccctctgag aggccctcct atgtccctac taaagccacc 1150  
 agcaagacat agctgacagg ggctaattggc tcagtgttgg cccaggaggt 1200  
 cagcaaggcc tgagagctga tcagaagggc ctgctgtgcg aacacggaaa 1250  
 tgcctccagt aagcacaggc tgcaaaatcc ccaggcaaag gactgtgtgg 1300  
 ctcaatttaa atcatgttct agtaattgga gctgtcccca agaccaaagg 1350  
 agctagagct tggttcaa at gatctccaag ggcccttata cccaggaga 1400  
 ctttgatttg aatttgaaac cccaaatcca aacctaaaga ccagggtgat 1450  
 taagaatcag ttattgccgg gtgtggtggc ctgtaatgcc aacatttttg 1500  
 gaggccgagg cgggtagatc acctgaggtc aggagttcaa gaccagcctg 1550  
 gccaacatgg tgaaaccct gtctctacta aaaatacaaa aaaactagcc 1600  
 aggcattgtg gtgtgtgcct gtatcccagc tactcgggag gctgagacag 1650  
 gagaattact tgaacctggg aggtgaagga ggctgagaca ggagaatcac 1700  
 ttcagcctga gcaacacagc gagactctgt ctcagaaaaa ataaaaaaag 1750  
 aattatgggtt atttgtaa 1768

<210> 304  
 <211> 109  
 <212> PRT  
 <213> Homo sapiens

<400> 304  
 Met Leu Trp Trp Leu Val Leu Leu Leu Leu Pro Thr Leu Lys Ser  
 1 5 10 15  
 Val Phe Cys Ser Leu Val Thr Ser Leu Tyr Leu Pro Asn Thr Glu  
 20 25 30  
 Asp Leu Ser Leu Trp Leu Trp Pro Lys Pro Asp Leu His Ser Gly  
 35 40 45  
 Thr Arg Thr Glu Val Ser Thr His Thr Val Pro Ser Lys Pro Gly  
 50 55 60  
 Thr Ala Ser Pro Cys Trp Pro Leu Ala Gly Ala Val Pro Ser Pro

	65		70		75
Thr Val Ser Arg Leu Glu Ala Leu Thr Arg Ala Val Gln Val Ala					
	80		85		90
Glu Pro Leu Gly Ser Cys Gly Phe Gln Gly Gly Pro Cys Pro Gly					
	95		100		105
Arg Arg Arg Asp					

<210> 305  
 <211> 989  
 <212> DNA  
 <213> Homo sapiens

<400> 305  
 gcgggcccgc gagtccgaga cctgtcccag gagctccagc tcacgtgacc 50  
 tgtcactgcc tcccgccgcc tcctgcccgc gccatgaccc agccggtgcc 100  
 ccggctctcc gtgcccgcgc cgctggccct gggctcagcc gcactgggcg 150  
 ccgccttcgc cactggcctc ttctgggga ggcggtgcc cccatggcga 200  
 ggccggcgag agcagtgcct gcttcccccc gaggacagcc gcctgtggca 250  
 gtatcttctg agccgctcca tgcgggagca cccggcgctg cgaagcctga 300  
 ggctgctgac cctggagcag ccgcaggggg attctatgat gacctgcgag 350  
 caggcccagc tcttgccaa cctggcgcg ctcattccagg ccaagaaggc 400  
 gctggacctg ggcaccttca cgggctactc cgccctggcc ctggccctgg 450  
 cgctgcccgc ggacgggcgc gtggtgacct gcgaggtgga cgcgcagccc 500  
 ccggagctgg gacggcccct gtggaggcag gccgaggcgg agcacaagat 550  
 cgacctccgg ctgaagccc ccttgagac cctggacgag ctgctggcgg 600  
 cgggcgaggc cggcaccttc gacgtggccg tgggtgatgc ggacaaggag 650  
 aactgctccg cctactacga gcgctgcctg cagctgctgc gaccggagg 700  
 catctcgcc gtcctcagag tcctgtggcg cgggaagggtg ctgcaacctc 750  
 cgaaagggga cgtggcggcc gactgtgtgc gaaacctaaa cgaacgcctc 800  
 cggcgggacg tcagggtcta catcagcctc ctgcccctgg gcgatggact 850  
 caccttgccc ttcaagatct agggctggcc cctagtgagt gggctcgagg 900  
 gagggttgcc tgggaacccc aggaattgac cctgagtttt aaattcgaaa 950  
 ataaagtggg gctgggacac aaaaaaaaaa aaaaaaaaaa 989

<210> 306  
<211> 262  
<212> PRT  
<213> Homo sapiens

<400> 306

Met	Thr	Gln	Pro	Val	Pro	Arg	Leu	Ser	Val	Pro	Ala	Ala	Leu	Ala
1				5					10					15
Leu	Gly	Ser	Ala	Ala	Leu	Gly	Ala	Ala	Phe	Ala	Thr	Gly	Leu	Phe
				20					25					30
Leu	Gly	Arg	Arg	Cys	Pro	Pro	Trp	Arg	Gly	Arg	Arg	Glu	Gln	Cys
				35					40					45
Leu	Leu	Pro	Pro	Glu	Asp	Ser	Arg	Leu	Trp	Gln	Tyr	Leu	Leu	Ser
				50					55					60
Arg	Ser	Met	Arg	Glu	His	Pro	Ala	Leu	Arg	Ser	Leu	Arg	Leu	Leu
				65					70					75
Thr	Leu	Glu	Gln	Pro	Gln	Gly	Asp	Ser	Met	Met	Thr	Cys	Glu	Gln
				80					85					90
Ala	Gln	Leu	Leu	Ala	Asn	Leu	Ala	Arg	Leu	Ile	Gln	Ala	Lys	Lys
				95					100					105
Ala	Leu	Asp	Leu	Gly	Thr	Phe	Thr	Gly	Tyr	Ser	Ala	Leu	Ala	Leu
				110					115					120
Ala	Leu	Ala	Leu	Pro	Ala	Asp	Gly	Arg	Val	Val	Thr	Cys	Glu	Val
				125					130					135
Asp	Ala	Gln	Pro	Pro	Glu	Leu	Gly	Arg	Pro	Leu	Trp	Arg	Gln	Ala
				140					145					150
Glu	Ala	Glu	His	Lys	Ile	Asp	Leu	Arg	Leu	Lys	Pro	Ala	Leu	Glu
				155					160					165
Thr	Leu	Asp	Glu	Leu	Leu	Ala	Ala	Gly	Glu	Ala	Gly	Thr	Phe	Asp
				170					175					180
Val	Ala	Val	Val	Asp	Ala	Asp	Lys	Glu	Asn	Cys	Ser	Ala	Tyr	Tyr
				185					190					195
Glu	Arg	Cys	Leu	Gln	Leu	Leu	Arg	Pro	Gly	Gly	Ile	Leu	Ala	Val
				200					205					210
Leu	Arg	Val	Leu	Trp	Arg	Gly	Lys	Val	Leu	Gln	Pro	Pro	Lys	Gly
				215					220					225
Asp	Val	Ala	Ala	Glu	Cys	Val	Arg	Asn	Leu	Asn	Glu	Arg	Ile	Arg
				230					235					240
Arg	Asp	Val	Arg	Val	Tyr	Ile	Ser	Leu	Leu	Pro	Leu	Gly	Asp	Gly
				245					250					255

Leu Thr Leu Ala Phe Lys Ile  
260

<210> 307

<211> 2272

<212> DNA

<213> Homo sapiens

<400> 307

ccgccgccgc agccgctacc gccgctgcag ccgctttccg cggcctgggc 50  
ctctcgccgt cagcatgcc aacgccttca agcccgggga cttggtgttc 100  
gctaagatga agggctaccc tcaactggcct gccaggatcg acgacatcgc 150  
ggatggcgcc gtgaagcccc cacccaacaa gtaccccatc tttttctttg 200  
gcacacacga aacagccttc ctgggaccca aggacctgtt cccctacgac 250  
aaatgtaaag acaagtacgg gaagcccaac aagaggaaag gcttcaatga 300  
agggctgtgg gagatccaga acaaccccc agccagctac agcgccctc 350  
cgccagtgag ctctccgac agcgaggccc ccgaggccaa ccccgccgac 400  
ggcagtgcag ctgacgagga cgatgaggac cgggggggtca tggccgtcac 450  
agcggtaacc gccacagctg ccagcgacag gatggagagc gactcagact 500  
cagacaagag tagcgacaac agtggcctga agaggaagac gcctgcgcta 550  
aagatgtcgg tctcgaaacg agcccgaag gcctccagcg acctggatca 600  
ggccagcgtg tccccatccg aagaggagaa ctcggaagc tcatctgagt 650  
cggagaagac cagcgaccag gacttcacac ctgagaagaa agcagcggtc 700  
cgggcgccac ggagggggccc tctgggggga cggaaaaaaaa agaaggcgcc 750  
gtcagcctcc gactccgact ccaaggccga ttcggacggg gccaagcctg 800  
agccggtggc catggcgcgg tcggcgctct cctcctctc ttcctcctcc 850  
tcctccgact ccgatgtgtc tgtgaagaag cctccgaggg gcaggaagcc 900  
agcggagaag cctctcccga agccgcgagg gcggaaaccg aagcctgaac 950  
ggcctccgtc cagctccagc agtgacagt acagcgacga ggtggaccgc 1000  
atcagtgagt ggaagcggcg ggacgaggcg cggaggcgcg agctggaggc 1050  
ccggcgggcg cgagagcagg aggaggagct gcggcgccctg cgggagcagg 1100  
agaaggagga gaaggagcgg aggcgcgagc gggccgaccg cggggagggt 1150  
gagcggggca gcggcggcag cagcggggac gagctcaggg aggacgatga 1200

gcccgctcaag aagcggggac gcaagggccg gggccggggt ccccgctcct 1250  
 cctctgactc cgagcccagag gccgagctgg agagagaggc caagaaatca 1300  
 gcgaagaagc cgcagtcctc aagcacagag cccgccagga aacctggcca 1350  
 gaaggagaag agagtgcggc ccgaggagaa gcaacaagcc aagcccgtga 1400  
 aggtggagcg gacccggaag cgggtccgagg gcttctcgat ggacaggaag 1450  
 gtagagaaga agaaagagcc ctccgtggag gagaagctgc agaagctgca 1500  
 cagtgaatc aagtttgccc taaaggtcga cagcccggac gtgaagaggt 1550  
 gcctgaatgc cctagaggag ctgggaaccc tgcaggtgac ctctcagatc 1600  
 ctccagaaga acacagacgt ggtggccacc ttgaagaaga ttcgccgtta 1650  
 caaagcgaac aaggacgtaa tggagaaggc agcagaagtc tatacccggc 1700  
 tcaagtcgag ggtcctcggc ccaaagatcg aggcggtgca gaaagtgaac 1750  
 aaggctggga tggagaagga gaaggccgag gagaagctgg ccggggagga 1800  
 gctggccggg gaggaggccc ccaggagaa ggcgaggagc aagcccagca 1850  
 ccgatctctc agccccagtg aatggcgagg ccacatcaca gaagggggag 1900  
 agcgagagg acaaggagca cgaggagggt cgggactcgg aggaggggcc 1950  
 aaggtgtggc tcctctgaag acctgcacga cagcgtacgg gaggggtccc 2000  
 acctggacag gcctgggagc gaccggcagg agcgcgagag ggcacggggg 2050  
 gactcggagg ccctggacga ggagagctga gccgcgggca gccaggccca 2100  
 gccccgccc gagctcaggc tgcccctctc cttccccggc tcgcaggaga 2150  
 gcagagcaga gaactgtggg gaacgctgtg ctgtttgtat ttgttcctt 2200  
 gggttttttt ttcctgccta atttctgtga tttccaacca acatgaaatg 2250  
 actataaacg gttttttaat ga 2272

<210> 308

<211> 671

<212> PRT

<213> Homo sapiens

<400> 308

Met	Pro	His	Ala	Phe	Lys	Pro	Gly	Asp	Leu	Val	Phe	Ala	Lys	Met
1					5				10					15

Lys	Gly	Tyr	Pro	His	Trp	Pro	Ala	Arg	Ile	Asp	Asp	Ile	Ala	Asp
				20					25					30

Gly Ala Val Lys Pro Pro Pro Asn Lys Tyr Pro Ile Phe Phe Phe

35										40					45				
Gly	Thr	His	Glu	Thr	Ala	Phe	Leu	Gly	Pro	Lys	Asp	Leu	Phe	Pro					
				50					55					60					
Tyr	Asp	Lys	Cys	Lys	Asp	Lys	Tyr	Gly	Lys	Pro	Asn	Lys	Arg	Lys					
				65					70					75					
Gly	Phe	Asn	Glu	Gly	Leu	Trp	Glu	Ile	Gln	Asn	Asn	Pro	His	Ala					
				80					85					90					
Ser	Tyr	Ser	Ala	Pro	Pro	Pro	Val	Ser	Ser	Ser	Asp	Ser	Glu	Ala					
				95					100					105					
Pro	Glu	Ala	Asn	Pro	Ala	Asp	Gly	Ser	Asp	Ala	Asp	Glu	Asp	Asp					
				110					115					120					
Glu	Asp	Arg	Gly	Val	Met	Ala	Val	Thr	Ala	Val	Thr	Ala	Thr	Ala					
				125					130					135					
Ala	Ser	Asp	Arg	Met	Glu	Ser	Asp	Ser	Asp	Ser	Asp	Lys	Ser	Ser					
				140					145					150					
Asp	Asn	Ser	Gly	Leu	Lys	Arg	Lys	Thr	Pro	Ala	Leu	Lys	Met	Ser					
				155					160					165					
Val	Ser	Lys	Arg	Ala	Arg	Lys	Ala	Ser	Ser	Asp	Leu	Asp	Gln	Ala					
				170					175					180					
Ser	Val	Ser	Pro	Ser	Glu	Glu	Glu	Asn	Ser	Glu	Ser	Ser	Ser	Glu					
				185					190					195					
Ser	Glu	Lys	Thr	Ser	Asp	Gln	Asp	Phe	Thr	Pro	Glu	Lys	Lys	Ala					
				200					205					210					
Ala	Val	Arg	Ala	Pro	Arg	Arg	Gly	Pro	Leu	Gly	Gly	Arg	Lys	Lys					
				215					220					225					
Lys	Lys	Ala	Pro	Ser	Ala	Ser	Asp	Ser	Asp	Ser	Lys	Ala	Asp	Ser					
				230					235					240					
Asp	Gly	Ala	Lys	Pro	Glu	Pro	Val	Ala	Met	Ala	Arg	Ser	Ala	Ser					
				245					250					255					
Ser	Ser	Ser	Ser	Ser	Ser	Ser	Ser	Ser	Asp	Ser	Asp	Val	Ser	Val					
				260					265					270					
Lys	Lys	Pro	Pro	Arg	Gly	Arg	Lys	Pro	Ala	Glu	Lys	Pro	Leu	Pro					
				275					280					285					
Lys	Pro	Arg	Gly	Arg	Lys	Pro	Lys	Pro	Glu	Arg	Pro	Pro	Ser	Ser					
				290					295					300					
Ser	Ser	Ser	Asp	Ser	Asp	Ser	Asp	Glu	Val	Asp	Arg	Ile	Ser	Glu					
				305					310					315					
Trp	Lys	Arg	Arg	Asp	Glu	Ala	Arg	Arg	Arg	Glu	Leu	Glu	Ala	Arg					

320	325	330
Arg Arg Arg Glu Gln Glu Glu Glu Leu	Arg Arg Leu Arg Glu Gln	
335	340	345
Glu Lys Glu Glu Lys Glu Arg Arg Arg	Glu Arg Ala Asp Arg Gly	
350	355	360
Glu Ala Glu Arg Gly Ser Gly Gly Ser	Ser Gly Asp Glu Leu Arg	
365	370	375
Glu Asp Asp Glu Pro Val Lys Lys Arg	Gly Arg Lys Gly Arg Gly	
380	385	390
Arg Gly Pro Pro Ser Ser Ser Asp Ser	Glu Pro Glu Ala Glu Leu	
395	400	405
Glu Arg Glu Ala Lys Lys Ser Ala Lys	Lys Pro Gln Ser Ser Ser	
410	415	420
Thr Glu Pro Ala Arg Lys Pro Gly Gln	Lys Glu Lys Arg Val Arg	
425	430	435
Pro Glu Glu Lys Gln Gln Ala Lys Pro	Val Lys Val Glu Arg Thr	
440	445	450
Arg Lys Arg Ser Glu Gly Phe Ser Met	Asp Arg Lys Val Glu Lys	
455	460	465
Lys Lys Glu Pro Ser Val Glu Glu Lys	Leu Gln Lys Leu His Ser	
470	475	480
Glu Ile Lys Phe Ala Leu Lys Val Asp	Ser Pro Asp Val Lys Arg	
485	490	495
Cys Leu Asn Ala Leu Glu Glu Leu Gly	Thr Leu Gln Val Thr Ser	
500	505	510
Gln Ile Leu Gln Lys Asn Thr Asp Val	Val Ala Thr Leu Lys Lys	
515	520	525
Ile Arg Arg Tyr Lys Ala Asn Lys Asp	Val Met Glu Lys Ala Ala	
530	535	540
Glu Val Tyr Thr Arg Leu Lys Ser Arg	Val Leu Gly Pro Lys Ile	
545	550	555
Glu Ala Val Gln Lys Val Asn Lys Ala	Gly Met Glu Lys Glu Lys	
560	565	570
Ala Glu Glu Lys Leu Ala Gly Glu Glu	Leu Ala Gly Glu Glu Ala	
575	580	585
Pro Gln Glu Lys Ala Glu Asp Lys Pro	Ser Thr Asp Leu Ser Ala	
590	595	600
Pro Val Asn Gly Glu Ala Thr Ser Gln	Lys Gly Glu Ser Ala Glu	



605	610	615
Asp Lys Glu His Glu Glu Gly Arg Asp Ser Glu Glu Gly Pro Arg		
620	625	630
Cys Gly Ser Ser Glu Asp Leu His Asp Ser Val Arg Glu Gly Pro		
635	640	645
Asp Leu Asp Arg Pro Gly Ser Asp Arg Gln Glu Arg Glu Arg Ala		
650	655	660
Arg Gly Asp Ser Glu Ala Leu Asp Glu Glu Ser		
665	670	

<210> 309  
 <211> 3871  
 <212> DNA  
 <213> Homo sapiens

<400> 309  
 gttggttctc ctggatcttc accttaccaa ctgcagatct tgggactcat 50  
 cagcctcaat aattatatta aattaacacc atttgaaaga gaacattggt 100  
 ttcacatga atgctaataa agatgaaaga cttaaagcca gaagccaaga 150  
 ttttcacctt tttcctgctt tgatgatgct aagcatgacc atgttgtttc 200  
 ttccagtcac tggcactttg aagcaaaata ttccaagact caagctaacc 250  
 taaaagact tgctgctttc aaatagctgt attccctttt tgggttcac 300  
 agaaggactg gattttcaaa ctcttctctt agatgaggaa agaggcaggc 350  
 tgctcttggg agccaaagac cacatctttc tactcagtct gggtgactta 400  
 aacaaaaatt ttaagaagat ttattggcct gctgcaaagg aacgggtgga 450  
 attatgtaaa ttagctggga aagatgcca tacagaatgt gcaaatttca 500  
 tcagagtact tcagccctat aacaaaactc acatatatgt gtgtggaact 550  
 ggagcatttc atccaatatg tgggtatatt gatcttgag tctacaagga 600  
 ggatattata ttcaaactag acacacataa tttggagtct ggcagactga 650  
 aatgtccttt cgatcctcag cagccttttg cttcagtaat gacagatgag 700  
 tacctctact ctggaacagc ttctgatttc cttggcaaag atactgcatt 750  
 cactcgatcc cttgggccta ctcatgacca ccactacatc agaactgaca 800  
 tttcagagca ctactggctc aatggagcaa aatttattgg aactttcttc 850  
 ataccagaca cctacaatcc agatgatgat aaaatatatt tcttctttcg 900  
 tgaatcatct caagaaggca gtacctccga taaaaccatc ctttctcgag 950

ttggaagagt ttgtaagaat gatgtaggag gacaacgcag cctgataaac 1000  
aagtggacga cttttcttaa ggccagactg atttgctcaa ttcttggaag 1050  
tgatggggca gatacttact ttgatgagct tcaagatatt tatttactcc 1100  
ccacaagaga tgaaagaaat cctgtagtat atggagtctt tactacaacc 1150  
agctccatct tcaaaggctc tgctgtttgt gtgtatagca tggctgacat 1200  
cagagcagtt tttaatggct catatgctca taaggaaagt gcagaccatc 1250  
gttgggtgca gtatgatggg agaattcctt atccacggcc tggtagatgt 1300  
ccaagcaaaa cctatgaccc actgattaag tccacccgag attttccaga 1350  
tgatgtcatc agtttcataa agcggcactc tgtgatgtat aagtccgtat 1400  
accagttgc aggaggacca acgttcaaga gaatcaatgt ggattacaga 1450  
ctgacacaga tagtggtgga tcatgtcatt gcagaagatg gccagtacga 1500  
tgtaatgttt cttggaacag acattggaac tgtcctcaaa gttgtcagca 1550  
tttcaaagga aaagtggaat atggaagagg tagtgctgga ggagttgcag 1600  
atattcaagc actcatcaat catcttgaac atggaattgt ctctgaagca 1650  
gcaacaattg tacattggtt cccgagatgg attagttcag ctctccttgc 1700  
acagatgcga cacttatggg aaagcttgcg cagactgttg tcttgccaga 1750  
gacccctact gtgcctggga tggaaatgca tgctctcgat atgctcctac 1800  
ttctaaaagg agagctagac gccaagatgt aaaatatggc gacccaatca 1850  
cccagtgctg ggacatcgaa gacagcatta gtcatgaaac tgctgatgaa 1900  
aaggtgattt ttggcattga atttaactca acctttctgg aatgtatacc 1950  
taaatcccaa caagcaacta ttaaattgta tatccagagg tcaggggatg 2000  
agcatcgaga ggagttgaag cccgatgaaa gaatcatcaa aacggaatat 2050  
gggctactga ttcgaagttt gcagaagaag gattctggga tgtattactg 2100  
caaagcccag gagcacactt tcatccacac catagtgaag ctgactttga 2150  
atgtcattga gaatgaacag atggaaaata cccagagggc agagcatgag 2200  
gaggggcagg tcaaggatct attggctgag tcacggttga gatacaaaga 2250  
ctacatccaa atccttagca gcccaaactt cagcctcgac cagtactgcg 2300  
aacagatgtg gcacaggag aagcggagac agagaaacaa ggggggcca 2350

aagtggaagc acatgcagga aatgaagaag aaacgaaatc gaagacatca 2400  
cagagacctg gatgagctcc ctagagctgt agccacgtag ttttctactt 2450  
aatttaaaga aaagaattcc ttacctataa aaacattgcc ttctgttttg 2500  
tatatccctt atagtaattc ataaatgctt cccatggagt ttgctaagg 2550  
cacaagacaa taatctgaat aagacaatat gtgatgaata taagaaagg 2600  
caaaaaattc atttgaacca gttttccaag aacaaatctt gcacaagcaa 2650  
agtataagaa ttatcctaaa aatagggggt ttacagttgt aaatgtttta 2700  
tgttttgagt tttggaattt attgtcatgt aaatagttga gctaagcaag 2750  
ccccgaattt gatagtgtat aagggtgctt attccctcga atgtccatta 2800  
agcatggaat ttaccatgca gttgtgctat gttcttatga acagatatat 2850  
cattcctatt gagaaccagc taccttgtgg tagggaataa gaggtcagac 2900  
acaaattaag acaactccca ttatcaacag gaactttctc agtgagccat 2950  
tcactcctgg agaattggtat aggaatttgg agaggtgcat tatttctttc 3000  
tggccactgg gggttaaattt agtgactac aacattgatt tactgaagg 3050  
cactaatgtt tccccagga tttctattga ctagtcagga gtaacagggt 3100  
cacagagaga agttggtgct tagttatgtg ttttttagag tatatactaa 3150  
gctctacagg gacagaatgc ttaataaata ctttaataag atatgggaaa 3200  
atattttaat aaaacaagga aaacataatg atgtataatg catcctgatg 3250  
ggaaggcatg cagatgggat ttgttagaag acagaaggaa agacagccat 3300  
aaattctggc tttggggaaa actcatatcc ccatgaaaag gaagaacaat 3350  
cacaaataaa gtgagagtaa tgtaatggag ctcttttcac tagggtataa 3400  
gtagctgcca atttgtaatt catctgttaa aaaaaatcta gattataaca 3450  
aactgctagc aaaatctgag gaaacataaa ttcttctgaa gaatcatagg 3500  
aagagtagac attttattta taaccaatga tatttcagta tatattttct 3550  
ctcttttaaa aaatatttat catactctgt atattatttc tttttactgc 3600  
ctttattctc tcctgtatat tggattttgt gattatattt gagtgaatag 3650  
gagaaaacaa tatataacac acagagaatt aagaaaatga catttctggg 3700  
gagtggggat atatatttgt tgaataacag aacgagtgt aaattttaac 3750  
aacggaaagg gttaaattaa ctctttgaca tcttcactca accttttctc 3800

attgctgagt taatctgttg taattgtagt attgtttttg taatttaaca 3850

ataaataagc ctgctacatg t 3871

<210> 310

<211> 777

<212> PRT

<213> Homo sapiens

<400> 310

Met	Asn	Ala	Asn	Lys	Asp	Glu	Arg	Leu	Lys	Ala	Arg	Ser	Gln	Asp
1				5					10					15

Phe	His	Leu	Phe	Pro	Ala	Leu	Met	Met	Leu	Ser	Met	Thr	Met	Leu
				20					25					30

Phe	Leu	Pro	Val	Thr	Gly	Thr	Leu	Lys	Gln	Asn	Ile	Pro	Arg	Leu
				35					40					45

Lys	Leu	Thr	Tyr	Lys	Asp	Leu	Leu	Leu	Ser	Asn	Ser	Cys	Ile	Pro
				50					55					60

Phe	Leu	Gly	Ser	Ser	Glu	Gly	Leu	Asp	Phe	Gln	Thr	Leu	Leu	Leu
				65					70					75

Asp	Glu	Glu	Arg	Gly	Arg	Leu	Leu	Leu	Gly	Ala	Lys	Asp	His	Ile
				80					85					90

Phe	Leu	Leu	Ser	Leu	Val	Asp	Leu	Asn	Lys	Asn	Phe	Lys	Lys	Ile
				95					100					105

Tyr	Trp	Pro	Ala	Ala	Lys	Glu	Arg	Val	Glu	Leu	Cys	Lys	Leu	Ala
				110					115					120

Gly	Lys	Asp	Ala	Asn	Thr	Glu	Cys	Ala	Asn	Phe	Ile	Arg	Val	Leu
				125					130					135

Gln	Pro	Tyr	Asn	Lys	Thr	His	Ile	Tyr	Val	Cys	Gly	Thr	Gly	Ala
				140					145					150

Phe	His	Pro	Ile	Cys	Gly	Tyr	Ile	Asp	Leu	Gly	Val	Tyr	Lys	Glu
				155					160					165

Asp	Ile	Ile	Phe	Lys	Leu	Asp	Thr	His	Asn	Leu	Glu	Ser	Gly	Arg
				170					175					180

Leu	Lys	Cys	Pro	Phe	Asp	Pro	Gln	Gln	Pro	Phe	Ala	Ser	Val	Met
				185					190					195

Thr	Asp	Glu	Tyr	Leu	Tyr	Ser	Gly	Thr	Ala	Ser	Asp	Phe	Leu	Gly
				200					205					210

Lys	Asp	Thr	Ala	Phe	Thr	Arg	Ser	Leu	Gly	Pro	Thr	His	Asp	His
				215					220					225

His Tyr Ile Arg Thr Asp Ile Ser Glu His Tyr Trp Leu Asn Gly

230										235				240			
Ala	Lys	Phe	Ile	Gly	Thr	Phe	Phe	Ile	Pro	Asp	Thr	Tyr	Asn	Pro			
				245					250					255			
Asp	Asp	Asp	Lys	Ile	Tyr	Phe	Phe	Phe	Arg	Glu	Ser	Ser	Gln	Glu			
				260					265					270			
Gly	Ser	Thr	Ser	Asp	Lys	Thr	Ile	Leu	Ser	Arg	Val	Gly	Arg	Val			
				275					280					285			
Cys	Lys	Asn	Asp	Val	Gly	Gly	Gln	Arg	Ser	Leu	Ile	Asn	Lys	Trp			
				290					295					300			
Thr	Thr	Phe	Leu	Lys	Ala	Arg	Leu	Ile	Cys	Ser	Ile	Pro	Gly	Ser			
				305					310					315			
Asp	Gly	Ala	Asp	Thr	Tyr	Phe	Asp	Glu	Leu	Gln	Asp	Ile	Tyr	Leu			
				320					325					330			
Leu	Pro	Thr	Arg	Asp	Glu	Arg	Asn	Pro	Val	Val	Tyr	Gly	Val	Phe			
				335					340					345			
Thr	Thr	Thr	Ser	Ser	Ile	Phe	Lys	Gly	Ser	Ala	Val	Cys	Val	Tyr			
				350					355					360			
Ser	Met	Ala	Asp	Ile	Arg	Ala	Val	Phe	Asn	Gly	Pro	Tyr	Ala	His			
				365					370					375			
Lys	Glu	Ser	Ala	Asp	His	Arg	Trp	Val	Gln	Tyr	Asp	Gly	Arg	Ile			
				380					385					390			
Pro	Tyr	Pro	Arg	Pro	Gly	Thr	Cys	Pro	Ser	Lys	Thr	Tyr	Asp	Pro			
				395					400					405			
Leu	Ile	Lys	Ser	Thr	Arg	Asp	Phe	Pro	Asp	Asp	Val	Ile	Ser	Phe			
				410					415					420			
Ile	Lys	Arg	His	Ser	Val	Met	Tyr	Lys	Ser	Val	Tyr	Pro	Val	Ala			
				425					430					435			
Gly	Gly	Pro	Thr	Phe	Lys	Arg	Ile	Asn	Val	Asp	Tyr	Arg	Leu	Thr			
				440					445					450			
Gln	Ile	Val	Val	Asp	His	Val	Ile	Ala	Glu	Asp	Gly	Gln	Tyr	Asp			
				455					460					465			
Val	Met	Phe	Leu	Gly	Thr	Asp	Ile	Gly	Thr	Val	Leu	Lys	Val	Val			
				470					475					480			
Ser	Ile	Ser	Lys	Glu	Lys	Trp	Asn	Met	Glu	Glu	Val	Val	Leu	Glu			
				485					490					495			
Glu	Leu	Gln	Ile	Phe	Lys	His	Ser	Ser	Ile	Ile	Leu	Asn	Met	Glu			
				500					505					510			
Leu	Ser	Leu	Lys	Gln	Gln	Gln	Leu	Tyr	Ile	Gly	Ser	Arg	Asp	Gly			

515					520					525				
Leu	Val	Gln	Leu	Ser	Leu	His	Arg	Cys	Asp	Thr	Tyr	Gly	Lys	Ala
				530					535					540
Cys	Ala	Asp	Cys	Cys	Leu	Ala	Arg	Asp	Pro	Tyr	Cys	Ala	Trp	Asp
				545					550					555
Gly	Asn	Ala	Cys	Ser	Arg	Tyr	Ala	Pro	Thr	Ser	Lys	Arg	Arg	Ala
				560					565					570
Arg	Arg	Gln	Asp	Val	Lys	Tyr	Gly	Asp	Pro	Ile	Thr	Gln	Cys	Trp
				575					580					585
Asp	Ile	Glu	Asp	Ser	Ile	Ser	His	Glu	Thr	Ala	Asp	Glu	Lys	Val
				590					595					600
Ile	Phe	Gly	Ile	Glu	Phe	Asn	Ser	Thr	Phe	Leu	Glu	Cys	Ile	Pro
				605					610					615
Lys	Ser	Gln	Gln	Ala	Thr	Ile	Lys	Trp	Tyr	Ile	Gln	Arg	Ser	Gly
				620					625					630
Asp	Glu	His	Arg	Glu	Glu	Leu	Lys	Pro	Asp	Glu	Arg	Ile	Ile	Lys
				635					640					645
Thr	Glu	Tyr	Gly	Leu	Leu	Ile	Arg	Ser	Leu	Gln	Lys	Lys	Asp	Ser
				650					655					660
Gly	Met	Tyr	Tyr	Cys	Lys	Ala	Gln	Glu	His	Thr	Phe	Ile	His	Thr
				665					670					675
Ile	Val	Lys	Leu	Thr	Leu	Asn	Val	Ile	Glu	Asn	Glu	Gln	Met	Glu
				680					685					690
Asn	Thr	Gln	Arg	Ala	Glu	His	Glu	Glu	Gly	Gln	Val	Lys	Asp	Leu
				695					700					705
Leu	Ala	Glu	Ser	Arg	Leu	Arg	Tyr	Lys	Asp	Tyr	Ile	Gln	Ile	Leu
				710					715					720
Ser	Ser	Pro	Asn	Phe	Ser	Leu	Asp	Gln	Tyr	Cys	Glu	Gln	Met	Trp
				725					730					735
His	Arg	Glu	Lys	Arg	Arg	Gln	Arg	Asn	Lys	Gly	Gly	Pro	Lys	Trp
				740					745					750
Lys	His	Met	Gln	Glu	Met	Lys	Lys	Lys	Arg	Asn	Arg	Arg	His	His
				755					760					765
Arg	Asp	Leu	Asp	Glu	Leu	Pro	Arg	Ala	Val	Ala	Thr			
				770					775					

<210> 311

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 311

caacgcagcc gtgataaaca agtgg 25

<210> 312

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 312

gcttggacat gtaccaggcc gtgg 24

<210> 313

<211> 45

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 313

ggccagactg atttgctcaa ttcctggaag tgatggggca gatac 45

<210> 314

<211> 3934

<212> DNA

<213> Homo sapiens

<400> 314

ccctgacctc cctgagccac actgagctgg aagccgcaga ggtcatcctg 50

gagcatgccc accgcgggga gcagacaacc tcccaggtaa gctgggagca 100

agacctgaag ctgtttcttc aggagcctgg tgtattttcc cccacccac 150

ctcagcagtt tcagccagca gggactgata aggtgtgtgt cctggagtgg 200

ggagcagaag gcgtggctgg caagagtggc ctggagaaag aggttcagcg 250

cttgaccagc cgagctgccc gtgactacaa gatccagaac catgggcatc 300

gggtgaggtg ggggggcaca ggtgtcatgt gcaccttctt gtctcagcaa 350

gaagagctga gagaggggat cttggagcca ttgaggggtgt catggagcta 400

cagaggggag ggaaaggat ttttaaggtaa cagtgtggca caatagttaa 450

gagcacagtt tttggagcta gaccgacata ggttcaaatt ctcttctgtt 500

gcttcctagt tctgtagccc caggtaaggg agtgacttaa cctctctgga 550

ctccaatttc ctcatcacta aagtagggcc aataatagca cccacctcat 600  
 aggaagatt aaatgacata atgtatgtga tgcaactagc aaagtaccag 650  
 toccatagta agtcatgccc cacagtattt ccacccaccc ctgttctctg 700  
 ccttcccaac caggtactgc aacgactgga gcagaggcgg cagcaggctt 750  
 cagagcgga ggctccaagc atagaacaga ggttacagga agtgcgagag 800  
 agcatccgcc gggcacaggt gagccaggtg aagggggctg cccggctggc 850  
 cctgctgcag ggggctggct tagatgtgga gcgctggctg aagccagcca 900  
 tgacccaggc ccaggatgag gtggagcagg agcggcggct cagtgaggct 950  
 cggctgtccc agagggacct ctctccaacc gctgaggatg ctgagctttc 1000  
 tgactttgag gaatgtgagg agacgggaga gctctttgag gacgctgccc 1050  
 cccaagccct ggccacgagg gccctcccct gccctgcaca cgtgggtattt 1100  
 cgctatcagg cagggcgtaga ggatgagctg acaatcacgg agggtagtg 1150  
 gctggaggtc atagaggagg gagatgctga cgaatgggtc aaggctcgga 1200  
 accagcacgg cgaggtaggc tttgtccctg agcgatatct caacttcccg 1250  
 gacctctccc tccagagag cagccaagac agtgacaatc cctgcggggc 1300  
 agagcccaca gcattcctgg cacaggccct gtacagctac accggacaga 1350  
 gtgcagagga gctgagcttc cctgaggggg cactcatccg tctgctgccc 1400  
 cgggcccagg atggagtaga tgacggcttc tggaggggag aatttggggg 1450  
 ccgtgttggg gtcttcccct ccctgctggt ggaagagctg cttggcccc 1500  
 cagggccacc tgaactctct gacctgaac agatgctgcc gtccccttct 1550  
 cctcccagct tctcccacc tgcacctacc tctgtgttg atgggcccc 1600  
 tgcacctgtc ctgcctgggg acaaagccct ggacttcctt gggttcctgg 1650  
 acatgatggc acctcgactc aggcgatgc gtccaccacc tccccgccg 1700  
 gctaaagccc cggatcctgg ccaccagat cccctcacct gaaggccagg 1750  
 gaagccttga ccccagtg tgctgctgtc cctatcttca agctgtcaga 1800  
 ccacaccatc aatgatccag agcaacacag ccaaaagctg gaatcgccct 1850  
 tatttccacc ctacactcca agggtggaat cttgcccctt cccatttcta 1900  
 gagctggaac ccactcctt ttttccatt gttctatcat ctctaggacc 1950  
 ggaactacta ccttctcttc tgtcatgacc ctatctaggg tggtgaaatg 2000



cctgaaatct ctggggctgg aaaccatcca tcaaggtctc tagtagttct 2050  
ggcccacctc tttccccacc ctggctccat gaccacccc actctggatg 2100  
ccagggtcac tggggttggg ctggggagag gaacaggcct tgggaatcag 2150  
gagctggagc caggatgcga agcagctgta atggtctgag cggttttatt 2200  
gacaatgaat aaagggcacg aaggccaggc cagggcctgg gcctcttggtg 2250  
ctaagagggc agggggccta cgggtctatt gctttagggg cccaccacgg 2300  
gcaggggcct gctcccagct gccacgctct atcatatgga gcgaggtggt 2350  
ggggaaggcg gggcaggcag cctgttgagc gcaggggaag gagaagagac 2400  
tgaggggctg tgacctctcc tgaggcccc agcctgagac tgtgcaactc 2450  
caggtggaag tagagctggt ccctcagctg gggggcagtg ctgtccagtg 2500  
gaggggaggg ctttcacgcc caccacccc ctggccctgc cagctggtag 2550  
tccatcagca caatgaagga gacttgagga agaggaagaa taacactggt 2600  
gcttcctggt caagctgtgt ccagcttttc ccctggggct ccaggacctt 2650  
ccctacctcc accaccaaac caagggattt atagcaaagg ctaagcctgc 2700  
agtttactct gggggttcag ggagccgaaa ggcttaaata gtttaagtag 2750  
gtgatgggaa gatgagatta cctcatttag ggctcaggca gactcacctc 2800  
acatactccc tgctccctgt ggtagagaca cctgagagaa aggggagggg 2850  
tcaacaatga gagaccagga gtaggtccta tcagtgcctc ccagagtaga 2900  
gagcaataag agcccagccc agtgcagtcc cggctgtggt ttcctacctg 2950  
gtgatcagaa gtgtctgggt tgcttggtg cccatttgcc tcttgagtgg 3000  
gcagccctgg gcttggggcc ctccctcgg ccctcagtggt tggctctgca 3050  
gaagctctgg ggttccttc aagtgcacga ggggttaggc tgctgtccct 3100  
gagtctcca ttctgtactg gggggctggc taggacctgg ggctgtggcc 3150  
tctcaggggg cagcctctcc atggcaggca tccctgcctt gggctgcctt 3200  
ccccagacc cctgaccacc ccctgggtcc tgtccccac cagagcccca 3250  
gtcctgtct gtgggggagc catcacggtg ttcgtgcagt ccatagcgct 3300  
tctcaatgtg tgtcaccgg aacctgggag gggagggaac actggggttt 3350  
aggaccacaa ctgagaggct gcttggccct cccctctgac cagggacatc 3400

ctgagtttgg tggctacttc cctctggcct aaggtagggg aggccttctc 3450  
 agattgtggg gcacattgtg tagcctgact tctgctggag ctcccagtcc 3500  
 aggaggaaag agccaaggcc cacttttggg atcaggtgcc tgatcactgg 3550  
 gccccctacc tcagcccccc tttccctgga gcacctgccc cacctgcca 3600  
 cagagaacac agtgggtctcc cctgtccggg ggcggtttt tccttccttg 3650  
 gagcgctcct gacggacaag tggaggcctc ttgctgcggc tgcaatggat 3700  
 gcaaggggct gcagagccca ggtgcactgt gtgatgatgg gagggggctc 3750  
 cgtcctgcag gctggaggtg gcattccacac tggacagcag gaggagggga 3800  
 gtgagggtaa catttccatt tcccttcatt ttttgtttct tacgttcttt 3850  
 cagcatgctc cttaaaaccc cagaagcccc aatttcccca agccccattt 3900  
 tttcttgtct ttatctaata aactcaatat taag 3934

<210> 315

<211> 370

<212> PRT

<213> Homo sapiens

<400> 315

Met	Gln	Leu	Ala	Lys	Tyr	Gln	Ser	His	Ser	Lys	Ser	Cys	Pro	Thr
1				5					10					15
Val	Phe	Pro	Pro	Thr	Pro	Val	Leu	Cys	Leu	Pro	Asn	Gln	Val	Leu
				20					25					30
Gln	Arg	Leu	Glu	Gln	Arg	Arg	Gln	Gln	Ala	Ser	Glu	Arg	Glu	Ala
				35					40					45
Pro	Ser	Ile	Glu	Gln	Arg	Leu	Gln	Glu	Val	Arg	Glu	Ser	Ile	Arg
				50					55					60
Arg	Ala	Gln	Val	Ser	Gln	Val	Lys	Gly	Ala	Ala	Arg	Leu	Ala	Leu
				65					70					75
Leu	Gln	Gly	Ala	Gly	Leu	Asp	Val	Glu	Arg	Trp	Leu	Lys	Pro	Ala
				80					85					90
Met	Thr	Gln	Ala	Gln	Asp	Glu	Val	Glu	Gln	Glu	Arg	Arg	Leu	Ser
				95					100					105
Glu	Ala	Arg	Leu	Ser	Gln	Arg	Asp	Leu	Ser	Pro	Thr	Ala	Glu	Asp
				110					115					120
Ala	Glu	Leu	Ser	Asp	Phe	Glu	Glu	Cys	Glu	Glu	Thr	Gly	Glu	Leu
				125					130					135
Phe	Glu	Glu	Pro	Ala	Pro	Gln	Ala	Leu	Ala	Thr	Arg	Ala	Leu	Pro
				140					145					150

Cys	Pro	Ala	His	Val	Val	Phe	Arg	Tyr	Gln	Ala	Gly	Arg	Glu	Asp	155	160	165
Glu	Leu	Thr	Ile	Thr	Glu	Gly	Glu	Trp	Leu	Glu	Val	Ile	Glu	Glu	170	175	180
Gly	Asp	Ala	Asp	Glu	Trp	Val	Lys	Ala	Arg	Asn	Gln	His	Gly	Glu	185	190	195
Val	Gly	Phe	Val	Pro	Glu	Arg	Tyr	Leu	Asn	Phe	Pro	Asp	Leu	Ser	200	205	210
Leu	Pro	Glu	Ser	Ser	Gln	Asp	Ser	Asp	Asn	Pro	Cys	Gly	Ala	Glu	215	220	225
Pro	Thr	Ala	Phe	Leu	Ala	Gln	Ala	Leu	Tyr	Ser	Tyr	Thr	Gly	Gln	230	235	240
Ser	Ala	Glu	Glu	Leu	Ser	Phe	Pro	Glu	Gly	Ala	Leu	Ile	Arg	Leu	245	250	255
Leu	Pro	Arg	Ala	Gln	Asp	Gly	Val	Asp	Asp	Gly	Phe	Trp	Arg	Gly	260	265	270
Glu	Phe	Gly	Gly	Arg	Val	Gly	Val	Phe	Pro	Ser	Leu	Leu	Val	Glu	275	280	285
Glu	Leu	Leu	Gly	Pro	Pro	Gly	Pro	Pro	Glu	Leu	Ser	Asp	Pro	Glu	290	295	300
Gln	Met	Leu	Pro	Ser	Pro	Ser	Pro	Pro	Ser	Phe	Ser	Pro	Pro	Ala	305	310	315
Pro	Thr	Ser	Val	Leu	Asp	Gly	Pro	Pro	Ala	Pro	Val	Leu	Pro	Gly	320	325	330
Asp	Lys	Ala	Leu	Asp	Phe	Pro	Gly	Phe	Leu	Asp	Met	Met	Ala	Pro	335	340	345
Arg	Leu	Arg	Pro	Met	Arg	Pro	Pro	Pro	Pro	Pro	Pro	Ala	Lys	Ala	350	355	360
Pro	Asp	Pro	Gly	His	Pro	Asp	Pro	Leu	Thr						365	370	

<210> 316

<211> 4407

<212> DNA

<213> Homo sapiens

<400> 316

cacagggaga cccacagaca catatgcacg agagagacag aggaggaaag 50

agacagagac aaaggcacag cggaagaagg cagagacagg gcaggcacag 100

aagcggccca gacagagtcc tacagagga gaggccagag aagctgcaga 150

agacacaggc agggagagac aaagatccag gaaaggagg ctcaggagga 200  
gagtttggag aagccagacc cctgggcacc tctcccaagc ccaaggacta 250  
agttttctcc atttccttta acggtcctca gcccttctga aaactttgcc 300  
tctgaccttg gcaggagtcc aagccccag gctacagaga ggagctttcc 350  
aaagctaggg tgtggaggac ttggtgccct agacggcctc agtccctccc 400  
agctgcagta ccagtgccat gtcccagaca ggctcgcata ccgggagggg 450  
cttggcaggg cgctggctgt ggggagccca accctgcctc ctgctcccca 500  
ttgtgccgct ctctggctg gtgtggctgc ttctgctact gctggcctct 550  
ctctgccct cagcccggct ggccagcccc ctccccggg aggaggagat 600  
cgtgtttcca gagaagctca acggcagcgt cctgcctggc tcgggcgccc 650  
ctgccaggct gttgtgccg ttgcaggcct ttggggagac gctgctacta 700  
gagctggagc aggactccgg tgtgcaggtc gaggggctga cagtgcagta 750  
cctgggccag gcgcctgagc tgctgggtgg agcagagcct ggcacctacc 800  
tgactggcac catcaatgga gatccggagt cgggtggcatc tctgcactgg 850  
gatgggggag ccctgttagg cgtgttaca tatcggggg ctgaactcca 900  
cctccagccc ctggagggag gcacccctaa ctctgctggg ggacctgggg 950  
ctcacatcct acgccggaag agtcctgcc a gcgtcaagg tcccatgtgc 1000  
aacgtcaagg ctctcttgg aagccccagc cccagacccc gaagagccaa 1050  
gcgctttgct tcaactgagta gatttgtgga gacactggtg gtggcagatg 1100  
acaagatggc cgcattccac ggtgcggggc taaagcgcta cctgctaaca 1150  
gtgatggcag cagcagccaa ggccttcaag cacccaagca tccgcaatcc 1200  
tgtcagcttg gtggtgactc ggctagtgat cctggggtca ggcgaggagg 1250  
ggccccaagt ggggcccagt gctgccaga ccctgcgcag cttctgtgcc 1300  
tggcagcggg gcctcaacac ccctgaggac tcgggccctg accactttga 1350  
cacagccatt ctgtttaccc gtcaggacct gtgtggagtc tccacttgcg 1400  
acacgctggg tatggctgat gtgggcaccg tctgtgacct ggctcggagc 1450  
tgtgccattg tggaggatga tgggctccag tcagccttca ctgctgctca 1500  
tgaactgggt catgtcttca acatgctcca tgacaactcc aagccatgca 1550

tcagtttgaa tgggcctttg agcacctctc gccatgtcat ggcccctgtg 1600  
atggctcatg tggatcctga ggagccctgg tccccctgca gtgcccgtt 1650  
catcactgac ttcttgaca atggctatgg gcactgtctc ttagacaaac 1700  
cagaggctcc attgcatctg cctgtgactt tccctggcaa ggactatgat 1750  
gctgaccgcc agtgccagct gaccttcggg cccgactcac gccattgtcc 1800  
acagctgccg ccgccctgtg ctgccctctg gtgctctggc cacctcaatg 1850  
gccatgccat gtgccagacc aaacactcgc cctggggccga tggcacaccc 1900  
tgccggcccg cacaggcctg catgggtggt cgctgcctcc acatggacca 1950  
gtccaggac ttcaatattc cacaggctgg tggctggggc ccttggggac 2000  
catggggtga ctgctctcgg acctgtgggg gtggtgtcca gttctcctcc 2050  
cgagactgca cgaggcctgt cccccggaat ggtggcaagt actgtgaggg 2100  
ccgccgtacc cgcttcgct cctgcaacac tgaggactgc ccaactggct 2150  
cagccctgac cttccgcgag gagcagtgtg ctgcctacaa ccaccgcacc 2200  
gacctcttca agagcttccc agggcccatg gactgggttc ctgctacac 2250  
aggcgtggcc cccaggacc agtgcaaaact cacctgccag gcccgggcac 2300  
tgggctacta ctatgtgctg gagccacggg tggtagatgg gaccccctgt 2350  
tccccggaca gtcctcgggt ctgtgtccag ggccgatgca tccatgctgg 2400  
ctgtgatcgc atcattggct ccaagaagaa gtttgacaag tgcattggtgt 2450  
gcggagggga cggttctggt tgcagcaagc agtcaggctc cttcaggaaa 2500  
ttcaggtagc gatacaacaa tgtggtcact atccccgagg gggccaacca 2550  
cattcttgtc cggcagcagg gaaaccctgg ccaccggagc atctacttgg 2600  
ccctgaagct gccagatggc tcctatgcc tcaatggtga atacacgtg 2650  
atgccctccc ccacagatgt ggtactgcct ggggcagtca gcttgcgcta 2700  
cagcggggcc actgcagcct cagagacact gtcaggccat gggccactgg 2750  
cccagccttt gacactgcaa gtccatgtgg ctggcaaccc ccaggacaca 2800  
cgctccgat acagcttctt cgtgccccgg ccgaccctt caacgccacg 2850  
ccccactccc caggactggc tgcaccgaag agcacagatt ctggagatcc 2900  
ttcggcggcg ccctggggcg ggcaggaaat aacctacta tcccggctgc 2950  
cctttctggg caccggggcc tcggacttag ctgggagaaa gagagagctt 3000

ctgttgctgc ctcatgctaa gactcagtgg ggaggggctg tgggcgtgag 3050  
acctgcccct cctctctgcc ctaatgcgca ggctggccct gccctggttt 3100  
cctgccctgg gaggcagtga tgggttagtg gatggaagg gctgacagac 3150  
agccctccat ctaaactgcc ccctctgccc tgcgggtcac aggagggagg 3200  
gggaaggcag ggagggcctg ggccccagtt gtatttattt agtatttatt 3250  
cacttttatt tagcaccagg gaaggggaca aggactaggg tcctggggaa 3300  
cctgaccctt gaccctcat agccctcacc ctggggctag gaaatccagg 3350  
gtggtggtga taggtataag tgggtgtgtgt atgcgtgtgt gtgtgtgtgt 3400  
gaaaatgtgt gtgtgcttat gtatgaggta caacctgttc tgctttcctc 3450  
ttcctgaatt ttatTTTTTt ggaaaagaaa agtcaagggt aggggtgggc 3500  
ttcaggaggt gagggattat cTTTTTTTTt ttttctttct ttctttcttt 3550  
TTTTTTTTt agacagaatc tcgctctgtc gcccaggctg gagtgcaatg 3600  
gcacaatctc ggctcactgc atcctccgcc tcccgggttc aagtgattct 3650  
catgcctcag cctcctgagt agctgggatt acaggctcct gccaccacgc 3700  
ccagctaatt tttgttttgt tttgtttgga gacagagtct cgctattgtc 3750  
accagggtg gaatgatttc agctcactgc aaccttcgcc acctgggttc 3800  
cagcaattct cctgcctcag cctcccgagt agctgagatt ataggcacct 3850  
accaccacgc ccggctaatt tttgtatttt tagtagagac ggggtttcac 3900  
catgttggtc aggtggtct cgaactcctg accttaggtg atccactcgc 3950  
cttcatctcc caaagtgtg ggattacagg cgtgagccac cgtgcctggc 4000  
cacgccaac taatttttgt atttttagta gagacagggt ttcaccatgt 4050  
tggccaggct gctctgaac tcctgacctc aggtaatcga cctgcctcgg 4100  
cctcccaaag tgctgggatt acagggtgtga gccaccacgc ccggtacata 4150  
TTTTTTaaat tgaattctac tatttatgtg atccttttgg agtcagacag 4200  
atgtggttgc atcctaactc catgtctctg agcattagat ttctcatttg 4250  
ccaataataa tacctccctt agaagtttgt tgtgaggatt aaataatgta 4300  
aataaagaac tagcataaca ctcaaaaaa aaaaaaaaaa aaaaaaaaaa 4350  
aaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 4400

aaggaaa 4407

<210> 317

<211> 837

<212> PRT

<213> Homo sapiens

<400> 317

Met	Ser	Gln	Thr	Gly	Ser	His	Pro	Gly	Arg	Gly	Leu	Ala	Gly	Arg
1				5					10					15

Trp	Leu	Trp	Gly	Ala	Gln	Pro	Cys	Leu	Leu	Leu	Pro	Ile	Val	Pro
			20						25					30

Leu	Ser	Trp	Leu	Val	Trp	Leu	Leu	Leu	Leu	Leu	Leu	Ala	Ser	Leu
			35						40					45

Leu	Pro	Ser	Ala	Arg	Leu	Ala	Ser	Pro	Leu	Pro	Arg	Glu	Glu	Glu
			50						55					60

Ile	Val	Phe	Pro	Glu	Lys	Leu	Asn	Gly	Ser	Val	Leu	Pro	Gly	Ser
			65						70					75

Gly	Ala	Pro	Ala	Arg	Leu	Leu	Cys	Arg	Leu	Gln	Ala	Phe	Gly	Glu
			80						85					90

Thr	Leu	Leu	Leu	Glu	Leu	Glu	Gln	Asp	Ser	Gly	Val	Gln	Val	Glu
			95						100					105

Gly	Leu	Thr	Val	Gln	Tyr	Leu	Gly	Gln	Ala	Pro	Glu	Leu	Leu	Gly
			110						115					120

Gly	Ala	Glu	Pro	Gly	Thr	Tyr	Leu	Thr	Gly	Thr	Ile	Asn	Gly	Asp
			125						130					135

Pro	Glu	Ser	Val	Ala	Ser	Leu	His	Trp	Asp	Gly	Gly	Ala	Leu	Leu
			140						145					150

Gly	Val	Leu	Gln	Tyr	Arg	Gly	Ala	Glu	Leu	His	Leu	Gln	Pro	Leu
			155						160					165

Glu	Gly	Gly	Thr	Pro	Asn	Ser	Ala	Gly	Gly	Pro	Gly	Ala	His	Ile
			170						175					180

Leu	Arg	Arg	Lys	Ser	Pro	Ala	Ser	Gly	Gln	Gly	Pro	Met	Cys	Asn
			185						190					195

Val	Lys	Ala	Pro	Leu	Gly	Ser	Pro	Ser	Pro	Arg	Pro	Arg	Arg	Ala
			200						205					210

Lys	Arg	Phe	Ala	Ser	Leu	Ser	Arg	Phe	Val	Glu	Thr	Leu	Val	Val
			215						220					225

Ala	Asp	Asp	Lys	Met	Ala	Ala	Phe	His	Gly	Ala	Gly	Leu	Lys	Arg
			230						235					240

Tyr Leu Leu Thr Val Met Ala Ala Ala Ala Lys Ala Phe Lys His

245	250	255
Pro Ser Ile Arg Asn Pro Val Ser Leu	Val Val Thr Arg Leu Val	
260	265	270
Ile Leu Gly Ser Gly Glu Glu Gly Pro	Gln Val Gly Pro Ser Ala	
275	280	285
Ala Gln Thr Leu Arg Ser Phe Cys Ala	Trp Gln Arg Gly Leu Asn	
290	295	300
Thr Pro Glu Asp Ser Gly Pro Asp His	Phe Asp Thr Ala Ile Leu	
305	310	315
Phe Thr Arg Gln Asp Leu Cys Gly Val	Ser Thr Cys Asp Thr Leu	
320	325	330
Gly Met Ala Asp Val Gly Thr Val Cys	Asp Pro Ala Arg Ser Cys	
335	340	345
Ala Ile Val Glu Asp Asp Gly Leu Gln	Ser Ala Phe Thr Ala Ala	
350	355	360
His Glu Leu Gly His Val Phe Asn Met	Leu His Asp Asn Ser Lys	
365	370	375
Pro Cys Ile Ser Leu Asn Gly Pro Leu	Ser Thr Ser Arg His Val	
380	385	390
Met Ala Pro Val Met Ala His Val Asp	Pro Glu Glu Pro Trp Ser	
395	400	405
Pro Cys Ser Ala Arg Phe Ile Thr Asp	Phe Leu Asp Asn Gly Tyr	
410	415	420
Gly His Cys Leu Leu Asp Lys Pro Glu	Ala Pro Leu His Leu Pro	
425	430	435
Val Thr Phe Pro Gly Lys Asp Tyr Asp	Ala Asp Arg Gln Cys Gln	
440	445	450
Leu Thr Phe Gly Pro Asp Ser Arg His	Cys Pro Gln Leu Pro Pro	
455	460	465
Pro Cys Ala Ala Leu Trp Cys Ser Gly	His Leu Asn Gly His Ala	
470	475	480
Met Cys Gln Thr Lys His Ser Pro Trp	Ala Asp Gly Thr Pro Cys	
485	490	495
Gly Pro Ala Gln Ala Cys Met Gly Gly	Arg Cys Leu His Met Asp	
500	505	510
Gln Leu Gln Asp Phe Asn Ile Pro Gln	Ala Gly Gly Trp Gly Pro	
515	520	525
Trp Gly Pro Trp Gly Asp Cys Ser Arg	Thr Cys Gly Gly Gly Val	



530										535					540				
Gln	Phe	Ser	Ser	Arg	Asp	Cys	Thr	Arg	Pro	Val	Pro	Arg	Asn	Gly					
545										550					555				
Gly	Lys	Tyr	Cys	Glu	Gly	Arg	Arg	Thr	Arg	Phe	Arg	Ser	Cys	Asn					
560										565					570				
Thr	Glu	Asp	Cys	Pro	Thr	Gly	Ser	Ala	Leu	Thr	Phe	Arg	Glu	Glu					
575										580					585				
Gln	Cys	Ala	Ala	Tyr	Asn	His	Arg	Thr	Asp	Leu	Phe	Lys	Ser	Phe					
590										595					600				
Pro	Gly	Pro	Met	Asp	Trp	Val	Pro	Arg	Tyr	Thr	Gly	Val	Ala	Pro					
605										610					615				
Gln	Asp	Gln	Cys	Lys	Leu	Thr	Cys	Gln	Ala	Arg	Ala	Leu	Gly	Tyr					
620										625					630				
Tyr	Tyr	Val	Leu	Glu	Pro	Arg	Val	Val	Asp	Gly	Thr	Pro	Cys	Ser					
635										640					645				
Pro	Asp	Ser	Ser	Ser	Val	Cys	Val	Gln	Gly	Arg	Cys	Ile	His	Ala					
650										655					660				
Gly	Cys	Asp	Arg	Ile	Ile	Gly	Ser	Lys	Lys	Lys	Phe	Asp	Lys	Cys					
665										670					675				
Met	Val	Cys	Gly	Gly	Asp	Gly	Ser	Gly	Cys	Ser	Lys	Gln	Ser	Gly					
680										685					690				
Ser	Phe	Arg	Lys	Phe	Arg	Tyr	Gly	Tyr	Asn	Asn	Val	Val	Thr	Ile					
695										700					705				
Pro	Ala	Gly	Ala	Thr	His	Ile	Leu	Val	Arg	Gln	Gln	Gly	Asn	Pro					
710										715					720				
Gly	His	Arg	Ser	Ile	Tyr	Leu	Ala	Leu	Lys	Leu	Pro	Asp	Gly	Ser					
725										730					735				
Tyr	Ala	Leu	Asn	Gly	Glu	Tyr	Thr	Leu	Met	Pro	Ser	Pro	Thr	Asp					
740										745					750				
Val	Val	Leu	Pro	Gly	Ala	Val	Ser	Leu	Arg	Tyr	Ser	Gly	Ala	Thr					
755										760					765				
Ala	Ala	Ser	Glu	Thr	Leu	Ser	Gly	His	Gly	Pro	Leu	Ala	Gln	Pro					
770										775					780				
Leu	Thr	Leu	Gln	Val	Leu	Val	Ala	Gly	Asn	Pro	Gln	Asp	Thr	Arg					
785										790					795				
Leu	Arg	Tyr	Ser	Phe	Phe	Val	Pro	Arg	Pro	Thr	Pro	Ser	Thr	Pro					
800										805					810				
Arg	Pro	Thr	Pro	Gln	Asp	Trp	Leu	His	Arg	Arg	Ala	Gln	Ile	Leu					

815

820

825

Glu Ile Leu Arg Arg Arg Pro Trp Ala Gly Arg Lys  
830 835

&lt;210&gt; 318

&lt;211&gt; 23

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Synthetic oligonucleotide probe

&lt;400&gt; 318

ccctgaagct gccagatggc tcc 23

&lt;210&gt; 319

&lt;211&gt; 24

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Synthetic oligonucleotide probe

&lt;400&gt; 319

ctgtgctctt cgggtgcagcc agtc 24

&lt;210&gt; 320

&lt;211&gt; 43

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Synthetic oligonucleotide probe

&lt;400&gt; 320

ccacagatgt ggtactgcct ggggcagtcg gcttgcgcta cag 43

&lt;210&gt; 321

&lt;211&gt; 1197

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 321

cagcagtggc ctctcagtc tctcaaagca aggaaagagt actgtgtgct 50

gagagaccat ggcaaagaat cctccagaga attgtgaaga ctgtcacatt 100

ctaaatgcag aagcttttaa atccaagaaa atatgtaaat cacttaagat 150

ttgtggactg gtgttttgta tcttgccct aactctaatt gtcctgtttt 200

gggggagcaa gcacttctgg ccggaggtac ccaaaaaagc ctatgacatg 250

gagcacactt tctacagcaa tggagagaag aagaagattt acatggaaat 300

tgatcctgtg accagaactg aaatattcag aagcggaaat ggcaactgatg 350

aaacattgga agtgcacgac tttaaaaacg gatacactgg catctacttc 400  
 gtgggtcttc aaaaatgttt tatcaaaact cagattaaag tgattcctga 450  
 attttctgaa ccagaagagg aaatagatga gaatgaagaa attaccacaa 500  
 ctttctttga acagtcagtg atttgggtcc cagcagaaaa gcctattgaa 550  
 aaccgagatt ttcttaaaaa ttccaaaatt ctggagattt gtgataacgt 600  
 gaccatgtat tggatcaatc ccactcta atcagtttct gagttacaag 650  
 actttgagga ggaggagaa gatcttcact ttcttgccaa cgaaaaaaaa 700  
 gggattgaac aaaatgaaca gtgggtgggc cctcaagtga aagtagagaa 750  
 gaccgcgtcac gccagacaag caagtgagga agaacttcca ataatgact 800  
 atactgaaaa tggaatagaa ttgatccca tgctggatga gagaggttat 850  
 tgttgtattt actgccgtcg aggcaaccgc tattgccgcc gcgtctgtga 900  
 accttacta ggctactacc catatccata ctgctaccaa ggaggacgag 950  
 tcactgtctg tgtcatcatg ccttgtaact ggtgggtggc ccgcatgctg 1000  
 gggaggggtct aataggaggt ttgagctcaa atgcttaa ac tgctggcaac 1050  
 atataataaa tgcatgctat tcaatgaatt tctgcctatg aggcattctg 1100  
 cccctggtag ccagctctcc agaattactt gtaggtaatt cctctcttca 1150  
 tgttctaata aacttctaca ttatcaccaa aaaaaaaaaa aaaaaaa 1197

<210> 322

<211> 317

<212> PRT

<213> Homo sapiens

<400> 322

Met	Ala	Lys	Asn	Pro	Pro	Glu	Asn	Cys	Glu	Asp	Cys	His	Ile	Leu
1				5					10					15

Asn	Ala	Glu	Ala	Phe	Lys	Ser	Lys	Lys	Ile	Cys	Lys	Ser	Leu	Lys
				20					25					30

Ile	Cys	Gly	Leu	Val	Phe	Gly	Ile	Leu	Ala	Leu	Thr	Leu	Ile	Val
				35					40					45

Leu	Phe	Trp	Gly	Ser	Lys	His	Phe	Trp	Pro	Glu	Val	Pro	Lys	Lys
				50					55					60

Ala	Tyr	Asp	Met	Glu	His	Thr	Phe	Tyr	Ser	Asn	Gly	Glu	Lys	Lys
				65					70					75

Lys Ile Tyr Met Glu Ile Asp Pro Val Thr Arg Thr Glu Ile Phe

80					85					90				
Arg	Ser	Gly	Asn	Gly	Thr	Asp	Glu	Thr	Leu	Glu	Val	His	Asp	Phe
				95					100					105
Lys	Asn	Gly	Tyr	Thr	Gly	Ile	Tyr	Phe	Val	Gly	Leu	Gln	Lys	Cys
				110					115					120
Phe	Ile	Lys	Thr	Gln	Ile	Lys	Val	Ile	Pro	Glu	Phe	Ser	Glu	Pro
				125					130					135
Glu	Glu	Glu	Ile	Asp	Glu	Asn	Glu	Glu	Ile	Thr	Thr	Thr	Phe	Phe
				140					145					150
Glu	Gln	Ser	Val	Ile	Trp	Val	Pro	Ala	Glu	Lys	Pro	Ile	Glu	Asn
				155					160					165
Arg	Asp	Phe	Leu	Lys	Asn	Ser	Lys	Ile	Leu	Glu	Ile	Cys	Asp	Asn
				170					175					180
Val	Thr	Met	Tyr	Trp	Ile	Asn	Pro	Thr	Leu	Ile	Ser	Val	Ser	Glu
				185					190					195
Leu	Gln	Asp	Phe	Glu	Glu	Glu	Gly	Glu	Asp	Leu	His	Phe	Pro	Ala
				200					205					210
Asn	Glu	Lys	Lys	Gly	Ile	Glu	Gln	Asn	Glu	Gln	Trp	Val	Val	Pro
				215					220					225
Gln	Val	Lys	Val	Glu	Lys	Thr	Arg	His	Ala	Arg	Gln	Ala	Ser	Glu
				230					235					240
Glu	Glu	Leu	Pro	Ile	Asn	Asp	Tyr	Thr	Glu	Asn	Gly	Ile	Glu	Phe
				245					250					255
Asp	Pro	Met	Leu	Asp	Glu	Arg	Gly	Tyr	Cys	Cys	Ile	Tyr	Cys	Arg
				260					265					270
Arg	Gly	Asn	Arg	Tyr	Cys	Arg	Arg	Val	Cys	Glu	Pro	Leu	Leu	Gly
				275					280					285
Tyr	Tyr	Pro	Tyr	Pro	Tyr	Cys	Tyr	Gln	Gly	Gly	Arg	Val	Ile	Cys
				290					295					300
Arg	Val	Ile	Met	Pro	Cys	Asn	Trp	Trp	Val	Ala	Arg	Met	Leu	Gly
				305					310					315

Arg Val

<210> 323

<211> 1174

<212> DNA

<213> Homo sapiens

<400> 323

gcggaactgg ctccggtggt cacctgagga gcggcgtgac cccgagggcc 50

caggagctg cccggctggc ctaggcaggc agccgcacca tggccagcac 100  
 ggccgtgcag cttctgggct tcctgctcag cttcctgggc atggtgggca 150  
 cgttgatcac caccatcctg ccgcactggc ggaggacagc gcacgtgggc 200  
 accaacaacc tcacggccgt gtcctacctg aaagggctct ggatggagtg 250  
 tgtgtggcac agcacaggca tctaccagtg ccagatctac cgatccctgc 300  
 tggcgctgcc ccaagacctc caggctgccc gcgccctcat ggtcatctcc 350  
 tgctgctctc cgggcatagc ctgcgcctgc gccgtcatcg ggatgaagtg 400  
 cacgcgctgc gccaaaggga caccgcgcaa gaccaccttt gccatcctcg 450  
 gcggcaccct cttcatcctg gccggcctcc tgtgcatggg ggccgtctcc 500  
 tggaccacca acgacgtggg gcagaacttc tacaaccgcg tgctgccagc 550  
 cggcatgaag tttgagattg gccaggccct gtacctgggc ttcattctct 600  
 cgtccctctc gctcattggg ggcaccctgc tttgctgtc ctgccaggac 650  
 gaggcaccct acaggcccta ccaggcccg ccaggggcca ccacgaccac 700  
 tgcaaacacc gcacctgcct accagccacc agctgcctac aaagacaatc 750  
 gggccccctc agtgacctcg gccacgcaca gcgggtacag gctgaacgac 800  
 tacgtgtgag tccccacagc ctgcttctcc cctgggctgc tgtgggctgg 850  
 gtccccggcg ggactgtcaa tggaggcagg ggttccagca caaagtttac 900  
 ttctgggcaa tttttgtatc caaggaaata atgtgaatgc gaggaaatgt 950  
 ctttagagca caggacaga gggggaaata agaggaggag aaagctctct 1000  
 ataccaaaga ctgaaaaaaaa aaatcctgtc tgtttttgta tttattatat 1050  
 atatttatgt ggggtgattg ataacaagtt taatataaag tgacttggga 1100  
 gtttggtcag tggggttggg ttgtgatcca ggaataaacc ttgcggatgt 1150  
 ggctgtttat gaaaaaaaaa aaaa 1174

<210> 324

<211> 239

<212> PRT

<213> Homo sapiens

<400> 324

Met	Ala	Ser	Thr	Ala	Val	Gln	Leu	Leu	Gly	Phe	Leu	Leu	Ser	Phe
1					5				10					15

Leu Gly Met Val Gly Thr Leu Ile Thr Thr Ile Leu Pro His Trp

	20	25	30
Arg Arg Thr Ala His Val Gly Thr Asn Ile Leu Thr Ala Val Ser	35	40	45
Tyr Leu Lys Gly Leu Trp Met Glu Cys Val Trp His Ser Thr Gly	50	55	60
Ile Tyr Gln Cys Gln Ile Tyr Arg Ser Leu Leu Ala Leu Pro Gln	65	70	75
Asp Leu Gln Ala Ala Arg Ala Leu Met Val Ile Ser Cys Leu Leu	80	85	90
Ser Gly Ile Ala Cys Ala Cys Ala Val Ile Gly Met Lys Cys Thr	95	100	105
Arg Cys Ala Lys Gly Thr Pro Ala Lys Thr Thr Phe Ala Ile Leu	110	115	120
Gly Gly Thr Leu Phe Ile Leu Ala Gly Leu Leu Cys Met Val Ala	125	130	135
Val Ser Trp Thr Thr Asn Asp Val Val Gln Asn Phe Tyr Asn Pro	140	145	150
Leu Leu Pro Ser Gly Met Lys Phe Glu Ile Gly Gln Ala Leu Tyr	155	160	165
Leu Gly Phe Ile Ser Ser Ser Leu Ser Leu Ile Gly Gly Thr Leu	170	175	180
Leu Cys Leu Ser Cys Gln Asp Glu Ala Pro Tyr Arg Pro Tyr Gln	185	190	195
Ala Pro Pro Arg Ala Thr Thr Thr Thr Ala Asn Thr Ala Pro Ala	200	205	210
Tyr Gln Pro Pro Ala Ala Tyr Lys Asp Asn Arg Ala Pro Ser Val	215	220	225
Thr Ser Ala Thr His Ser Gly Tyr Arg Leu Asn Asp Tyr Val	230	235	

<210> 325

<211> 2121

<212> DNA

<213> Homo sapiens

<400> 325

gagctcccct caggagcgcg ttagcttcac accttcggca gcaggagggc 50

ggcagcttct cgcaggcggc agggcgggcg gccaggatca tgtccaccac 100

cacatgccaa gtggtggcgt tcctcctgtc catcctgggg ctggccggct 150

gcatgcggc caccgggatg gacatgtgga gcaccaggga cctgtacgac 200

aaccccgta cctccgtgtt ccagtagcaa gggctctgga ggagctgcgt 250  
gaggcagagt tcaggcttca ccgaatgcag gccctatttc accatcctgg 300  
gacttccagc catgctgcag gcagtgcgag ccctgatgat cgtaggcatc 350  
gtcctgggtg ccattggcct cctggatatcc atctttgccc tgaaatgcat 400  
ccgcattggc agcatggagg actctgcaa agccaacatg aactgacct 450  
ccgggatcat gttcattgtc tcaggctctt gtgcaattgc tggagtgtct 500  
gtgtttgcca acatgctggt gactaacttc tggatgtcca cagctaacat 550  
gtacaccggc atgggtggga tgggtgcagac tggtcagacc aggtacacat 600  
ttgggtgcggc tctgttcgtg ggctgggtcg ctggaggcct cacactaatt 650  
gggggtgtga tgatgtgcat cgctgccgg ggctggcac cagaagaaac 700  
caactacaaa gccgtttctt atcatgcctc aggccacagt gttgcctaca 750  
agcctggagg cttcaaggcc agcactggct ttgggtccaa caccaaaaac 800  
aagaagatat acgatggagg tgccgcaca gaggacgagg tacaatctta 850  
tcctccaag cagactatg tgtaatgtc taagacctct cagcacgggc 900  
ggaagaaact cccggagagc tcacccaaaa aacaaggaga tcccatctag 950  
atttcttctt gcttttgact cacagctgga agttagaaaa gcctcgattt 1000  
catctttgga gaggccaaat ggtcttagcc tcagtctctg tctctaaata 1050  
ttccaccata aaacagctga gttatttatg aattagaggc tatagctcac 1100  
atcttcaatc ctctatttct ttttttaaata ataactttct actctgatga 1150  
gagaatgtgg ttttaatctc tctctcacat tttgatgatt tagacagact 1200  
ccccctcttc ctctagtca ataaaccat tgatgatcta tttcccagct 1250  
tatccccaag aaaacttttg aaaggaaaga gtagaccaa agatgttatt 1300  
ttctgctggt tgaattttgt ctccccacc ccaacttggc tagtaataaa 1350  
cacttactga agaagaagca ataagagaaa gatatttgta atctctccag 1400  
cccatgatct cggttttctt aactgtgat cttaaaagt accaaaccaa 1450  
agtcattttc agtttgaggc aacaaacct ttctactgct gttgacatct 1500  
tcttattaca gcaacacat tctaggagt tctgagctc tccactggag 1550  
tcctctttct gtcgcggtc agaaattgtc cctagatgaa tgagaaaatt 1600

atttttttta atttaagtcc taaatatagt taaaataaat aatgttttag 1650  
 taaaatgata cactatctct gtgaaatagc ctcacccta catgtggata 1700  
 gaaggaaatg aaaaaataat tgctttgaca ttgtctatat ggtactttgt 1750  
 aaagtcatgc ttaagtacaa attccatgaa aagctcacac ctgtaatcct 1800  
 agcacttttg gaggctgagg aggaaggatc acttgagccc agaagttcga 1850  
 gactagcctg ggcaacatgg agaagccctg tctctacaaa atacagagag 1900  
 aaaaaatcag ccagtcatgg tggcatacac ctgtagtccc agcattccgg 1950  
 gaggctgagg tgggaggatc acttgagccc agggaggttg gggctgcagt 2000  
 gagccatgat cacaccactg cactccagcc aggtgacata gcgagatcct 2050  
 gtctaaaaaa ataaaaaata aataatggaa cacagcaagt cctaggaagt 2100  
 aggttaaaac taattcttta a 2121

<210> 326

<211> 261

<212> PRT

<213> Homo sapiens

<400> 326

Met	Ser	Thr	Thr	Thr	Cys	Gln	Val	Val	Ala	Phe	Leu	Leu	Ser	Ile
1				5					10					15
Leu	Gly	Leu	Ala	Gly	Cys	Ile	Ala	Ala	Thr	Gly	Met	Asp	Met	Trp
				20					25					30
Ser	Thr	Gln	Asp	Leu	Tyr	Asp	Asn	Pro	Val	Thr	Ser	Val	Phe	Gln
				35					40					45
Tyr	Glu	Gly	Leu	Trp	Arg	Ser	Cys	Val	Arg	Gln	Ser	Ser	Gly	Phe
				50					55					60
Thr	Glu	Cys	Arg	Pro	Tyr	Phe	Thr	Ile	Leu	Gly	Leu	Pro	Ala	Met
				65					70					75
Leu	Gln	Ala	Val	Arg	Ala	Leu	Met	Ile	Val	Gly	Ile	Val	Leu	Gly
				80					85					90
Ala	Ile	Gly	Leu	Leu	Val	Ser	Ile	Phe	Ala	Leu	Lys	Cys	Ile	Arg
				95					100					105
Ile	Gly	Ser	Met	Glu	Asp	Ser	Ala	Lys	Ala	Asn	Met	Thr	Leu	Thr
				110					115					120
Ser	Gly	Ile	Met	Phe	Ile	Val	Ser	Gly	Leu	Cys	Ala	Ile	Ala	Gly
				125					130					135
Val	Ser	Val	Phe	Ala	Asn	Met	Leu	Val	Thr	Asn	Phe	Trp	Met	Ser
				140					145					150



Thr	Ala	Asn	Met	Tyr	Thr	Gly	Met	Gly	Gly	Met	Val	Gln	Thr	Val
				155					160					165
Gln	Thr	Arg	Tyr	Thr	Phe	Gly	Ala	Ala	Leu	Phe	Val	Gly	Trp	Val
				170					175					180
Ala	Gly	Gly	Leu	Thr	Leu	Ile	Gly	Gly	Val	Met	Met	Cys	Ile	Ala
				185					190					195
Cys	Arg	Gly	Leu	Ala	Pro	Glu	Glu	Thr	Asn	Tyr	Lys	Ala	Val	Ser
				200					205					210
Tyr	His	Ala	Ser	Gly	His	Ser	Val	Ala	Tyr	Lys	Pro	Gly	Gly	Phe
				215					220					225
Lys	Ala	Ser	Thr	Gly	Phe	Gly	Ser	Asn	Thr	Lys	Asn	Lys	Lys	Ile
				230					235					240
Tyr	Asp	Gly	Gly	Ala	Arg	Thr	Glu	Asp	Glu	Val	Gln	Ser	Tyr	Pro
				245					250					255
Ser	Lys	His	Asp	Tyr	Val									
				260										

<210> 327

<211> 2010

<212> DNA

<213> Homo sapiens

<400> 327

```

ggaaaaactg ttctcttctg tggcacagag aaccctgctt caaagcagaa 50
gtagcagttc cggagtccag ctggctaaaa ctcacccag aggataatgg 100
caacccatgc cttagaaatc gctgggctgt ttcttggtgg tgttggaatg 150
gtgggcacag tggctgtcac tgtcatgcct cagtggagag tgtcggcctt 200
cattgaaaac aacatcgtgg tttttgaaaa cttctgggaa ggactgtgga 250
tgaattgcgt gaggcaggct aacatcagga tgcagtcaa aatctatgat 300
tcctgtctgg ctctttctcc ggacctacag gcagccagag gactgatgtg 350
tgctgcttcc gtgatgtcct tcttggtttt catgatggcc atccttgcca 400
tgaaatgcac caggtgcacg ggggacaatg agaagtgaa ggctcacatt 450
ctgctgacgg ctggaatcat cttcatcatc acgggcatgg tgggtgctcat 500
ccctgtgagc tgggttgcca atgcatcat cagagatttc tataactcaa 550
tagtgaatgt tgccaaaaaa cgtgagcttg gagaagctct ctacttagga 600
tggaccacgg cactggtgct gattgttgga ggagctctgt tctgctgcgt 650

```

tttttgttgc aacgaaaaga gcagtagcta cagatactcg ataccttccc 700  
 atcgcacaaac ccaaaaaagt tatcacaccg gaaagáagtc accgagcgtc 750  
 tactccagaa gtcagtatgt gtagttgtgt atgttttttt aactttacta 800  
 taaagccatg caaatgacaa aaatctatat tactttctca aaatggaccc 850  
 caaagaaact ttgatttact gttcttaact gcctaactctt aattacagga 900  
 actgtgcac agctatttat gattctataa gctatttcag cagaatgaga 950  
 tattaaaccc aatgctttga ttgttctaga aagtatagta atttgttttc 1000  
 taagggtggtt caagcatcta ctctttttat catttacttc aaaatgacat 1050  
 tgctaaagac tgcattattt tactactgta atttctccac gacatagcat 1100  
 tatgtacata gatgagtgtg acatttatat ctcacataga gacatgctta 1150  
 tatggtttta tttaaaatga aatgccagtc cattacactg aataaataga 1200  
 actcaactat tgcttttcag ggaaatcatg gatagggttg aagaaggtta 1250  
 ctattaattg tttaaaaaca gcttagggat taatgtcctc catttataat 1300  
 gaagattaaa atgaaggctt taatcagcat tgtaaaggaa attgaatggc 1350  
 tttctgatat gctgtttttt agcctaggag ttagaaatcc taacttcttt 1400  
 atcctcttct cccagaggct ttttttttct tgtgtattaa attaacattt 1450  
 ttaaaacgca gatattttgt caaggggctt tgcattcaaa ctgcttttcc 1500  
 agggctatac tcagaagaaa gataaaagtg tgatctaaga aaaagtgatg 1550  
 gttttaggaa agtgaaaata tttttgtttt tgtatttgaa gaagaatgat 1600  
 gcattttgac aagaaatcat atatgtatgg atatatttta ataagtattt 1650  
 gagtacagac tttgagggtt catcaatata aataaaagag cagaaaaata 1700  
 tgtcttggtt ttcatttgct taccaaaaaa acaacaacaa aaaaagttgt 1750  
 cctttgagaa cttcacctgc tctatgtgg gtacctgagt caaaattgtc 1800  
 atttttgttc tgtgaaaaat aaatttcctt cttgtaccat ttctgtttag 1850  
 ttttactaaa atctgtaaat actgtatttt tctgtttatt ccaaatttga 1900  
 tgaaactgac aatccaattt gaaagtttgt gtcgacgtct gtctagctta 1950  
 aatgaatgtg ttctatttgc tttatacatt tatattaata aattgtacat 2000  
 ttttctaatt 2010

<211> 225  
<212> PRT  
<213> Homo sapiens

<400> 328

Met	Ala	Thr	His	Ala	Leu	Glu	Ile	Ala	Gly	Leu	Phe	Leu	Gly	Gly	
1				5					10					15	
Val	Gly	Met	Val	Gly	Thr	Val	Ala	Val	Thr	Val	Met	Pro	Gln	Trp	
				20					25					30	
Arg	Val	Ser	Ala	Phe	Ile	Glu	Asn	Asn	Ile	Val	Val	Phe	Glu	Asn	
				35					40					45	
Phe	Trp	Glu	Gly	Leu	Trp	Met	Asn	Cys	Val	Arg	Gln	Ala	Asn	Ile	
				50					55					60	
Arg	Met	Gln	Cys	Lys	Ile	Tyr	Asp	Ser	Leu	Leu	Ala	Leu	Ser	Pro	
				65					70					75	
Asp	Leu	Gln	Ala	Ala	Arg	Gly	Leu	Met	Cys	Ala	Ala	Ser	Val	Met	
				80					85					90	
Ser	Phe	Leu	Ala	Phe	Met	Met	Ala	Ile	Leu	Gly	Met	Lys	Cys	Thr	
				95					100					105	
Arg	Cys	Thr	Gly	Asp	Asn	Glu	Lys	Val	Lys	Ala	His	Ile	Leu	Leu	
				110					115					120	
Thr	Ala	Gly	Ile	Ile	Phe	Ile	Ile	Thr	Gly	Met	Val	Val	Leu	Ile	
				125					130					135	
Pro	Val	Ser	Trp	Val	Ala	Asn	Ala	Ile	Ile	Arg	Asp	Phe	Tyr	Asn	
				140					145					150	
Ser	Ile	Val	Asn	Val	Ala	Gln	Lys	Arg	Glu	Leu	Gly	Glu	Ala	Leu	
				155					160					165	
Tyr	Leu	Gly	Trp	Thr	Thr	Ala	Leu	Val	Leu	Ile	Val	Gly	Gly	Ala	
				170					175					180	
Leu	Phe	Cys	Cys	Val	Phe	Cys	Cys	Asn	Glu	Lys	Ser	Ser	Ser	Tyr	
				185					190					195	
Arg	Tyr	Ser	Ile	Pro	Ser	His	Arg	Thr	Thr	Gln	Lys	Ser	Tyr	His	
				200					205					210	
Thr	Gly	Lys	Lys	Ser	Pro	Ser	Val	Tyr	Ser	Arg	Ser	Gln	Tyr	Val	
				215					220					225	

<210> 329  
<211> 1315  
<212> DNA  
<213> Homo sapiens

<400> 329

tcgccatggc ctctgccgga atgcagatcc tgggagtcgt cctgacactg 50

ctgggctggg tgaatggcct ggtctcctgt gccctgccca tgtggaaggt 100  
 gaccgctttc atcggaaca gcatcgtggt ggcccagggt gtgtgggagg 150  
 gcctgtggat gtctgcgtg gtgcagagca ccggccagat gcagtgaag 200  
 gtgtacgact cactgctggc gctgccacag gacctgcagg ctgcacgtgc 250  
 cctctgtgtc atcgccctcc ttgtggccct gttcggcttg ctggtctacc 300  
 ttgtgggggc caagtgtacc acctgtgtgg aggagaagga ttccaaggcc 350  
 cgctggtgc tcacctctgg gattgtcttt gtcactctag gggtcctgac 400  
 gctaataccc gtgtgctgga cggcgcatgc catcatccgg gacttctata 450  
 accccctggt ggctgaggcc caaaagcggg agctgggggc ctccctctac 500  
 ttgggctggg cggcctcagg ccttttgttg ctgggtgggg ggttgctgtg 550  
 ctgcacttgc cctcggggg ggtcccaggg cccagccat tacatggccc 600  
 gctactcaac atctgcccct gccatctctc gggggccctc tgagtaccct 650  
 accaagaatt acgtctgacg tggaggggaa tgggggctcc gctggcgcta 700  
 gagccatcca gaagtggcag tgcccaacag ctttgggatg ggttcgtacc 750  
 ttttgtttct gcctcctgct attttcttt tgactgagga tatttaaaat 800  
 tcatttgaaa actgagccaa ggtgttgact cagactctca cttaggctct 850  
 gctgtttctc acccttgat gatggagcca aagaggggat gctttgagat 900  
 tctggatctt gacatgccca tcttagaagc cagtcaagct atggaactaa 950  
 tgcggagggt gcttgctgtg ctggctttgc aacaagacag actgtcccca 1000  
 agagtctctg ctgtgctgtg gggctgggct tccctagatg tcaactggaca 1050  
 gctgcccccc atcctactca ggtctctgga gctcctctct tcaccctgg 1100  
 aaaaacaaat catctgttaa caaaggactg cccacctccg gaacttctga 1150  
 cctctgtttc ctccgtcctg ataagacgtc cccccccag ggccagggtcc 1200  
 cagctatgta gacccccgcc cccacctcca aactgcacc cttctgccct 1250  
 gccccctcg tctaccccc tttaactca cttttttatc aaataaagca 1300  
 tgttttggtta gtgca 1315

<210> 330

<211> 220

<212> PRT

<213> Homo sapiens

<400> 330

Met	Ala	Ser	Ala	Gly	Met	Gln	Ile	Leu	Gly	Val	Val	Leu	Thr	Leu
1				5					10					15
Leu	Gly	Trp	Val	Asn	Gly	Leu	Val	Ser	Cys	Ala	Leu	Pro	Met	Trp
				20					25					30
Lys	Val	Thr	Ala	Phe	Ile	Gly	Asn	Ser	Ile	Val	Val	Ala	Gln	Val
				35					40					45
Val	Trp	Glu	Gly	Leu	Trp	Met	Ser	Cys	Val	Val	Gln	Ser	Thr	Gly
				50					55					60
Gln	Met	Gln	Cys	Lys	Val	Tyr	Asp	Ser	Leu	Leu	Ala	Leu	Pro	Gln
				65					70					75
Asp	Leu	Gln	Ala	Ala	Arg	Ala	Leu	Cys	Val	Ile	Ala	Leu	Leu	Val
				80					85					90
Ala	Leu	Phe	Gly	Leu	Leu	Val	Tyr	Leu	Ala	Gly	Ala	Lys	Cys	Thr
				95					100					105
Thr	Cys	Val	Glu	Glu	Lys	Asp	Ser	Lys	Ala	Arg	Leu	Val	Leu	Thr
				110					115					120
Ser	Gly	Ile	Val	Phe	Val	Ile	Ser	Gly	Val	Leu	Thr	Leu	Ile	Pro
				125					130					135
Val	Cys	Trp	Thr	Ala	His	Ala	Ile	Ile	Arg	Asp	Phe	Tyr	Asn	Pro
				140					145					150
Leu	Val	Ala	Glu	Ala	Gln	Lys	Arg	Glu	Leu	Gly	Ala	Ser	Leu	Tyr
				155					160					165
Leu	Gly	Trp	Ala	Ala	Ser	Gly	Leu	Leu	Leu	Leu	Gly	Gly	Gly	Leu
				170					175					180
Leu	Cys	Cys	Thr	Cys	Pro	Ser	Gly	Gly	Ser	Gln	Gly	Pro	Ser	His
				185					190					195
Tyr	Met	Ala	Arg	Tyr	Ser	Thr	Ser	Ala	Pro	Ala	Ile	Ser	Arg	Gly
				200					205					210
Pro	Ser	Glu	Tyr	Pro	Thr	Lys	Asn	Tyr	Val					
				215					220					

<210> 331

<211> 1160

<212> DNA

<213> Homo sapiens

<400> 331

gccaaggaga acatcatcaa agacttctct agactcaaaa ggcttccacg 50

ttctacatct tgagcatctt ctaccactcc gaattgaacc agtcttcaaa 100

gtaaaggcaa tggcatttta tcccttgcaa attgctgggc tggttcttgg 150  
 gttccttggc atggtgggga ctcttgccac aacccttctg cctcagtggg 200  
 ggagtatcag cttttgttgg cagcaacatt attgtctttg agaggctctg 250  
 ggaagggtc tggatgaatt gcatccgaca agccagggtc cggttgcaat 300  
 gcaagtctta tagctccttg ttggctctcc cgctgccct ggaaacagcc 350  
 cgggccctca tgtgtgtggc tgttgctctc tccttgatcg ccttgcttat 400  
 tggcatctgt ggcatagaag aggtccagt caccaggctc aacgagaggg 450  
 ccaaagcata ccttctggga acttcaggag tcctcttcat cctgacgggt 500  
 atcttcgttc tgattccggt gagctggaca gccaatataa tcatcagaga 550  
 tttctacaac ccagccatcc acatagggtc gaaacgagag ctgggagcag 600  
 cacttttct tggctgggca agcgtgctg tcctcttcat tggagggggg 650  
 ctgctttgtg gatcttgctg ctgcaacaga aagaagcaag ggtacagata 700  
 tccagtgcct ggctaccgtg tgccacacac agataagcga agaaatacga 750  
 caatgcttag taagacctcc accagttatg tctaatagct ccttttgggt 800  
 ccaagtatgg actatgggtc atgtttttta taaagtcttg ctagaaactg 850  
 taagtatgtg aggcaggaga acttgcttta tgtctagatt tacattgata 900  
 cgaaagtctt aatttggtac tgggtgtagg aatgaaaatg acttacttgg 950  
 acattctgac ttcaggtgta ttaaatacat tgactattgt tggaccaat 1000  
 cgctgtcca attttcatat tctaaattca agtataccca taatcattag 1050  
 caagtgtaca atgatggact acttattact ttttgaccat catgtattat 1100  
 ctgataagaa tctaaagttg aaattgatat tctataacaa taaaacatat 1150  
 acctattcta 1160

<210> 332

<211> 173

<212> PRT

<213> Homo sapiens

<400> 332

Met	Asn	Cys	Ile	Arg	Gln	Ala	Arg	Val	Arg	Leu	Gln	Cys	Lys	Phe
1				5					10					15

Tyr	Ser	Ser	Leu	Leu	Ala	Leu	Pro	Pro	Ala	Leu	Glu	Thr	Ala	Arg
			20						25					30

Ala Leu Met Cys Val Ala Val Ala Leu Ser Leu Ile Ala Leu Leu

35										40					45				
Ile	Gly	Ile	Cys	Gly	Met	Lys	Gln	Val	Gln	Cys	Thr	Gly	Ser	Asn					
				50					55					60					
Glu	Arg	Ala	Lys	Ala	Tyr	Leu	Leu	Gly	Thr	Ser	Gly	Val	Leu	Phe					
				65					70					75					
Ile	Leu	Thr	Gly	Ile	Phe	Val	Leu	Ile	Pro	Val	Ser	Trp	Thr	Ala					
				80					85					90					
Asn	Ile	Ile	Ile	Arg	Asp	Phe	Tyr	Asn	Pro	Ala	Ile	His	Ile	Gly					
				95					100					105					
Gln	Lys	Arg	Glu	Leu	Gly	Ala	Ala	Leu	Phe	Leu	Gly	Trp	Ala	Ser					
				110					115					120					
Ala	Ala	Val	Leu	Phe	Ile	Gly	Gly	Gly	Leu	Leu	Cys	Gly	Phe	Cys					
				125					130					135					
Cys	Cys	Asn	Arg	Lys	Lys	Gln	Gly	Tyr	Arg	Tyr	Pro	Val	Pro	Gly					
				140					145					150					
Tyr	Arg	Val	Pro	His	Thr	Asp	Lys	Arg	Arg	Asn	Thr	Thr	Met	Leu					
				155					160					165					
Ser	Lys	Thr	Ser	Thr	Ser	Tyr	Val												
				170															

<210> 333

<211> 535

<212> DNA

<213> Homo sapiens

<400> 333

```

agtgacaatc tcagagcagc ttctacacca cagccatttc cagcatgaag 50
atcactgggg gtctccttct gctctgtaca gtggtctatt tctgtagcag 100
ctcagaagct gctagtctgt ctccaaaaaa agtggactgc agcatttaca 150
agaagtatcc agtgggtggcc atcccctgcc ccatcacata cctaccagtt 200
tgtggttctg actacatcac ctatgggaat gaatgtcact tgtgtaccga 250
gagcttgaaa agtaatggaa gagttcagtt tcttcacgat ggaagttgct 300
aaattctcca tggacataga gagaaaggaa tgatattctc atcatcatct 350
tcatcatccc aggctctgac tgagtttctt tcagttttac tgatgttctg 400
ggtggggggac agagccagat tcagagtaat cttgactgaa tggagaaagt 450
ttctgtgcta cccctacaaa cccatgcctc actgacagac cagcattttt 500
ttttaacac gtcaataaaa aaataatctc ccaga 535

```

<210> 334  
<211> 85  
<212> PRT  
<213> Homo sapiens

<400> 334  
Met Lys Ile Thr Gly Gly Leu Leu Leu Cys Thr Val Val Tyr  
1 5 10 15  
Phe Cys Ser Ser Ser Glu Ala Ala Ser Leu Ser Pro Lys Lys Val  
20 25 30  
Asp Cys Ser Ile Tyr Lys Lys Tyr Pro Val Val Ala Ile Pro Cys  
35 40 45  
Pro Ile Thr Tyr Leu Pro Val Cys Gly Ser Asp Tyr Ile Thr Tyr  
50 55 60  
Gly Asn Glu Cys His Leu Cys Thr Glu Ser Leu Lys Ser Asn Gly  
65 70 75  
Arg Val Gln Phe Leu His Asp Gly Ser Cys  
80 85

<210> 335  
<211> 742  
<212> DNA  
<213> Homo sapiens

<400> 335  
ccgcgcgcgc gttctccctc gcagcacctc gaagtgcgcc cctcgccctc 50  
ctgctcgcgc cccgcgcgca tggctgcctc cccgcgcggg cctgctgtcc 100  
tggccctgac cgggctggcg ctgctcctgc tcctgtgctg gggcccaggt 150  
ggcataagtg gaaataaact caagctgatg cttcaaaaac gagaagcacc 200  
tgttccaact aagactaaag tggccgttga tgagaataaa gccaaagaat 250  
tccttggcag cctgaagcgc cagaagcggc agctgtggga ccggactcgg 300  
cccgaggtgc agcagtggta ccagcagttt ctctacatgg gctttgatga 350  
agcgaaattt gaagatgaca tcacctattg gcttaacaga gatcgaaatg 400  
gacatgaata ctatggcgat tactaccaac gtcactatga tgaagactct 450  
gcaattggtc cccggagccc ctacggcttt aggcattggag ccagcgtcaa 500  
ctacgatgac tactaaccat gacttgccac acgctgtaca agaagcaaat 550  
agcgattctc ttcatgtatc tcctaatagcc ttacactact tggtttctga 600  
tttgctctat ttcagcagat cttttctacc tactttgtgt gatcaaaaaa 650  
gaagagttaa aacaacacat gtaaatgcct tttgatattt catgggaatg 700



cctctcattt aaaaatagaa ataaagcatt ttgttaaaaa ga 742

<210> 336

<211> 148

<212> PRT

<213> Homo sapiens

<400> 336

Met	Ala	Ala	Ser	Pro	Ala	Arg	Pro	Ala	Val	Leu	Ala	Leu	Thr	Gly
1				5					10					15
Leu	Ala	Leu	Leu	Leu	Leu	Leu	Cys	Trp	Gly	Pro	Gly	Gly	Ile	Ser
			20						25					30
Gly	Asn	Lys	Leu	Lys	Leu	Met	Leu	Gln	Lys	Arg	Glu	Ala	Pro	Val
			35						40					45
Pro	Thr	Lys	Thr	Lys	Val	Ala	Val	Asp	Glu	Asn	Lys	Ala	Lys	Glu
				50					55					60
Phe	Leu	Gly	Ser	Leu	Lys	Arg	Gln	Lys	Arg	Gln	Leu	Trp	Asp	Arg
				65					70					75
Thr	Arg	Pro	Glu	Val	Gln	Gln	Trp	Tyr	Gln	Gln	Phe	Leu	Tyr	Met
				80					85					90
Gly	Phe	Asp	Glu	Ala	Lys	Phe	Glu	Asp	Asp	Ile	Thr	Tyr	Trp	Leu
				95					100					105
Asn	Arg	Asp	Arg	Asn	Gly	His	Glu	Tyr	Tyr	Gly	Asp	Tyr	Tyr	Gln
				110					115					120
Arg	His	Tyr	Asp	Glu	Asp	Ser	Ala	Ile	Gly	Pro	Arg	Ser	Pro	Tyr
				125					130					135
Gly	Phe	Arg	His	Gly	Ala	Ser	Val	Asn	Tyr	Asp	Asp	Tyr		
				140					145					

<210> 337

<211> 1310

<212> DNA

<213> Homo sapiens

<400> 337

cggtcgcgagc ccgcccggaa gtgcccgcagg ggccgcgatg gagctggggg 50

agccggggcgc tcggtagcgc ggcgggcaag gcaggcgcca tgaccctgat 100

tgaaggggtg ggtgatgagg tgaccgtcct tttctcgggtg cttgcctgcc 150

ttctggtgct ggcccttgcc tgggtctcaa cgcacaccgc tgagggcggg 200

gacccactgc cccagccgtc agggaccca acgcatccc agcccagcgc 250

agccatggca gctaccgaca gcatgagagg ggaggcccca ggggcagaga 300

```

ccccagcct gagacacaga ggtcaagctg cacagccaga gccagcacg 350
gggttcacag caacaccgcc agccccggac tccccgcagg agcccctcgt 400
gctacggctg aaattcctca atgattcaga gcaggtggcc agggcctggc 450
cccacgacac cattggctcc ttgaaaagga cccagtttcc cggccgggaa 500
cagcaggtgc gactcatcta ccaagggcag ctgctaggcg acgacacca 550
gaccctgggc agccttcacc tccctcccaa ctgcgttctc cactgccacg 600
tgtccacgag agtcgggtccc ccaaatcccc cctgcccgcc ggggtccgag 650
cccggcccct ccgggctgga aatcggcagc ctgctgctgc ccctgctgct 700
cctgctgttg ctgctgctct ggtactgcca gatccagtac cggcccttct 750
ttccccigac cgccactctg ggcttgccg gcttcaccct gtcctcagt 800
ctcctggcct ttgccatgta ccgcccgtag tgcctccgcg ggcgcttggc 850
agcgtcgccg gccctccgg accttgctcc ccgcgccgcg gcgggagctg 900
ctgcctgccc agggccgcct ctccggcctg cctcttcccg ctgccctgga 950
gccagccct gcgccgcaga ggactcccgg gactggcgga ggccccgccc 1000
tgcgaccgcc ggggctcggg gccacctccc ggggctgctg aacctcagcc 1050
cgactggga gtgggctcct cggggctcggg catctgctgt cgctgcctcg 1100
gccccgggca gagccgggcc gccccggggg cccgtcttag tgttctgccg 1150
gaggaccag ccgcctcaa tccctgacag ctccctgggc tgagttgggg 1200
acgccaggtc ggtgggaggc tgggaaggg gagcggggag gggcagagga 1250
gttccccgga acccgtgcag attaaagtaa ctgtgaagtt taaaaaaaaa 1300
aaaaaaaaa 1310

```

<210> 338

<211> 246

<212> PRT

<213> Homo sapiens

<400> 338

```

Met Thr Leu Ile Glu Gly Val Gly Asp Glu Val Thr Val Leu Phe
  1                      5                      10                      15

Ser Val Leu Ala Cys Leu Leu Val Leu Ala Leu Ala Trp Val Ser
                20                      25                      30

Thr His Thr Ala Glu Gly Gly Asp Pro Leu Pro Gln Pro Ser Gly
                35                      40                      45

```

Thr	Pro	Thr	Pro	Ser	Gln	Pro	Ser	Ala	Ala	Met	Ala	Ala	Thr	Asp	
				50					55					60	
Ser	Met	Arg	Gly	Glu	Ala	Pro	Gly	Ala	Glu	Thr	Pro	Ser	Leu	Arg	
				65					70					75	
His	Arg	Gly	Gln	Ala	Ala	Gln	Pro	Glu	Pro	Ser	Thr	Gly	Phe	Thr	
				80					85					90	
Ala	Thr	Pro	Pro	Ala	Pro	Asp	Ser	Pro	Gln	Glu	Pro	Leu	Val	Leu	
				95					100					105	
Arg	Leu	Lys	Phe	Leu	Asn	Asp	Ser	Glu	Gln	Val	Ala	Arg	Ala	Trp	
				110					115					120	
Pro	His	Asp	Thr	Ile	Gly	Ser	Leu	Lys	Arg	Thr	Gln	Phe	Pro	Gly	
				125					130					135	
Arg	Glu	Gln	Gln	Val	Arg	Leu	Ile	Tyr	Gln	Gly	Gln	Leu	Leu	Gly	
				140					145					150	
Asp	Asp	Thr	Gln	Thr	Leu	Gly	Ser	Leu	His	Leu	Pro	Pro	Asn	Cys	
				155					160					165	
Val	Leu	His	Cys	His	Val	Ser	Thr	Arg	Val	Gly	Pro	Pro	Asn	Pro	
				170					175					180	
Pro	Cys	Pro	Pro	Gly	Ser	Glu	Pro	Gly	Pro	Ser	Gly	Leu	Glu	Ile	
				185					190					195	
Gly	Ser	Leu	Leu	Leu	Pro	Leu	Leu	Leu	Leu	Leu	Leu	Leu	Leu	Leu	
				200					205					210	
Trp	Tyr	Cys	Gln	Ile	Gln	Tyr	Arg	Pro	Phe	Phe	Pro	Leu	Thr	Ala	
				215					220					225	
Thr	Leu	Gly	Leu	Ala	Gly	Phe	Thr	Leu	Leu	Leu	Ser	Leu	Leu	Ala	
				230					235					240	
Phe	Ala	Met	Tyr	Arg	Pro										
				245											

<210> 339

<211> 849

<212> DNA

<213> Homo sapiens

<400> 339

gagattggaa acagccaggt tggagcagtg agtgagtaag gaaacctggc 50

tgccctctcc agattcccca ggctctcaga gaagatcagc agaaagtctg 100

caagacccta agaaccatca gccctcagct gcacctctc cctccaagg 150

atgacaaagg cgctactcat ctatttggtc agcagctttc ttgccctaaa 200

tcaggccagc ctcatcagtc gctgtgactt ggcccaggtg ctgcagctgg 250

aggacttgga tgggtttgag ggttactccc tgagtgactg gctgtgcctg 300  
gcttttgtgg aaagcaagtt caacatatca aagataaatg aaaatgcgga 350  
tggaagcttt gactatggcc tcttcagat caacagccac tactggtgca 400  
acgattataa gagttactcg gaaaaccttt gccacgtaga ctgtcaagat 450  
ctgctgaatc ccaaccttct tgcaggcatc cactgcgcaa aaaggattgt 500  
gtccggagca cgggggatga acaactgggt agaatggagg ttgcactggt 550  
caggccggcc actctcctac tggctgacag gatgccgcct gagatgaaac 600  
aggggtgcggg tgcaccgtgg agtcattcca agactcctgt cctcactcag 650  
ggattcttca tttcttcttc ctactgcctc cacttcatgt tattttcttc 700  
ccttcccatt tacaactaaa actgaccaga gccccaggaa taaatggttt 750  
tcttggttc ctccttactc ccatctggac ccagtcccct gggttcctgtc 800  
tgttatttgt aaactgagga ccacaataaa gaaatcttta tatttatcg 849

<210> 340

<211> 148

<212> PRT

<213> Homo sapiens

<400> 340

Met	Thr	Lys	Ala	Leu	Leu	Ile	Tyr	Leu	Val	Ser	Ser	Phe	Leu	Ala
1				5					10					15
Leu	Asn	Gln	Ala	Ser	Leu	Ile	Ser	Arg	Cys	Asp	Leu	Ala	Gln	Val
				20					25					30
Leu	Gln	Leu	Glu	Asp	Leu	Asp	Gly	Phe	Glu	Gly	Tyr	Ser	Leu	Ser
				35					40					45
Asp	Trp	Leu	Cys	Leu	Ala	Phe	Val	Glu	Ser	Lys	Phe	Asn	Ile	Ser
				50					55					60
Lys	Ile	Asn	Glu	Asn	Ala	Asp	Gly	Ser	Phe	Asp	Tyr	Gly	Leu	Phe
				65					70					75
Gln	Ile	Asn	Ser	His	Tyr	Trp	Cys	Asn	Asp	Tyr	Lys	Ser	Tyr	Ser
				80					85					90
Glu	Asn	Leu	Cys	His	Val	Asp	Cys	Gln	Asp	Leu	Leu	Asn	Pro	Asn
				95					100					105
Leu	Leu	Ala	Gly	Ile	His	Cys	Ala	Lys	Arg	Ile	Val	Ser	Gly	Ala
				110					115					120
Arg	Gly	Met	Asn	Asn	Trp	Val	Glu	Trp	Arg	Leu	His	Cys	Ser	Gly
				125					130					135

Arg Pro Leu Ser Tyr Trp Leu Thr Gly Cys Arg Leu Arg  
140 145

<210> 341

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 341

ccctccaagg atgacaaagg cgc 23

<210> 342

<211> 29

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 342

ggtcagcagc tttcttgccc taaatcagg 29

<210> 343

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 343

atctcaggcg gcatcctgtc agcc 24

<210> 344

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 344

gtggatgcct gcaagaaggt tggg 24

<210> 345

<211> 45

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 345

agctttcttg ccctaaatca ggccagcctc atcagtcgct gtgac 45

<210> 346

<211> 2575

<212> DNA

<213> Homo sapiens

<400> 346

tctgacctga ctggaagcgt ccaaagaggg acggctgtca gccctgcttg 50

actgagaacc caccagctca tcccagacac ctcatagcaa cctatttata 100

caaaggggga aagaaacacc tgagcagaat ggaatcatta tttttttccc 150

aaggagaaaa ccggggtaaa gggaggggaag caattcaatt tgaagtcctt 200

gtgaatgggc tttcagaagg caattaaaga aatccactca gagaggactt 250

ggggtgaaac ttgggtcctg tggttttctg attgtaagtg gaagcaggtc 300

ttgcacacgc tgttggcaaa tgtcaggacc aggttaagtg actggcagaa 350

aaacttcag gtggaacaag caacccatgt tctgctgcaa gcttgaagga 400

gcctggagcg ggagaaagct aacttgaaca tgacctgttg catttgcaa 450

gttctagcaa catgctccta aggaagcgat acaggcacag accatgcaga 500

ctccagttcc tctgctgct cctgatgctg ggatgctcc tgatgatggt 550

ggcgatgttg caccctcccc accacacct gcaccagact gtcacagccc 600

aagccagcaa gcacagccct gaagccaggt accgcctgga ctttggggaa 650

tcccaggatt ggggtactgga agctgaggat gaggggtgaag agtacagccc 700

tctggagggc ctgccaccct ttatctcact gcgggaggat cagctgctgg 750

tggccgtggc cttaccccag gccagaagga accagagcca gggcaggaga 800

ggtgggagct accgcctcat caagcagcca aggaggcagg ataaggaagc 850

cccaaagagg gactgggggg ctgatgagga cggggaggtg tctgaagaag 900

aggagttgac ccggttcagc ctggaccac gtggcctcca ggaggcactc 950

agtgcccgca tccccctcca gagggctctg cccgaggtgc ggcacccact 1000

gtgtctgcag cagcacctc aggacagcct gccacagcc agcgtcatcc 1050

tctgtttcca tgatgaggcc tggccactc tctgcggac tgtacacagc 1100

atcctcgaca cagtgccag ggccttcctg aaggagatca tcctcgtgga 1150

cgacctcagc cagcaaggac aactcaagtc tgctctcagc gaatatgtgg 1200

ccaggctgga ggggggtgaag ttactcagga gcaacaagag gctgggtgcc 1250

atcagggccc ggatgctggg ggccaccaga gccaccgggg atgtgctcgt 1300  
 cttcatggat gcccactgcg agtgccaccc aggctggctg gagcccctcc 1350  
 tcagcagaat agctggtgac aggagccgag tggatatctcc ggtgatagat 1400  
 gtgattgact ggaagacttt ccagtattac ccctcaaagg acctgcagcg 1450  
 tgggggtgttg gactggaagc tggatttcca ctgggaacct ttgccagagc 1500  
 atgtgaggaa ggccctccag tccccataa gcccacatcag gagccctgtg 1550  
 gtgcccggag aggtggtggc catggacaga cattacttcc aaaacactgg 1600  
 agcgtatgac tctcttatgt cgctgcgagg tggtgaaaac ctcgaactgt 1650  
 ctttcaaggc ctggctctgt ggtggctctg ttgaaatcct tccctgctct 1700  
 cgggtaggac acatctacca aaatcaggat tccattccc ccctcgacca 1750  
 ggaggccacc ctgaggaaca gggttcgcat tgctgagacc tggctgggg 1800  
 cattcaaaga aaccttctac aagcatagcc cagaggcctt ctccttgagc 1850  
 aaggctgaga agccagactg catggaacgc ttgcagctgc aaaggagact 1900  
 gggttgtcgg acattccact ggtttctggc taatgtctac cctgagctgt 1950  
 acccatctga acccaggccc agtttctctg gaaagctcca caacactgga 2000  
 cttgggctct gtgcagactg ccaggcagaa ggggacatcc tgggctgtcc 2050  
 catggtgttg gctccttgca gtgacagccg gcagcaacag tacctgcagc 2100  
 acaccagcag gaaggagatt cactttggca gccacagca cctgtgcttt 2150  
 gctgtcaggc aggagcaggt gattcttcag aactgcacgg aggaaggcct 2200  
 ggccatccac cagcagcact gggacttcca ggagaatggg atgattgtcc 2250  
 acattctttc tgggaaatgc atggaagctg tggtgcaaga aaacaataaa 2300  
 gatttgtacc tgcgtccgtg tgatggaaaa gcccgccagc agtggcgatt 2350  
 tgaccagata aatgctgtgg atgaacgatg aatgtcaatg tcagaaggaa 2400  
 aagagaatth tggccatcaa aatccagctc caagtgaacg taaagagctt 2450  
 atatatttca tgaagctgat cttttgtgt gtgtgctcct tgtgttagga 2500  
 gagaaaaaag ctctatgaaa gaatatagga agtttctcct tttcacacct 2550  
 tatttcattg actgctggct gctta 2575

<210> 347

<211> 639

<212> PRT

<213> Homo sapiens

<400> 347

Met	Leu	Leu	Arg	Lys	Arg	Tyr	Arg	His	Arg	Pro	Cys	Arg	Leu	Gln
1				5					10					15
Phe	Leu	Leu	Leu	Leu	Leu	Met	Leu	Gly	Cys	Val	Leu	Met	Met	Val
				20					25					30
Ala	Met	Leu	His	Pro	Pro	His	His	Thr	Leu	His	Gln	Thr	Val	Thr
				35					40					45
Ala	Gln	Ala	Ser	Lys	His	Ser	Pro	Glu	Ala	Arg	Tyr	Arg	Leu	Asp
				50					55					60
Phe	Gly	Glu	Ser	Gln	Asp	Trp	Val	Leu	Glu	Ala	Glu	Asp	Glu	Gly
				65					70					75
Glu	Glu	Tyr	Ser	Pro	Leu	Glu	Gly	Leu	Pro	Pro	Phe	Ile	Ser	Leu
				80					85					90
Arg	Glu	Asp	Gln	Leu	Leu	Val	Ala	Val	Ala	Leu	Pro	Gln	Ala	Arg
				95					100					105
Arg	Asn	Gln	Ser	Gln	Gly	Arg	Arg	Gly	Gly	Ser	Tyr	Arg	Leu	Ile
				110					115					120
Lys	Gln	Pro	Arg	Arg	Gln	Asp	Lys	Glu	Ala	Pro	Lys	Arg	Asp	Trp
				125					130					135
Gly	Ala	Asp	Glu	Asp	Gly	Glu	Val	Ser	Glu	Glu	Glu	Glu	Leu	Thr
				140					145					150
Pro	Phe	Ser	Leu	Asp	Pro	Arg	Gly	Leu	Gln	Glu	Ala	Leu	Ser	Ala
				155					160					165
Arg	Ile	Pro	Leu	Gln	Arg	Ala	Leu	Pro	Glu	Val	Arg	His	Pro	Leu
				170					175					180
Cys	Leu	Gln	Gln	His	Pro	Gln	Asp	Ser	Leu	Pro	Thr	Ala	Ser	Val
				185					190					195
Ile	Leu	Cys	Phe	His	Asp	Glu	Ala	Trp	Ser	Thr	Leu	Leu	Arg	Thr
				200					205					210
Val	His	Ser	Ile	Leu	Asp	Thr	Val	Pro	Arg	Ala	Phe	Leu	Lys	Glu
				215					220					225
Ile	Ile	Leu	Val	Asp	Asp	Leu	Ser	Gln	Gln	Gly	Gln	Leu	Lys	Ser
				230					235					240
Ala	Leu	Ser	Glu	Tyr	Val	Ala	Arg	Leu	Glu	Gly	Val	Lys	Leu	Leu
				245					250					255
Arg	Ser	Asn	Lys	Arg	Leu	Gly	Ala	Ile	Arg	Ala	Arg	Met	Leu	Gly
				260					265					270



Ala Thr Arg Ala	Thr Gly Asp Val Leu Val Phe Met Asp Ala His	275	280	285
Cys Glu Cys His	Pro Gly Trp Leu Glu Pro Leu Leu Ser Arg Ile	290	295	300
Ala Gly Asp Arg	Ser Arg Val Val Ser Pro Val Ile Asp Val Ile	305	310	315
Asp Trp Lys Thr	Phe Gln Tyr Tyr Pro Ser Lys Asp Leu Gln Arg	320	325	330
Gly Val Leu Asp	Trp Lys Leu Asp Phe His Trp Glu Pro Leu Pro	335	340	345
Glu His Val Arg	Lys Ala Leu Gln Ser Pro Ile Ser Pro Ile Arg	350	355	360
Ser Pro Val Val	Pro Gly Glu Val Val Ala Met Asp Arg His Tyr	365	370	375
Phe Gln Asn Thr	Gly Ala Tyr Asp Ser Leu Met Ser Leu Arg Gly	380	385	390
Gly Glu Asn Leu	Glu Leu Ser Phe Lys Ala Trp Leu Cys Gly Gly	395	400	405
Ser Val Glu Ile	Leu Pro Cys Ser Arg Val Gly His Ile Tyr Gln	410	415	420
Asn Gln Asp Ser	His Ser Pro Leu Asp Gln Glu Ala Thr Leu Arg	425	430	435
Asn Arg Val Arg	Ile Ala Glu Thr Trp Leu Gly Ser Phe Lys Glu	440	445	450
Thr Phe Tyr Lys	His Ser Pro Glu Ala Phe Ser Leu Ser Lys Ala	455	460	465
Glu Lys Pro Asp	Cys Met Glu Arg Leu Gln Leu Gln Arg Arg Leu	470	475	480
Gly Cys Arg Thr	Phe His Trp Phe Leu Ala Asn Val Tyr Pro Glu	485	490	495
Leu Tyr Pro Ser	Glu Pro Arg Pro Ser Phe Ser Gly Lys Leu His	500	505	510
Asn Thr Gly Leu	Gly Leu Cys Ala Asp Cys Gln Ala Glu Gly Asp	515	520	525
Ile Leu Gly Cys	Pro Met Val Leu Ala Pro Cys Ser Asp Ser Arg	530	535	540
Gln Gln Gln Tyr	Leu Gln His Thr Ser Arg Lys Glu Ile His Phe	545	550	555

Gly	Ser	Pro	Gln	His	Leu	Cys	Phe	Ala	Val	Arg	Gln	Glu	Gln	Val
				560					565					570
Ile	Leu	Gln	Asn	Cys	Thr	Glu	Glu	Gly	Leu	Ala	Ile	His	Gln	Gln
				575					580					585
His	Trp	Asp	Phe	Gln	Glu	Asn	Gly	Met	Ile	Val	His	Ile	Leu	Ser
				590					595					600
Gly	Lys	Cys	Met	Glu	Ala	Val	Val	Gln	Glu	Asn	Asn	Lys	Asp	Leu
				605					610					615
Tyr	Leu	Arg	Pro	Cys	Asp	Gly	Lys	Ala	Arg	Gln	Gln	Trp	Arg	Phe
				620					625					630
Asp	Gln	Ile	Asn	Ala	Val	Asp	Glu	Arg						
				635										

<210> 348  
 <211> 23  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 348  
 ggagaggtgg tggccatgga cag 23

<210> 349  
 <211> 24  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 349  
 ctgtcactgc aaggagccaa cacc 24

<210> 350  
 <211> 45  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 350  
 tatgtcgctg cgaggtggtg aaaacctcga actgtctttc aaggc 45

<210> 351  
 <211> 2524  
 <212> DNA  
 <213> Homo sapiens

<400> 351

cgccaagcat gcagtaaagg ctgaaaatct gggtcacagc tgaggaagac 50  
ctcagacatg gagtccagga tgtggcctgc gctgctgctg tcccacctcc 100  
tccctctctg gccactgctg ttgctgcccc tcccaccgcc tgctcagggc 150  
tcttcatcct cccctcgaac cccaccagcc ccagcccgcc ccccggtgtgc 200  
caggggaggg ccctcgcccc cagtcattgt gtgctgtgtg gagcgagcac 250  
ctccaccaag ccgatctcct cgggtcccaa gatcacgtcg gcaagtcctg 300  
cctggcactg cccccccagc cccccatca ggctttgagg aggggccgcc 350  
ctcatcccaa taccctgagg ctatcgtgtg gggteccacc gtgtctcgag 400  
aggatggagg ggacccaac tctgccaatc ccggatttct ggactatggg 450  
tttgagccc ctcatgggct cgcaaccca caccacaact cagactccat 500  
gcgaggtgat ggagatgggc ttatccttgg agaggcacct gccaccctgc 550  
ggccattcct gttcgggggc cgtggggaag gtgtggaccc ccagctctat 600  
gtcacaatta ccattccat catcattgtt ctctgggcca ctggcatcat 650  
cttcaagttc tgctgggacc gcagccagaa gcgacgcaga ccctcagggc 700  
agcaaggtgc cctgaggcag gaggagagcc agcagccact gacagacctg 750  
tccccggtg gagtcaactgt gctggggggc ttcggggact cacctacccc 800  
caccctgac catgaggagc cccgaggggg accccggcct gggatgcccc 850  
acccaaggg ggctccagcc ttccagttga accggtgagg gcaggggcaa 900  
tgggatggga gggcaaagag ggaaggcaac ttaggtcttc agagctgggg 950  
tgggggtgcc ctctggatgg gtagtgagga ggcaggcgtg gcctcccaca 1000  
gcccctggcc ctcccaaggg ggctggacca gctcctctct gggaggcacc 1050  
cttccttctc ccagtctctc aggatctgtg tcctattctc tgctgcccac 1100  
aactccaact ctgccctctt tggtttttct tcatgccacc ttgtctaaga 1150  
caactctgcc ctcttaacct tgattcccc tctttgtctt gaacttcccc 1200  
ttctattctg gcctaccct tggttcctga ctgtgccctt tccctcttcc 1250  
tctcaggatt cccctggtga atctgtgatg ccccaatgt tggggtgcag 1300  
ccaagcagga ggccaagggg ccggcacagc ccccatcca ctgaggggtg 1350  
ggcagctgtg gggagctggg gccacagggg ctctggctc ctgccccttg 1400

cacaccaccc ggaacactcc ccagccccac gggcaatcct atctgctcgc 1450  
 cctcctgcag gtgggggcct cacatatctg tgacttcggg tccctgtccc 1500  
 cacccttggtg cactcacatg aaagccttgc acactcacct ccaccttcac 1550  
 aggccatttg cacacgctcc tgcaccctct ccccgctccat accgctccgc 1600  
 tcagctgact ctcatgttct ctggtctcac atttgcactc tctccttccc 1650  
 acattctgtg ctgagctcac tcagtgttca gcgtttcctg cacactttac 1700  
 ctctcatgtg cgtttcccggt cctgatgttg tgggtggtgtg cggcgtgctc 1750  
 actctctccc tcatgaacac ccacccacct cgtttccgca gcccctgcgt 1800  
 gctgctccag aggtgggtgg gaggtgagct gggggctcct tgggccctca 1850  
 tcggtcatgg tctcgtccca ttccacacca tttgtttctc tgtctcccca 1900  
 tcctactcca aggatgccgg catcacctg agggctcccc cttgggaatg 1950  
 gggtagtgag gcccagact tcacccccag cccactgcta aaatctgttt 2000  
 tctgacagat gggttttggg gagtcgcctg ctgcactaca tgagaaagg 2050  
 actccatttt gcccttcctt ttctcttaca gtcccttttg tcttgtctgt 2100  
 cctggctgtc tgtgtgtgtg ccattctctg gacttcagag cccctgagc 2150  
 cagtcctccc ttccagcct ccttttgggc ctccctaact ccacctaggc 2200  
 tgccagggac cggagtcagc tggttcaagg ccacgggag ctctgcctcc 2250  
 aagtctaccc ttcccttccc ggactccctc ctgtccctc ctttccctcc 2300  
 tccttccctc cactctcctt ccttttgctt cctgcccctt tccccctcct 2350  
 caggttcttc cctccttctc actggttttt ccaccttccct ccttcccttc 2400  
 ttccctggct cctaggctgt gatatatatt tttgtattat ctctttcttc 2450  
 ttcttgtggt gatcatcttg aattactgtg ggatgtaagt ttcaaaattt 2500  
 tcaaataaag cctttgcaag ataa 2524

<210> 352

<211> 243

<212> PRT

<213> Homo sapiens

<400> 352

Met	Arg	Pro	Gln	Gly	Pro	Ala	Ala	Ser	Pro	Gln	Arg	Leu	Arg	Gly
1				5					10					15

Leu	Leu	Leu	Leu	Leu	Leu	Leu	Gln	Leu	Pro	Ala	Pro	Ser	Ser	Ala
				20					25					30

Ser	Glu	Ile	Pro	Lys	Gly	Lys	Gln	Lys	Ala	Gln	Leu	Arg	Gln	Arg	35	40	45
Glu	Val	Val	Asp	Leu	Tyr	Asn	Gly	Met	Cys	Leu	Gln	Gly	Pro	Ala	50	55	60
Gly	Val	Pro	Gly	Arg	Asp	Gly	Ser	Pro	Gly	Ala	Asn	Val	Ile	Pro	65	70	75
Gly	Thr	Pro	Gly	Ile	Pro	Gly	Arg	Asp	Gly	Phe	Lys	Gly	Glu	Lys	80	85	90
Gly	Glu	Cys	Leu	Arg	Glu	Ser	Phe	Glu	Glu	Ser	Trp	Thr	Pro	Asn	95	100	105
Tyr	Lys	Gln	Cys	Ser	Trp	Ser	Ser	Leu	Asn	Tyr	Gly	Ile	Asp	Leu	110	115	120
Gly	Lys	Ile	Ala	Glu	Cys	Thr	Phe	Thr	Lys	Met	Arg	Ser	Asn	Ser	125	130	135
Ala	Leu	Arg	Val	Leu	Phe	Ser	Gly	Ser	Leu	Arg	Leu	Lys	Cys	Arg	140	145	150
Asn	Ala	Cys	Cys	Gln	Arg	Trp	Tyr	Phe	Thr	Phe	Asn	Gly	Ala	Glu	155	160	165
Cys	Ser	Gly	Pro	Leu	Pro	Ile	Glu	Ala	Ile	Ile	Tyr	Leu	Asp	Gln	170	175	180
Gly	Ser	Pro	Glu	Met	Asn	Ser	Thr	Ile	Asn	Ile	His	Arg	Thr	Ser	185	190	195
Ser	Val	Glu	Gly	Leu	Cys	Glu	Gly	Ile	Gly	Ala	Gly	Leu	Val	Asp	200	205	210
Val	Ala	Ile	Trp	Val	Gly	Thr	Cys	Ser	Asp	Tyr	Pro	Lys	Gly	Asp	215	220	225
Ala	Ser	Thr	Gly	Trp	Asn	Ser	Val	Ser	Arg	Ile	Ile	Ile	Glu	Glu	230	235	240

Leu Pro Lys

<210> 353

<211> 480

<212> DNA

<213> Homo sapiens

<400> 353

gttaaccagc gcagtcctcc gtgcgtcccg cccgccgctg ccctcaactcc 50

cggccaggat ggcatacctgt ctggccctgc gcatggcgct gctgctggtc 100

tccgggggttc tggcccctgc ggtgctcaca gacgatgttc cacaggagcc 150

cgtgcccacg ctgtggaacg agccggccga gctgccgtcg ggagaaggcc 200  
 ccgtggagag caccagcccc ggccgggagc ccgtggacac cggcccccca 250  
 gccccaccg tcgcgccagg acccgaggac agcaccgcgc aggagcggct 300  
 ggaccagggc ggcgggtcgc tggggcccgg cgctatcgcg gccatcgtga 350  
 tcgccgccct gctggccacc tgcgtggtgc tggcgctcgt ggtcgtcgcg 400  
 ctgagaaagt tttctgcctc ctgaagcgaa taaagggggc gcgcccggcc 450  
 gcggcgcgac tcggcaaaaa aaaaaaaaaa 480

<210> 354

<211> 121

<212> PRT

<213> Homo sapiens

<400> 354

Met	Ala	Ser	Cys	Leu	Ala	Leu	Arg	Met	Ala	Leu	Leu	Leu	Val	Ser	1	5	10	15
Gly	Val	Leu	Ala	Pro	Ala	Val	Leu	Thr	Asp	Asp	Val	Pro	Gln	Glu	20	25	30	
Pro	Val	Pro	Thr	Leu	Trp	Asn	Glu	Pro	Ala	Glu	Leu	Pro	Ser	Gly	35	40	45	
Glu	Gly	Pro	Val	Glu	Ser	Thr	Ser	Pro	Gly	Arg	Glu	Pro	Val	Asp	50	55	60	
Thr	Gly	Pro	Pro	Ala	Pro	Thr	Val	Ala	Pro	Gly	Pro	Glu	Asp	Ser	65	70	75	
Thr	Ala	Gln	Glu	Arg	Leu	Asp	Gln	Gly	Gly	Gly	Ser	Leu	Gly	Pro	80	85	90	
Gly	Ala	Ile	Ala	Ala	Ile	Val	Ile	Ala	Ala	Leu	Leu	Ala	Thr	Cys	95	100	105	
Val	Val	Leu	Ala	Leu	Val	Val	Val	Ala	Leu	Arg	Lys	Phe	Ser	Ala	110	115	120	
Ser																		

<210> 355

<211> 2134

<212> DNA

<213> Homo sapiens

<400> 355

ggccgttggt tgggtgcgcg ctgaaggggtg tggcgcgagc agcgtcgttg 50  
 gttggccggc ggccgggccc gacgggcatg gccctgctgc tgtgcctggg 100

gtgcctgacg gcggcgctgg cccacggctg tctgcaactg cacagcaact 150  
tctccaagaa gttctccttc taccgccacc atgtgaactt caagtctctg 200  
tgggtgggcg acatccccgt gtcaggggcg ctgctcaccg actggagcga 250  
cgacacgatg aaggagctgc acctggccat ccccgccaag atcaccggg 300  
agaagctgga ccaagtggcg acagcagtgt accagatgat ggatcagctg 350  
taccagggga agatgtactt ccccggtat ttcccaacg agctgcgaaa 400  
catcttccg gagcaggtgc acctcatcca gaacgccatc atcgaaaggc 450  
acctggcacc aggcagctgg ggaggagggc agctctccag ggagggaccc 500  
agcctagcac ctgaaggatc aatgccatca ccccgcgggg acctccccta 550  
agtagcccc agaggcgctg ggagtgttg caccgccctc ccctgaagtt 600  
tgctccatct cacgctggg gtcaacctgg ggaccccttc cctccgggccc 650  
atggacacac atacatgaaa accaggccgc atcgactgtc agcaccgctg 700  
tggcatcttc cagtacgaga ccatctcctg caacaactgc acagactcgc 750  
acgtgcctg ctttggtat aactgcgagt agggctcagg catcacacc 800  
accgtgccca gggccctact gtccctgggg tcccaggctc tccttgagg 850  
gggctccccg ccttccacct ggctgtcatc gggtagggcg gggccgtggg 900  
ttcaggggcg caccacttcc aagcctgtgt cccacaggctc ctcggcgcag 950  
tggaagtcag ctgtccaggg cctcctgaac tacataaata actggcacia 1000  
gtaagtcccc tcctcaaacc aacacaggca gtgtgtgtat gtgagcacct 1050  
cgtgggtgag tatgtgtgg gcacaggctg gctccctcag ctcccacgtc 1100  
ctagaggggc tcccaggag gtggaacctc aaccagctc tgcgcaggag 1150  
gcggctgcag tccttttctc cctcaaaggc ctccgaccct cagctggagg 1200  
cgggcatctt tcctaaaggg tcccataagg gtctggttcc acccatccc 1250  
aggtctgtgg tcagagcctg ggagggttcc ctacgatggt taggggtgcc 1300  
ccatggaggg gctgactgcc ccacattgcc tttcagacag gacacgagca 1350  
tgaggtaagg ccgccctgac ctggacttca gggggagggg gtaaaggag 1400  
agaggagggg ggctagggg tcctctagat cagtgggggc actgcaggtg 1450  
gggctctccc tatacctggg acacctgctg gatgtcacct ctgcaaccac 1500

acccatgtgg tggtttcatg aacagaccac gtcctctgc cttctcctgg 1550  
 cctgggacac acagagccac cccggccttg tgagtgaccc agagaaggga 1600  
 ggcctcggga gaaggggtgc tcgtaagcca acaccagcgt gccgcggcct 1650  
 gcacaccctt cggacatccc aggcacgagg gtgtcgtgga tgtggccaca 1700  
 cataggacca cacgtcccag ctgggaggag aggcctgggg ccccaggga 1750  
 gggaggcagg ggggtggggga catggagagc tgaggcagcc tcgtctcccc 1800  
 gcagcctggt atcgccagcc ttaaggtgtc tggagcccc acacttggcc 1850  
 aacctgacct tggaagatgc tgctgagtgt ctcaagcagc actgacagca 1900  
 gctgggcctg cccaggggca acgtgggggc ggagactcag ctggacagcc 1950  
 cctgcctgtc actctggagc tgggctgctg ctgcctcagg accccctctc 2000  
 cgaccccgga cagagctgag ctggccaggg ccaggagggc gggagggagg 2050  
 gaatgggggt gggctgtgcg cagcatcagc gcctgggcag gtccgcagag 2100  
 ctgcgggatg tgattaaagt ccctgatgtt tctc 2134

<210> 356

<211> 157

<212> PRT

<213> Homo sapiens

<400> 356

Met	Ala	Leu	Leu	Leu	Cys	Leu	Val	Cys	Leu	Thr	Ala	Ala	Leu	Ala
1				5					10					15

His	Gly	Cys	Leu	His	Cys	His	Ser	Asn	Phe	Ser	Lys	Lys	Phe	Ser
			20						25					30

Phe	Tyr	Arg	His	His	Val	Asn	Phe	Lys	Ser	Trp	Trp	Val	Gly	Asp
			35						40					45

Ile	Pro	Val	Ser	Gly	Ala	Leu	Leu	Thr	Asp	Trp	Ser	Asp	Asp	Thr
			50						55					60

Met	Lys	Glu	Leu	His	Leu	Ala	Ile	Pro	Ala	Lys	Ile	Thr	Arg	Glu
			65						70					75

Lys	Leu	Asp	Gln	Val	Ala	Thr	Ala	Val	Tyr	Gln	Met	Met	Asp	Gln
			80						85					90

Leu	Tyr	Gln	Gly	Lys	Met	Tyr	Phe	Pro	Gly	Tyr	Phe	Pro	Asn	Glu
			95						100					105

Leu	Arg	Asn	Ile	Phe	Arg	Glu	Gln	Val	His	Leu	Ile	Gln	Asn	Ala
			110						115					120

Ile	Ile	Glu	Arg	His	Leu	Ala	Pro	Gly	Ser	Trp	Gly	Gly	Gly	Gln
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----



	125		130		135
Leu Ser Arg Glu Gly Pro Ser Leu Ala Pro Glu Gly Ser Met Pro					
	140		145		150
Ser Pro Arg Gly Asp Leu Pro					
	155				

<210> 357

<211> 1536

<212> DNA

<213> Homo sapiens

<400> 357

```

agcaggagca ggagagggac aatggaagct gccccgtcca ggttcatgtt 50
cctcttattt ctctcacgt gtgagctggc tgcagaagtt gctgcagaag 100
ttgagaaatc ctcatggtt cctggtgctg cccaggaacc cacgtggctc 150
acagatgtcc cagctgccat ggaattcatt gctgccactg aggtggctgt 200
cataggcttc ttccaggatt tagaaatacc agcagtgcc atactccata 250
gcatggtgca aaaattccca ggcgtgtcat ttgggatcag cactgattct 300
gaggttctga cactactaca catcactggg aacaccatct gcctctttcg 350
cctggtagac aatgaacaac tgaatttaga ggacgaagac attgaaagca 400
ttgatgccac caaattgagc cgtttcattg agatcaacag cctccacatg 450
gtgacagagt acaaccctgt gactgtgatt gggttattca acagcgtaat 500
tcagattcat ctctctctga taatgaacaa ggctcccca gagtatgaag 550
agaacatgca cagataccag aaggcagcca agctcttcca ggggaagatt 600
ctctttattc tgggtggacag tggatatgaaa gaaaatggga aggtgatatc 650
atcttttcaa ctaaaggagt ctcaactgcc agctttggca atttaccaga 700
ctctagatga cgagtgggat aactgcccc cagcagaagt ttccgtagag 750
catgtgcaaa acttttgtga tggattccta agtggaatat tgttgaaaga 800
aaatcgtgaa tcagaaggaa agactccaaa ggtggaactc tgacttctcc 850
ttggaactac atatggccaa gtatctactt tatgcaaagt aaaaaggcac 900
aactcaaatc tcagagacac taaacaacag gatcactagg cctgccaacc 950
acacacacac gcacgtgcac acacgcacgc acgcgtgcac acacacacgc 1000
gcacacacac acacacacag agcttcattt cctgtcttaa aatctcgttt 1050
tctcttcttc cttcttttaa atttcatatc ctcaactcct atccaatttc 1100

```

cttcttatcg tgcattcata ctctgtaagc ccatctgtaa cacacctaga 1150  
 tcaaggcttt aagagactca ctgtgatgcc tctatgaaag agaggcattc 1200  
 ctagagaaag attgttccaa tttgtcattt aatatcaagt ttgtatactg 1250  
 cacatgactt acacacaaca tagttcctgc tcttttaagg ttacctaaagg 1300  
 gttgaaactc taccttcttt cataagcaca tgtccgtctc tgactcagga 1350  
 tcaaaaacca aaggatgggt ttaaacacct ttgtgaaatt gtctttttgc 1400  
 cagaagttaa aggctgtctc caagtccttg aactcagcag aaatagacca 1450  
 tgtgaaaact ccatgcttgg ttagcatctc caactcccta tgtaaataca 1500  
 caacctgcat aataaataaa aggcaatcat gttata 1536

<210> 358

<211> 273

<212> PRT

<213> Homo sapiens

<400> 358

Met	Glu	Ala	Ala	Pro	Ser	Arg	Phe	Met	Phe	Leu	Leu	Phe	Leu	Leu	1	5	10	15
Thr	Cys	Glu	Leu	Ala	Ala	Glu	Val	Ala	Ala	Glu	Val	Glu	Lys	Ser	20	25	30	
Ser	Asp	Gly	Pro	Gly	Ala	Ala	Gln	Glu	Pro	Thr	Trp	Leu	Thr	Asp	35	40	45	
Val	Pro	Ala	Ala	Met	Glu	Phe	Ile	Ala	Ala	Thr	Glu	Val	Ala	Val	50	55	60	
Ile	Gly	Phe	Phe	Gln	Asp	Leu	Glu	Ile	Pro	Ala	Val	Pro	Ile	Leu	65	70	75	
His	Ser	Met	Val	Gln	Lys	Phe	Pro	Gly	Val	Ser	Phe	Gly	Ile	Ser	80	85	90	
Thr	Asp	Ser	Glu	Val	Leu	Thr	His	Tyr	Asn	Ile	Thr	Gly	Asn	Thr	95	100	105	
Ile	Cys	Leu	Phe	Arg	Leu	Val	Asp	Asn	Glu	Gln	Leu	Asn	Leu	Glu	110	115	120	
Asp	Glu	Asp	Ile	Glu	Ser	Ile	Asp	Ala	Thr	Lys	Leu	Ser	Arg	Phe	125	130	135	
Ile	Glu	Ile	Asn	Ser	Leu	His	Met	Val	Thr	Glu	Tyr	Asn	Pro	Val	140	145	150	
Thr	Val	Ile	Gly	Leu	Phe	Asn	Ser	Val	Ile	Gln	Ile	His	Leu	Leu	155	160	165	

Leu	Ile	Met	Asn	Lys	Ala	Ser	Pro	Glu	Tyr	Glu	Glu	Asn	Met	His
				170					175					180
Arg	Tyr	Gln	Lys	Ala	Ala	Lys	Leu	Phe	Gln	Gly	Lys	Ile	Leu	Phe
				185					190					195
Ile	Leu	Val	Asp	Ser	Gly	Met	Lys	Glu	Asn	Gly	Lys	Val	Ile	Ser
				200					205					210
Phe	Phe	Lys	Leu	Lys	Glu	Ser	Gln	Leu	Pro	Ala	Leu	Ala	Ile	Tyr
				215					220					225
Gln	Thr	Leu	Asp	Asp	Glu	Trp	Asp	Thr	Leu	Pro	Thr	Ala	Glu	Val
				230					235					240
Ser	Val	Glu	His	Val	Gln	Asn	Phe	Cys	Asp	Gly	Phe	Leu	Ser	Gly
				245					250					255
Lys	Leu	Leu	Lys	Glu	Asn	Arg	Glu	Ser	Glu	Gly	Lys	Thr	Pro	Lys
				260					265					270

Val Glu Leu

<210> 359

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 359

ccagcagtgc ccatactcca tagc 24

<210> 360

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 360

tgacgagtgg gatacactgc 20

<210> 361

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 361

gctctacgga aacttctgct gtgg 24

<210> 362  
<211> 50  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 362  
attcccaggc gtgtcatttg ggatcagcac tgattctgag gttctgacac 50

<210> 363  
<211> 1777  
<212> DNA  
<213> Homo sapiens

<400> 363  
ggagagccgc ggctgggacc ggagtgggga gcgcggcgctg gaggtgccac 50  
ccggcgcggg tggcggagag atcagaagcc tcttcccca gccgagccaa 100  
cctcagcggg gacccgggct cagggacgcg gcggcgggcg cggcgactgc 150  
agtggctgga cgatggcagc gtccgccgga gccggggcg tgattgcagc 200  
cccagacagc cggcgctggc tgtggtcggt gctggcgggc gcgcttgggc 250  
tcttgacagc tggagtatca gccttggaa tatatacgcc aaaagaaatc 300  
ttcgtggcaa atggtacaca agggaagctg acctgcaagt tcaagtctac 350  
tagtacgact ggcgggttga cctcagtctc ctggagcttc cagccagagg 400  
gggccgacac tactgtgtcg tttttccact actcccaagg gcaagtgtac 450  
cttgggaatt atccaccatt taaagacaga atcagctggg ctggagacct 500  
tgacaagaaa gatgcatcaa tcaacataga aaatatgcag ttatacaca 550  
atggcaccta tatctgtgat gtcaaaaacc ctctgacat cgttgtccag 600  
cctggacaca ttaggctcta tgtcgtagaa aaagagaatt tgctgtgtt 650  
tccagtttgg gtagtggtgg gcatagttac tgctgtggtc ctaggtctca 700  
ctctgctcat cagcatgatt ctggctgtcc tctatagaag gaaaaactct 750  
aaacgggatt aactggctg cagtacatca gagagtttgt caccagttaa 800  
gcaggctcct cggaagtccc cctccgacac tgagggtctt gtaaagagtc 850  
tgcttcttgg atctcaccag ggcccagtc tatatgcaca gttagaccac 900  
tccggcggac atcacagtga caagattaac aagtcagagt ctgtggtgta 950  
tgcgatatc cgaaagaatt aagagaatac ctagaacata tcctcagcaa 1000

gaaacaaaac caaactggac tctcgtgcag aaaatgtagc ccattaccac 1050  
 atgtagcctt ggagaccag gcaaggacaa gtacacgtgt actcacagag 1100  
 ggagagaaaag atgtgtacaa aggatatgta taaatattct atttagtcat 1150  
 cctgatatga ggagccagtg ttgcatgatg aaaagatggg atgattctac 1200  
 atatgtaccc attgtcttgc tgtttttgta ctttcttttc aggtcattta 1250  
 caattgggag atttcagaaa cattcctttc accatcattt agaaatgggt 1300  
 tgccttaatg gagacaatag cagatcctgt agtattttcca gtagacatgg 1350  
 ccttttaatc taagggttta agactgatta gtcttagcat ttactgtagt 1400  
 tggaggatgg agatgctatg atggaagcat acccaggggtg gccttttagca 1450  
 cagtatcagt accatttatt tgtctgccgc ttttaaaaaa taccattgg 1500  
 ctatgccact tgaaaacaat ttgagaagtt tttttgaagt ttttctcact 1550  
 aaaatatggg gcaattgtta gccttacatg ttgtgtagac ttactttaag 1600  
 tttgcaccct tgaaatgtgt catatcaatt tctggattca taatagcaag 1650  
 attagcaaag gataaatgcc gaaggctact tcattctgga cacagttgga 1700  
 tcaatactga ttaagtagaa aatccaagct ttgcttgaga acttttgtaa 1750  
 cgtggagagt aaaaagtatc ggtttta 1777

<210> 364

<211> 269

<212> PRT

<213> Homo sapiens

<400> 364

Met	Ala	Ala	Ser	Ala	Gly	Ala	Gly	Ala	Val	Ile	Ala	Ala	Pro	Asp
1				5					10					15

Ser	Arg	Arg	Trp	Leu	Trp	Ser	Val	Leu	Ala	Ala	Ala	Leu	Gly	Leu
				20					25					30

Leu	Thr	Ala	Gly	Val	Ser	Ala	Leu	Glu	Val	Tyr	Thr	Pro	Lys	Glu
				35					40					45

Ile	Phe	Val	Ala	Asn	Gly	Thr	Gln	Gly	Lys	Leu	Thr	Cys	Lys	Phe
				50					55					60

Lys	Ser	Thr	Ser	Thr	Thr	Gly	Gly	Leu	Thr	Ser	Val	Ser	Trp	Ser
				65					70					75

Phe	Gln	Pro	Glu	Gly	Ala	Asp	Thr	Thr	Val	Ser	Phe	Phe	His	Tyr
				80					85					90

Ser	Gln	Gly	Gln	Val	Tyr	Leu	Gly	Asn	Tyr	Pro	Pro	Phe	Lys	Asp	
				95					100					105	
Arg	Ile	Ser	Trp	Ala	Gly	Asp	Leu	Asp	Lys	Lys	Asp	Ala	Ser	Ile	
				110					115					120	
Asn	Ile	Glu	Asn	Met	Gln	Phe	Ile	His	Asn	Gly	Thr	Tyr	Ile	Cys	
				125					130					135	
Asp	Val	Lys	Asn	Pro	Pro	Asp	Ile	Val	Val	Gln	Pro	Gly	His	Ile	
				140					145					150	
Arg	Leu	Tyr	Val	Val	Glu	Lys	Glu	Asn	Leu	Pro	Val	Phe	Pro	Val	
				155					160					165	
Trp	Val	Val	Val	Gly	Ile	Val	Thr	Ala	Val	Val	Leu	Gly	Leu	Thr	
				170					175					180	
Leu	Leu	Ile	Ser	Met	Ile	Leu	Ala	Val	Leu	Tyr	Arg	Arg	Lys	Asn	
				185					190					195	
Ser	Lys	Arg	Asp	Tyr	Thr	Gly	Cys	Ser	Thr	Ser	Glu	Ser	Leu	Ser	
				200					205					210	
Pro	Val	Lys	Gln	Ala	Pro	Arg	Lys	Ser	Pro	Ser	Asp	Thr	Glu	Gly	
				215					220					225	
Leu	Val	Lys	Ser	Leu	Pro	Ser	Gly	Ser	His	Gln	Gly	Pro	Val	Ile	
				230					235					240	
Tyr	Ala	Gln	Leu	Asp	His	Ser	Gly	Gly	His	His	Ser	Asp	Lys	Ile	
				245					250					255	
Asn	Lys	Ser	Glu	Ser	Val	Val	Tyr	Ala	Asp	Ile	Arg	Lys	Asn		
				260					265						

<210> 365

<211> 1321

<212> DNA

<213> Homo sapiens

<400> 365

```

gccggctgtg cagagacgcc atgtaccggc tctgtcagc agtgactgcc 50
cgggctgccg cccccggggg cttggcctca agctgcggac gacgcggggt 100
ccatcagcgc gccgggctgc cgcctctcgg ccacggctgg gtcggggggc 150
tcgggctggg gctggggctg gcgctcgggg tgaagctggc aggtgggctg 200
aggggcgcgg ccccggcgca gtccccgcg gccccgacc ctgaggcgtc 250
gcctctggcc gagecgccac aggagcagtc cctcgccccg tggctctcgc 300
agaccccggc gccgcctgc tccaggtgct tcgccagagc catcgagagc 350
agccgcgacc tgctgcacag gatcaaggat gaggtgggcg caccgggcat 400

```

agtggttgga gtttctgtag atggaaaaga agtctggtca gaaggtttag 450  
 gttatgctga tggtgagaac cgtgtaccat gtaaaccaga gacagttag 500  
 cgaattgcta gcatcagcaa aagtctcacc atggttgctc ttgccaaatt 550  
 gtgggaagca gggaaactgg atcttgatat tccagtacaa cattatgttc 600  
 ccgaattccc agaaaaagaa tatgaagggtg aaaagggttc tgtcacaaca 650  
 agattactga tttcccatTTT aagtggaatt cgtcattatg aaaaggacat 700  
 aaaaaagggtg aaagaagaga aagcttataa agccttgaag atgatgaaag 750  
 agaatgttgc atttgagcaa gaaaaagaag gcaaaagtaa tgaaaagaat 800  
 gatTTTacta aatttaaaac agagcaggag aatgaagcca aatgccggaa 850  
 ttcaaaacct ggcaagaaaa agaatgattt tgaacaaggc gaattatatt 900  
 tgagagaaaa gtttgaaaat tcaattgaat ccctaagatt atttaaaaat 950  
 gatcctttgt tcttcaaacc tggtagtcag tttttgtatt caacttttgg 1000  
 ctatacccta ctggcagcca tagtagagag agcttcagga tgtaaattatt 1050  
 tggactatat gcagaaaata ttccatgact tggatatgct gacgactgtg 1100  
 caggaagaaa acgagccagt gatttacaat agagcaagggt aaatgaatac 1150  
 cttctgctgt gtctagctat atcgcatctt aacactatTTT tattaattaa 1200  
 aagtcaaatt ttctttgttt ccattccaaa atcaacctgc cacattttgg 1250  
 gagcttttct acatgtctgt tttctcatct gtaaagtga ggaagtaaaa 1300  
 catgTTTata aagtaaaaaa a 1321

<210> 366

<211> 373

<212> PRT

<213> Homo sapiens

<400> 366

Met	Tyr	Arg	Leu	Leu	Ser	Ala	Val	Thr	Ala	Arg	Ala	Ala	Ala	Pro
1				5					10					15

Gly	Gly	Leu	Ala	Ser	Ser	Cys	Gly	Arg	Arg	Gly	Val	His	Gln	Arg
				20					25					30

Ala	Gly	Leu	Pro	Pro	Leu	Gly	His	Gly	Trp	Val	Gly	Gly	Leu	Gly
				35					40					45

Leu	Gly	Leu	Gly	Leu	Ala	Leu	Gly	Val	Lys	Leu	Ala	Gly	Gly	Leu
				50					55					60

Arg Gly Ala Ala	Pro Ala Gln Ser Pro Ala Ala Pro Asp Pro Glu	65	70	75
Ala Ser Pro Leu	Ala Glu Pro Pro Gln Glu Gln Ser Leu Ala Pro	80	85	90
Trp Ser Pro Gln	Thr Pro Ala Pro Pro Cys Ser Arg Cys Phe Ala	95	100	105
Arg Ala Ile Glu	Ser Ser Arg Asp Leu Leu His Arg Ile Lys Asp	110	115	120
Glu Val Gly Ala	Pro Gly Ile Val Val Gly Val Ser Val Asp Gly	125	130	135
Lys Glu Val Trp	Ser Glu Gly Leu Gly Tyr Ala Asp Val Glu Asn	140	145	150
Arg Val Pro Cys	Lys Pro Glu Thr Val Met Arg Ile Ala Ser Ile	155	160	165
Ser Lys Ser Leu	Thr Met Val Ala Leu Ala Lys Leu Trp Glu Ala	170	175	180
Gly Lys Leu Asp	Leu Asp Ile Pro Val Gln His Tyr Val Pro Glu	185	190	195
Phe Pro Glu Lys	Glu Tyr Glu Gly Glu Lys Val Ser Val Thr Thr	200	205	210
Arg Leu Leu Ile	Ser His Leu Ser Gly Ile Arg His Tyr Glu Lys	215	220	225
Asp Ile Lys Lys	Val Lys Glu Glu Lys Ala Tyr Lys Ala Leu Lys	230	235	240
Met Met Lys Glu	Asn Val Ala Phe Glu Gln Glu Lys Glu Gly Lys	245	250	255
Ser Asn Glu Lys	Asn Asp Phe Thr Lys Phe Lys Thr Glu Gln Glu	260	265	270
Asn Glu Ala Lys	Cys Arg Asn Ser Lys Pro Gly Lys Lys Lys Asn	275	280	285
Asp Phe Glu Gln	Gly Glu Leu Tyr Leu Arg Glu Lys Phe Glu Asn	290	295	300
Ser Ile Glu Ser	Leu Arg Leu Phe Lys Asn Asp Pro Leu Phe Phe	305	310	315
Lys Pro Gly Ser	Gln Phe Leu Tyr Ser Thr Phe Gly Tyr Thr Leu	320	325	330
Leu Ala Ala Ile	Val Glu Arg Ala Ser Gly Cys Lys Tyr Leu Asp	335	340	345



Tyr Met Gln Lys Ile Phe His Asp Leu Asp Met Leu Thr Thr Val  
350 355 360

Gln Glu Glu Asn Glu Pro Val Ile Tyr Asn Arg Ala Arg  
365 370

<210> 367

<211> 30

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 367

tggaagaagaa gtctggtcag aaggttagg 30

<210> 368

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 368

catttggtt cattctcctg ctctg 25

<210> 369

<211> 28

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 369

aaaacctcag aacaactcat ttgcacc 28

<210> 370

<211> 41

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 370

gtctcaccat gggtgctctt gccaaattgt gggaagcagg g 41

<210> 371

<211> 1150

<212> DNA

<213> Homo sapiens

<400> 371

gtgacactat agaagagcta tgacgtcgca tgcacgcgta cgtaagctcg 50

gaattcggct cgaggctggt gggaagaagc cgagatggcg gcagccagcg 100  
 ctggggcaac ccggtgctc ctgctcttgc tgatggcggt agcagcgccc 150  
 agtcgagccc ggggcagcgg ctgccgggcc gggactggtg cgcgaggggc 200  
 tggggcgga ggtcgagagg gcgaggcctg tggcacggtg gggctgctgc 250  
 tggagcactc atttgagatc gatgacagtg ccaacttccg gaagcggggc 300  
 tcaactgctct ggaaccagca ggatggtacc ttgtccctgt cacagcgga 350  
 gctcagcgag gaggagcggg gccgactccg ggatgtggca gccctgaatg 400  
 gcctgtaccg ggtccggatc ccaaggcgac ccggggccct ggatggcctg 450  
 gaagctggtg gctatgtctc ctctttgtc cctgcgtgct ccctggtgga 500  
 gtcgcacctg tcggaccagc tgaccctgca cgtggatgtg gccggcaacg 550  
 tgggtggcgt gtcggtggtg acgcaccccg ggggctgccg gggccatgag 600  
 gtggaggacg tggacctgga gctgttcaac acctcggtgc agctgcagcc 650  
 gccaccaca gcccaggcc ctgagacggc ggccttcatt gagcgcttg 700  
 agatggaaca ggcccagaag gccaagaacc ccaggagca gaagtccttc 750  
 ttcgccaaat actggatgta catcattccc gtcgtcctgt tcctcatgat 800  
 gtcaggagcg ccagacaccg ggggccaggg tgggggtggg ggtgggggtg 850  
 gtggtggggg tagtggcctt tgctgtgtgc caccctccct gtaagtctat 900  
 ttaaaaacat cgacgataca ttgaaatgtg tgaacgtttt gaaaagctac 950  
 agcttcagc agccaaaagc aactgttggt ttggcaagac ggtcctgatg 1000  
 tacaagcttg attgaaattc actgctcact tgatacgtta ttcagaaacc 1050  
 caaggaatgg ctgtcccat cctcatgtgg ctgtgtggag ctcagctgtg 1100  
 ttgtgtggca gtttattaaa ctgtcccca gatcgacacg caaaaaaaaa 1150

<210> 372

<211> 269

<212> PRT

<213> Homo sapiens

<400> 372

Met	Ala	Ala	Ala	Ser	Ala	Gly	Ala	Thr	Arg	Leu	Leu	Leu	Leu	Leu
1				5					10					15

Leu	Met	Ala	Val	Ala	Ala	Pro	Ser	Arg	Ala	Arg	Gly	Ser	Gly	Cys
				20					25					30

Arg	Ala	Gly	Thr	Gly	Ala	Arg	Gly	Ala	Gly	Ala	Glu	Gly	Arg	Glu			
				35					40					45			
Gly	Glu	Ala	Cys	Gly	Thr	Val	Gly	Leu	Leu	Leu	Glu	His	Ser	Phe			
				50					55					60			
Glu	Ile	Asp	Asp	Ser	Ala	Asn	Phe	Arg	Lys	Arg	Gly	Ser	Leu	Leu			
				65					70					75			
Trp	Asn	Gln	Gln	Asp	Gly	Thr	Leu	Ser	Leu	Ser	Gln	Arg	Gln	Leu			
				80					85					90			
Ser	Glu	Glu	Glu	Arg	Gly	Arg	Leu	Arg	Asp	Val	Ala	Ala	Leu	Asn			
				95					100					105			
Gly	Leu	Tyr	Arg	Val	Arg	Ile	Pro	Arg	Arg	Pro	Gly	Ala	Leu	Asp			
				110					115					120			
Gly	Leu	Glu	Ala	Gly	Gly	Tyr	Val	Ser	Ser	Phe	Val	Pro	Ala	Cys			
				125					130					135			
Ser	Leu	Val	Glu	Ser	His	Leu	Ser	Asp	Gln	Leu	Thr	Leu	His	Val			
				140					145					150			
Asp	Val	Ala	Gly	Asn	Val	Val	Gly	Val	Ser	Val	Val	Thr	His	Pro			
				155					160					165			
Gly	Gly	Cys	Arg	Gly	His	Glu	Val	Glu	Asp	Val	Asp	Leu	Glu	Leu			
				170					175					180			
Phe	Asn	Thr	Ser	Val	Gln	Leu	Gln	Pro	Pro	Thr	Thr	Ala	Pro	Gly			
				185					190					195			
Pro	Glu	Thr	Ala	Ala	Phe	Ile	Glu	Arg	Leu	Glu	Met	Glu	Gln	Ala			
				200					205					210			
Gln	Lys	Ala	Lys	Asn	Pro	Gln	Glu	Gln	Lys	Ser	Phe	Phe	Ala	Lys			
				215					220					225			
Tyr	Trp	Met	Tyr	Ile	Ile	Pro	Val	Val	Leu	Phe	Leu	Met	Met	Ser			
				230					235					240			
Gly	Ala	Pro	Asp	Thr	Gly	Gly	Gln	Gly	Gly	Gly	Gly	Gly	Gly	Gly			
				245					250					255			
Gly	Gly	Gly	Gly	Ser	Gly	Leu	Cys	Cys	Val	Pro	Pro	Ser	Leu				
				260					265								

<210> 373

<211> 1706

<212> DNA

<213> Homo sapiens

<400> 373

ggagcgctgc tggaacccga gccggagccg gagccacagc ggggaggggtg 50

gcctggcggc ctggagccgg acgtgtccgg gccgtccccg cagaccgggg 100

cagcaggctg tccgggggcc caccatgctg gtgactgcct accttgcttt 150  
tgtaggcctc ctggcctcct gcctggggct ggaactgtca agatgccggg 200  
ctaaaccccc tggaagggcc tgcagcaatc cctccttctc tcggtttcaa 250  
ctggacttct atcaggctca cttcctggcc ctggcagctg attggcttca 300  
ggccccctac ctctataaac tctaccagca ttactacttc ctggaaggctc 350  
aaattgccat cctctatgtc tgtggccttg cctctacagt cctctttggc 400  
ctagtggcct cctcccttgt ggattggctg ggtcgcaaga attcttgtgt 450  
cctcttctcc ctgacttact cactatgctg cttaaccaaa ctctctcaag 500  
actactttgt gctgctagtg gggcgagcac ttggtgggct gtccacagcc 550  
ctgctcttct cagccttcga ggcctgggat atccatgagc acgtggaacg 600  
gcatgacttc cctgctgagt ggatcccagc tacctttgct cgagctgcct 650  
tctggaacca tgtgctggct gtagtggcag gtgtggcagc tgaggctgta 700  
gccagctgga tagggctggg gcctgtagcg ccctttgtgg ctgccatccc 750  
tctcctggct ctggcagggg ccttggccct tcgaaactgg ggggagaact 800  
atgaccggca gcgtgccttc tcaaggacct gtgctggagg cctgcgctgc 850  
ctcctgtcgg accgccgcgt gctgctgctg ggcaccatac aagctctatt 900  
tgagagtgtc atcttcatct ttgtcttctc ctggacacct gtgctggacc 950  
cacacggggc ccctctgggc attatcttct ccagcttcat ggcagccagc 1000  
ctgcttggct ctccctgta ccgtatcgcc acctccaaga ggtaccacct 1050  
tcagcccatg cacctgctgt cccttgctgt gctcatcgtc gtcttctctc 1100  
tcttcatgtt gactttctct accagcccag gccaggagag tccggtggag 1150  
tccttcatag cctttctact tattgagttg gcttgtggat tatactttcc 1200  
cagcatgagc ttctacgga gaaaggatgat ccctgagaca gagcaggctg 1250  
gtgtactcaa ctggttccgg gtacctctgc actcactggc ttgcctaggg 1300  
ctccttgtcc tccatgacag tgatcgaaaa acaggcactc ggaatatgtt 1350  
cagcatttgc tctgctgtca tggatgatggc tctgctggca gtggtgggac 1400  
tcttcaccgt ggtaaggcat gatgctgagc tgcgggtacc ttcacctact 1450  
gaggagccct atgccctga gctgtaacct cactccagga caagatagct 1500

gggacagact cttgaattcc agctatccgg gattgtacag atctctctgt 1550  
 gactgacttt gtgactgtcc tgtgggttct cctgccattg ctttgtgttt 1600  
 gggaggacat gatgggggtg atggactgga aagaagggtgc caaaagttcc 1650  
 ctctgtgtta ctccattta gaaaataaac acttttaaata gatcaaaaaa 1700  
 aaaaaa 1706

<210> 374

<211> 450

<212> PRT

<213> Homo sapiens

<400> 374

Met	Leu	Val	Thr	Ala	Tyr	Leu	Ala	Phe	Val	Gly	Leu	Leu	Ala	Ser	
1				5					10					15	
Cys	Leu	Gly	Leu	Glu	Leu	Ser	Arg	Cys	Arg	Ala	Lys	Pro	Pro	Gly	
				20					25					30	
Arg	Ala	Cys	Ser	Asn	Pro	Ser	Phe	Leu	Arg	Phe	Gln	Leu	Asp	Phe	
				35					40					45	
Tyr	Gln	Val	Tyr	Phe	Leu	Ala	Leu	Ala	Ala	Asp	Trp	Leu	Gln	Ala	
				50					55					60	
Pro	Tyr	Leu	Tyr	Lys	Leu	Tyr	Gln	His	Tyr	Tyr	Phe	Leu	Glu	Gly	
				65					70					75	
Gln	Ile	Ala	Ile	Leu	Tyr	Val	Cys	Gly	Leu	Ala	Ser	Thr	Val	Leu	
				80					85					90	
Phe	Gly	Leu	Val	Ala	Ser	Ser	Leu	Val	Asp	Trp	Leu	Gly	Arg	Lys	
				95					100					105	
Asn	Ser	Cys	Val	Leu	Phe	Ser	Leu	Thr	Tyr	Ser	Leu	Cys	Cys	Leu	
				110					115					120	
Thr	Lys	Leu	Ser	Gln	Asp	Tyr	Phe	Val	Leu	Leu	Val	Gly	Arg	Ala	
				125					130					135	
Leu	Gly	Gly	Leu	Ser	Thr	Ala	Leu	Leu	Phe	Ser	Ala	Phe	Glu	Ala	
				140					145					150	
Trp	Tyr	Ile	His	Glu	His	Val	Glu	Arg	His	Asp	Phe	Pro	Ala	Glu	
				155					160					165	
Trp	Ile	Pro	Ala	Thr	Phe	Ala	Arg	Ala	Ala	Phe	Trp	Asn	His	Val	
				170					175					180	
Leu	Ala	Val	Val	Ala	Gly	Val	Ala	Ala	Glu	Ala	Val	Ala	Ser	Trp	
				185					190					195	
Ile	Gly	Leu	Gly	Pro	Val	Ala	Pro	Phe	Val	Ala	Ala	Ile	Pro	Leu	
				200					205					210	

Leu	Ala	Leu	Ala	Gly	Ala	Leu	Ala	Leu	Arg	Asn	Trp	Gly	Glu	Asn	
				215					220					225	
Tyr	Asp	Arg	Gln	Arg	Ala	Phe	Ser	Arg	Thr	Cys	Ala	Gly	Gly	Leu	
				230					235					240	
Arg	Cys	Leu	Leu	Ser	Asp	Arg	Arg	Val	Leu	Leu	Leu	Gly	Thr	Ile	
				245					250					255	
Gln	Ala	Leu	Phe	Glu	Ser	Val	Ile	Phe	Ile	Phe	Val	Phe	Leu	Trp	
				260					265					270	
Thr	Pro	Val	Leu	Asp	Pro	His	Gly	Ala	Pro	Leu	Gly	Ile	Ile	Phe	
				275					280					285	
Ser	Ser	Phe	Met	Ala	Ala	Ser	Leu	Leu	Gly	Ser	Ser	Leu	Tyr	Arg	
				290					295					300	
Ile	Ala	Thr	Ser	Lys	Arg	Tyr	His	Leu	Gln	Pro	Met	His	Leu	Leu	
				305					310					315	
Ser	Leu	Ala	Val	Leu	Ile	Val	Val	Phe	Ser	Leu	Phe	Met	Leu	Thr	
				320					325					330	
Phe	Ser	Thr	Ser	Pro	Gly	Gln	Glu	Ser	Pro	Val	Glu	Ser	Phe	Ile	
				335					340					345	
Ala	Phe	Leu	Leu	Ile	Glu	Leu	Ala	Cys	Gly	Leu	Tyr	Phe	Pro	Ser	
				350					355					360	
Met	Ser	Phe	Leu	Arg	Arg	Lys	Val	Ile	Pro	Glu	Thr	Glu	Gln	Ala	
				365					370					375	
Gly	Val	Leu	Asn	Trp	Phe	Arg	Val	Pro	Leu	His	Ser	Leu	Ala	Cys	
				380					385					390	
Leu	Gly	Leu	Leu	Val	Leu	His	Asp	Ser	Asp	Arg	Lys	Thr	Gly	Thr	
				395					400					405	
Arg	Asn	Met	Phe	Ser	Ile	Cys	Ser	Ala	Val	Met	Val	Met	Ala	Leu	
				410					415					420	
Leu	Ala	Val	Val	Gly	Leu	Phe	Thr	Val	Val	Arg	His	Asp	Ala	Glu	
				425					430					435	
Leu	Arg	Val	Pro	Ser	Pro	Thr	Glu	Glu	Pro	Tyr	Ala	Pro	Glu	Leu	
				440					445					450	

<210> 375

<211> 1098

<212> DNA

<213> Homo sapiens

<400> 375

gcgacgcgcg gcggggcggc gagaggaaac gcggcgcccg gccgggcccg 50

gccctggaga tgggtccccg cgccgcgggc tgggtgtgtc tegtgtctctg 100  
 gctccccgcg tgcgtcgcgg ccacagcgtt ccgtatccat gattatttgt 150  
 actttcaagt gctgagtcct ggggacattc gatacatctt cacagccaca 200  
 cctgccaagg actttggtgg tatctttcac acaaggtag agcagattca 250  
 ccttggtccc gctgaacctc cagaggcctg cggggaactc agcaacggtt 300  
 tcttcatcca ggaccagatt gctctggtgg agaggggggg ctgctccttc 350  
 ctctccaaga ctcggtggtt ccaggagcac ggcgggcggg cggtgatcat 400  
 ctctgacaac gcagttgaca atgacagctt ctacgtggag atgatccagg 450  
 acagtacca gcgcacagct gacatccccg ccctcttctt gctcgccga 500  
 gacggctaca tgatccgccg ctctctggaa cagcatgggc tgccatgggc 550  
 catcatttcc atcccagtc atgtcaccag catccccacc tttgagctgc 600  
 tgcaaccgcc ctggaccttc tggtagaaga gtttgtccca cattccagcc 650  
 ataagtgact ctgagctggg aaggggaaac ccaggaattt tgctacttgg 700  
 aatttgga tagcatctgg ggacaagtgg agccaggtag aggaaaagg 750  
 tttgggcgtt gctaggtga aagggaagcc acaccactgg cttcccttc 800  
 cccagggccc ccaagggtgt ctcatgctac aagaagaggc aagagacagg 850  
 cccagggct tctggctaga acccgaaaca aaaggagctg aaggcaggtg 900  
 gctgagagc catctgtgac ctgtcacact cacctggctc cagcctcccc 950  
 taccaggggt ctctgcacag tgaccttcac agcagttggt ggagtgggtt 1000  
 aaagagctgg tgtttgggga ctcaataaac cctcactgac ttttagcaa 1050  
 taaagcttct catcagggtt gcaaaaaaaaa aaaaaaaaaa aaaaaaaa 1098

<210> 376

<211> 188

<212> PRT

<213> Homo sapiens

<400> 376

Met	Val	Pro	Gly	Ala	Ala	Gly	Trp	Cys	Cys	Leu	Val	Leu	Trp	Leu
1				5				10					15	
Pro	Ala	Cys	Val	Ala	Ala	His	Gly	Phe	Arg	Ile	His	Asp	Tyr	Leu
				20				25					30	
Tyr	Phe	Gln	Val	Leu	Ser	Pro	Gly	Asp	Ile	Arg	Tyr	Ile	Phe	Thr
				35				40					45	

Ala Thr Pro Ala Lys Asp Phe Gly Gly Ile Phe His Thr Arg Tyr		
	50	55 60
Glu Gln Ile His Leu Val Pro Ala Glu Pro Pro Glu Ala Cys Gly		
	65	70 75
Glu Leu Ser Asn Gly Phe Phe Ile Gln Asp Gln Ile Ala Leu Val		
	80	85 90
Glu Arg Gly Gly Cys Ser Phe Leu Ser Lys Thr Arg Val Val Gln		
	95	100 105
Glu His Gly Gly Arg Ala Val Ile Ile Ser Asp Asn Ala Val Asp		
	110	115 120
Asn Asp Ser Phe Tyr Val Glu Met Ile Gln Asp Ser Thr Gln Arg		
	125	130 135
Thr Ala Asp Ile Pro Ala Leu Phe Leu Leu Gly Arg Asp Gly Tyr		
	140	145 150
Met Ile Arg Arg Ser Leu Glu Gln His Gly Leu Pro Trp Ala Ile		
	155	160 165
Ile Ser Ile Pro Val Asn Val Thr Ser Ile Pro Thr Phe Glu Leu		
	170	175 180
Leu Gln Pro Pro Trp Thr Phe Trp		
	185	

<210> 377  
 <211> 496  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> unsure  
 <222> 396  
 <223> unknown base

<400> 377  
 tctgcctcca ctgctctgtg ctgggatcat ggaacttgca ctgctgtgtg 50  
 ggctggtggt gatggctggt gtgattccaa tccagggcgg gatcctgaac 100  
 ctgaacaaga tggtaagca agtgactggg aaaatgccca tcctctccta 150  
 ctggccctac ggctgtcact gcggactagg tggcagaggc caacccaaag 200  
 atgccacgga ctggtgctgc cagacccatg actgctgcta tgaccacctg 250  
 aagaccacgg ggtgcggcat ctacaaggac aacaacaaaa gcagcataca 300  
 ttgtatggat ttatctcaac gctattgttt aatggctgtg tttaatgtga 350  
 tctatctgga aaatgaggac tccgaataaa aagctattac tawttnaaaa 400



aaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 450

aaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaa 496

<210> 378

<211> 116

<212> PRT

<213> Homo sapiens

<400> 378

Met	Glu	Leu	Ala	Leu	Leu	Cys	Gly	Leu	Val	Val	Met	Ala	Gly	Val
1				5				10					15	

Ile	Pro	Ile	Gln	Gly	Gly	Ile	Leu	Asn	Leu	Asn	Lys	Met	Val	Lys
			20					25					30	

Gln	Val	Thr	Gly	Lys	Met	Pro	Ile	Leu	Ser	Tyr	Trp	Pro	Tyr	Gly
			35					40					45	

Cys	His	Cys	Gly	Leu	Gly	Gly	Arg	Gly	Gln	Pro	Lys	Asp	Ala	Thr
			50					55					60	

Asp	Trp	Cys	Cys	Gln	Thr	His	Asp	Cys	Cys	Tyr	Asp	His	Leu	Lys
			65					70					75	

Thr	Gln	Gly	Cys	Gly	Ile	Tyr	Lys	Asp	Asn	Asn	Lys	Ser	Ser	Ile
			80					85						90

His	Cys	Met	Asp	Leu	Ser	Gln	Arg	Tyr	Cys	Leu	Met	Ala	Val	Phe
			95					100					105	

Asn	Val	Ile	Tyr	Leu	Glu	Asn	Glu	Asp	Ser	Glu
			110					115		

<210> 379

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 379

ctgcctccac tgctctgtgc tggg 24

<210> 380

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 380

cagagcagtg gatgttcccc tggg 24

<210> 381

<211> 45  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 381  
ctgaacaaga tgggtcaagca agtgactggg aaaatgccca tcctc 45

<210> 382  
<211> 764  
<212> DNA  
<213> Homo sapiens

<400> 382  
ctcgtcttctt ccttctggat gggggcccag ggggccagg agagtataaa 50  
ggcgatgtgg aggggtgccc gcacaaccag acgccagtc acaggcgaga 100  
gccctgggat gcaccggcca gaggccatgc tgctgctgct cacgcttgcc 150  
ctcctggggg gcccacactg ggcagggaag atgtatggcc ctggaggagg 200  
caagtatttc agcaccactg aagactacga ccatgaaatc acagggctgc 250  
gggtgtctgt aggtcttctc ctggtgaaaa gtgtccaggt gaaacttgga 300  
gactcctggg acgtgaaact gggagcctta ggtgggaata cccaggaagt 350  
caccctgcag ccaggcgaat acatcacaaa agtctttgtc gccttccaag 400  
ctttcctccg gggataggtc atgtacacca gcaaggaccg ctatttctat 450  
tttggaagc ttgatggcca gatctcctct gcctaccca gccagaggg 500  
gcagggtgctg gtgggcatct atggccagta tcaactcctt ggcataaga 550  
gcattggctt tgaatggaat tatccactag aggagccgac cactgagcca 600  
ccagttaatc tcacatactc agcaaaactca cccgtgggtc gctaggggtg 650  
ggatggggc catccgagct gaggccatct gtgtgggtgg ggctgatgg 700  
actggagtaa ctgagtcggg acgctgaatc tgaatccacc aataaataaa 750  
gcttctgcag aaaa 764

<210> 383  
<211> 178  
<212> PRT  
<213> Homo sapiens

<400> 383  
Met His Arg Pro Glu Ala Met Leu Leu Leu Thr Leu Ala Leu  
1 5 10 15

Leu	Gly	Gly	Pro	Thr	Trp	Ala	Gly	Lys	Met	Tyr	Gly	Pro	Gly	Gly	20	25	30
Gly	Lys	Tyr	Phe	Ser	Thr	Thr	Glu	Asp	Tyr	Asp	His	Glu	Ile	Thr	35	40	45
Gly	Leu	Arg	Val	Ser	Val	Gly	Leu	Leu	Leu	Val	Lys	Ser	Val	Gln	50	55	60
Val	Lys	Leu	Gly	Asp	Ser	Trp	Asp	Val	Lys	Leu	Gly	Ala	Leu	Gly	65	70	75
Gly	Asn	Thr	Gln	Glu	Val	Thr	Leu	Gln	Pro	Gly	Glu	Tyr	Ile	Thr	80	85	90
Lys	Val	Phe	Val	Ala	Phe	Gln	Ala	Phe	Leu	Arg	Gly	Met	Val	Met	95	100	105
Tyr	Thr	Ser	Lys	Asp	Arg	Tyr	Phe	Tyr	Phe	Gly	Lys	Leu	Asp	Gly	110	115	120
Gln	Ile	Ser	Ser	Ala	Tyr	Pro	Ser	Gln	Glu	Gly	Gln	Val	Leu	Val	125	130	135
Gly	Ile	Tyr	Gly	Gln	Tyr	Gln	Leu	Leu	Gly	Ile	Lys	Ser	Ile	Gly	140	145	150
Phe	Glu	Trp	Asn	Tyr	Pro	Leu	Glu	Glu	Pro	Thr	Thr	Glu	Pro	Pro	155	160	165
Val	Asn	Leu	Thr	Tyr	Ser	Ala	Asn	Ser	Pro	Val	Gly	Arg			170	175	

<210> 384

<211> 2379

<212> DNA

<213> Homo sapiens

<400> 384

gctgagcgtg tgcgcggtac ggggctctcc tgccttctgg gctccaacgc 50

agctctgtgg ctgaactggg tgctcatcac gggaactgct gggctatgga 100

atacagatgt ggcagctcag gtagcccca attgcctgga agaatacatc 150

atgtttttcg ataagaagaa attgtaggat ccagtttttt ttttaaccgc 200

cccctcccca ccccccaaaa aaactgtaaa gatgcaaaaa cgtaatatcc 250

atgaagatcc tattacctag gaagattttg atgttttgct gcgaatgcgg 300

tgttgggatt tatttgttct tggagtgttc tgcgtggctg gcaaagaata 350

atgttccaaa atcgggtccat ctccaagggt gtccaatttt tcttctctggg 400

tgtcagcgag ccctgactca ctacagtgcg gctgacaggg gctgtcatgc 450

aactggcccc taagccaaag caaaagacct aaggacgacc tttgaacaat 500  
acaaaggatg ggtttcaatg taattaggct actgagcgga tcagctgtag 550  
cactggttat agccccact gtcttactga caatgctttc ttctgccgaa 600  
cgaggatgcc ctaagggctg taggtgtgaa ggcaaaatgg tatattgtga 650  
atctcagaaa ttacaggaga taccctcaag tataatctgct ggttgcttag 700  
gtttgtccct tcgctataac agccttcaaa aacttaagta taatcaattt 750  
aaagggctca accagctcac ctggctatac cttgaccata accatatcag 800  
caatattgac gaaaatgctt ttaatggaat acgcagactc aaagagctga 850  
ttcttagttc caatagaatc tcctattttc ttaacaatac cttcagacct 900  
gtgacaaatt tacggaactt ggatctgtcc tataatcagc tgcattctct 950  
gggatctgaa cagtttcggg gcttgcgga gctgctgagt ttacatttac 1000  
ggtctaactc cctgagaacc atccctgtgc gaatattcca agactgccgc 1050  
aacctggaac ttttggacct gggatataac cggatccgaa gtttagccag 1100  
gaatgtcttt gctggcatga tcagactcaa agaacttcac ctggagcaca 1150  
atcaattttc caagctcaac ctggcccttt ttccaagggt ggtcagcctt 1200  
cagaaccttt acttgcatg gaataaaatc agtgtcatag gacagaccat 1250  
gtcctggacc tggagctcct taciaaggct tgatttatca ggcaatgaga 1300  
tcgaagcttt cagtggacct agtgttttcc agtgtgtccc gaatctgcag 1350  
cgctcaacc tggattccaa caagctcaca tttattggtc aagagatttt 1400  
ggattcttgg atatccctca atgacatcag tcttgctggg aatatatggg 1450  
aatgcagcag aaatatattgc tcccttgtaa actggctgaa aagttttaaa 1500  
ggtctaaggg agaatacaat tatctgtgcc agtcccaaag agctgcaagg 1550  
agtaaatgtg atcgatgcag tgaagaacta cagcatctgt ggcaaaagta 1600  
ctacagagag gtttgatctg gccagggtc tcccaaagcc gacgtttaag 1650  
cccaagctcc ccaggccgaa gcatgagagc aaacccctt tgccccgcac 1700  
ggtgggagcc acagagcccg gccagagac cgatgctgac gccagacaca 1750  
tctctttcca taaaatcatc gcgggcagcg tggcgctttt cctgtccgtg 1800  
ctcgtcatcc tgctggttat ctacgtgtca tggaagcggg accctgcgag 1850  
catgaagcag ctgcagcagc gctccctcat gcgaaggcac aggaaaaaga 1900

aaagacagtc cctaaagcaa atgactccca gcacccagga attttatgta 1950  
 gattataaac ccaccaacac ggagaccagc gagatgctgc tgaatgggac 2000  
 gggaccctgc acctataaca aatcgggctc cagggagtgt gaggtatgaa 2050  
 ccattgtgat aaaaagagct cttaaaagct gggaaataag tgggtgcttta 2100  
 ttgaactctg gtgactatca agggaacgcg atgccccccc tccccttccc 2150  
 tctccctctc actttgggtgg caagatcctt ccttgtccgt tttagtgcac 2200  
 tcataatact ggtcattttc ctctcataca taatcaaccc attgaaattt 2250  
 aaataccaca atcaatgtga agcttgaact ccggtttaat ataataccta 2300  
 ttgtataaga ccctttactg attccattaa tgtcgcattt gttttaagat 2350  
 aaaacttctt tcataggtaa aaaaaaaaa 2379

<210> 385

<211> 513

<212> PRT

<213> Homo sapiens

<400> 385

Met	Gly	Phe	Asn	Val	Ile	Arg	Leu	Leu	Ser	Gly	Ser	Ala	Val	Ala
1				5					10					15
Leu	Val	Ile	Ala	Pro	Thr	Val	Leu	Leu	Thr	Met	Leu	Ser	Ser	Ala
				20					25					30
Glu	Arg	Gly	Cys	Pro	Lys	Gly	Cys	Arg	Cys	Glu	Gly	Lys	Met	Val
				35					40					45
Tyr	Cys	Glu	Ser	Gln	Lys	Leu	Gln	Glu	Ile	Pro	Ser	Ser	Ile	Ser
				50					55					60
Ala	Gly	Cys	Leu	Gly	Leu	Ser	Leu	Arg	Tyr	Asn	Ser	Leu	Gln	Lys
				65					70					75
Leu	Lys	Tyr	Asn	Gln	Phe	Lys	Gly	Leu	Asn	Gln	Leu	Thr	Trp	Leu
				80					85					90
Tyr	Leu	Asp	His	Asn	His	Ile	Ser	Asn	Ile	Asp	Glu	Asn	Ala	Phe
				95					100					105
Asn	Gly	Ile	Arg	Arg	Leu	Lys	Glu	Leu	Ile	Leu	Ser	Ser	Asn	Arg
				110					115					120
Ile	Ser	Tyr	Phe	Leu	Asn	Asn	Thr	Phe	Arg	Pro	Val	Thr	Asn	Leu
				125					130					135
Arg	Asn	Leu	Asp	Leu	Ser	Tyr	Asn	Gln	Leu	His	Ser	Leu	Gly	Ser
				140					145					150

Glu Gln Phe Arg Gly Leu Arg Lys Leu Leu Ser Leu His Leu Arg	155	160	165
Ser Asn Ser Leu Arg Thr Ile Pro Val Arg Ile Phe Gln Asp Cys	170	175	180
Arg Asn Leu Glu Leu Leu Asp Leu Gly Tyr Asn Arg Ile Arg Ser	185	190	195
Leu Ala Arg Asn Val Phe Ala Gly Met Ile Arg Leu Lys Glu Leu	200	205	210
His Leu Glu His Asn Gln Phe Ser Lys Leu Asn Leu Ala Leu Phe	215	220	225
Pro Arg Leu Val Ser Leu Gln Asn Leu Tyr Leu Gln Trp Asn Lys	230	235	240
Ile Ser Val Ile Gly Gln Thr Met Ser Trp Thr Trp Ser Ser Leu	245	250	255
Gln Arg Leu Asp Leu Ser Gly Asn Glu Ile Glu Ala Phe Ser Gly	260	265	270
Pro Ser Val Phe Gln Cys Val Pro Asn Leu Gln Arg Leu Asn Leu	275	280	285
Asp Ser Asn Lys Leu Thr Phe Ile Gly Gln Glu Ile Leu Asp Ser	290	295	300
Trp Ile Ser Leu Asn Asp Ile Ser Leu Ala Gly Asn Ile Trp Glu	305	310	315
Cys Ser Arg Asn Ile Cys Ser Leu Val Asn Trp Leu Lys Ser Phe	320	325	330
Lys Gly Leu Arg Glu Asn Thr Ile Ile Cys Ala Ser Pro Lys Glu	335	340	345
Leu Gln Gly Val Asn Val Ile Asp Ala Val Lys Asn Tyr Ser Ile	350	355	360
Cys Gly Lys Ser Thr Thr Glu Arg Phe Asp Leu Ala Arg Ala Leu	365	370	375
Pro Lys Pro Thr Phe Lys Pro Lys Leu Pro Arg Pro Lys His Glu	380	385	390
Ser Lys Pro Pro Leu Pro Pro Thr Val Gly Ala Thr Glu Pro Gly	395	400	405
Pro Glu Thr Asp Ala Asp Ala Glu His Ile Ser Phe His Lys Ile	410	415	420
Ile Ala Gly Ser Val Ala Leu Phe Leu Ser Val Leu Val Ile Leu	425	430	435

Leu Val Ile Tyr Val Ser Trp Lys Arg Tyr Pro Ala Ser Met Lys  
440 445 450

Gln Leu Gln Gln Arg Ser Leu Met Arg Arg His Arg Lys Lys Lys  
455 460 465

Arg Gln Ser Leu Lys Gln Met Thr Pro Ser Thr Gln Glu Phe Tyr  
470 475 480

Val Asp Tyr Lys Pro Thr Asn Thr Glu Thr Ser Glu Met Leu Leu  
485 490 495

Asn Gly Thr Gly Pro Cys Thr Tyr Asn Lys Ser Gly Ser Arg Glu  
500 505 510

Cys Glu Val

<210> 386

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 386

ctgggatctg aacagtttcg gggc 24

<210> 387

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 387

ggtccccagg acatggtctg tccc 24

<210> 388

<211> 48

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 388

gctgagttta catttacggt ctaactccct gagaaccatc cctgtgcg 48

<210> 389

<211> 1449

<212> DNA

<213> Homo sapiens

<400> 389

agttctgaga aagaaggaaa taaacacagg caccaaacca ctatcctaag 50  
ttgactgtcc tttaaataatg tcaagatcca gacttttcag tgtcacctca 100  
gcgatctcaa cgatagggat cttgtgtttg ccgctattcc agttggtgct 150  
ctcggaccta ccatgcgaag aagatgaaat gtgtgtaaat tataatgacc 200  
aacaccctaa tggctggtat atctggatcc tcctgctgct ggttttggtg 250  
gcagctcttc tctgtggagc tgtggtcctc tgcctccagt gctggctgag 300  
gagacccoga attgattctc acaggcgcac catggcagtt tttgctgttg 350  
gagacttga ctctatttat gggacagaag cagctgtgag tccaactgtt 400  
ggaattcacc ttcaaactca aaccctgac ctatatcctg ttctgctcc 450  
atgttttggc cctttaggct cccacctcc atatgaagaa attgtaaaaa 500  
caacctgatt ttaggtgtgg attatcaatt taaagtatta acgacatctg 550  
taattccaaa acatcaaatt taggaatagt tatttcagtt gttggaaatg 600  
tccagagatc tattcatata gtctgaggaa ggacaattcg aaaaaagaat 650  
ggatgttga aaaaattttg gtcattggaga tgtttaaata gtaaagtagc 700  
aggcttttga tgtgtcactg ctgtatcata cttttatgct acacaaccaa 750  
attaatgctt ctccactagt atccaaacag gcaacaatta ggtgctggaa 800  
gtagtttcca tcacatttag gactccactg cagtatacag cacaccattt 850  
tctgctttaa actctttcct agcatggggt ccataaaaat tattataatt 900  
taacaatagc ccaagccgag aatccaacat gtccagaacc agaaccagaa 950  
agatagtatt tgaatgaagg tgaggggaga gagtaggaaa aagaaaagtt 1000  
tggagttgaa gggtaaagga taaatgaaga ggaaaaggaa aagattacaa 1050  
gtctcagcaa aaacaagagg ttttatgccc caacctgaag aggaagaaat 1100  
tgtagataga aggtgaagga gattgctgaa gatatagagc acatataatg 1150  
ccaacacggg gagaaaagaa aatttcccct ttacagtaa tgaatgtggc 1200  
ctccatagtc catagtgttt ctctggagcc tcagggcttg gcatttattg 1250  
cagcatcatg ctaagaacct tcggcatagg tatctgttcc catgaggact 1300  
gcagaagtag caatgagaca tcttcaagtg gcattttggc agtggccatc 1350  
agcaggggga cagacaaaaa catccatcac agatgacata tgatcttcag 1400  
ctgacaaatt tgttgaacaa aacaataaac atcaatagat atctaaaaa 1449



<210> 390  
<211> 146  
<212> PRT  
<213> Homo sapiens

<400> 390  
Met Ser Arg Ser Arg Leu Phe Ser Val Thr Ser Ala Ile Ser Thr  
1 5 10 15  
Ile Gly Ile Leu Cys Leu Pro Leu Phe Gln Leu Val Leu Ser Asp  
20 25 30  
Leu Pro Cys Glu Glu Asp Glu Met Cys Val Asn Tyr Asn Asp Gln  
35 40 45  
His Pro Asn Gly Trp Tyr Ile Trp Ile Leu Leu Leu Leu Val Leu  
50 55 60  
Val Ala Ala Leu Leu Cys Gly Ala Val Val Leu Cys Leu Gln Cys  
65 70 75  
Trp Leu Arg Arg Pro Arg Ile Asp Ser His Arg Arg Thr Met Ala  
80 85 90  
Val Phe Ala Val Gly Asp Leu Asp Ser Ile Tyr Gly Thr Glu Ala  
95 100 105  
Ala Val Ser Pro Thr Val Gly Ile His Leu Gln Thr Gln Thr Pro  
110 115 120  
Asp Leu Tyr Pro Val Pro Ala Pro Cys Phe Gly Pro Leu Gly Ser  
125 130 135  
Pro Pro Pro Tyr Glu Glu Ile Val Lys Thr Thr  
140 145

<210> 391  
<211> 26  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 391  
cttttcagtg tcacctcagc gatctc 26

<210> 392  
<211> 23  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 392

ccaaaacatg gagcaggaac agg 23

<210> 393

<211> 47

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 393

ccagttggtg ctctcggacc taccatgcga agaagatgaa atgtgtg 47

<210> 394

<211> 2340

<212> DNA

<213> Homo sapiens

<400> 394

gagcggagta aaatctccac aagctgggaa caaacctcgt cccaactccc 50  
accacccggc gtttctccag ctcgatctgg aggctgcttc gccagtgtgg 100  
gaocgagctg acgcccgctt attagctctc gctgcgtcgc cccggctcag 150  
aagctccgtg gcggcggcga ccgtgacgag aagcccacgg ccagctcagt 200  
tctctttctac tttgggagag agagaaagtc agatgccctt tttaaactcc 250  
ctcttcaaaa ctcatctcct gggtgactga gttaatagag tggatacaac 300  
cttgctgaag atgaagaata tacaatattg aggatatattt tttctttttt 350  
ttttcaagtc ttgatttggt gcttacctca agttaccatt tttcagtcaa 400  
gtctgtttgt ttgcttcttc agaaatgttt tttacaatct caagaaaaaa 450  
tatgtcccag aaattgagtt tactgttgct tgtatttgga ctcatattggg 500  
gattgatgtt actgcactat acttttcaac aaccaagaca tcaaagcagt 550  
gtcaagttac gtgagcaaat actagactta agcaaaagat atgttaaagc 600  
tctagcagag gaaaataaga acacagtggg tgtcgagaac ggtgcttcta 650  
tggcaggata tgcggatctg aaaagaacaa ttgctgtcct tctggatgac 700  
attttgcaac gattgggtgaa gctggagaac aaagttgact atattgttgt 750  
gaatggctca gcagccaaca ccaccaatgg tactagtggg aatttggtgc 800  
cagtaaccac aaataaaaga acgaatgtct cgggcagtat cagatagcag 850  
ttgaaaatca ctttgtgctg ctccatccac tgtggattat atcctatggc 900  
agaaaagctt tataattgct ggcttaggac agagcaatac tttacaataa 950

aagctctaca cattttcaag gagtatgctg gattcatgga actctaattc 1000  
tgtacataaa aatttttaaag ttatttggtt gctttcaggc aagtctgttc 1050  
aatgctgtac tatgtcctta aagagaattt ggtaacttgg ttgatgtggt 1100  
aagcagatag gtgagttttg tataaatctt ttgtgtttga gatcaagctg 1150  
aaatgaaaac actgaaaaac atggattcat ttctataaca catttattta 1200  
agtatataac acgttttttg gacaagtga gaatgtttaa tcattctgtc 1250  
atgtgttctc aatagatgta actgttagac tacggctatt tgaaaaaatg 1300  
tgcttattgt actatatttt gttattccaa ttatgagcag agaaaggaaa 1350  
tataatgttg aaaataatgt ttgaaatca tgacccaaag aatgtattga 1400  
tttgcactat ccttcagaat aactgaaggt taattattgt atatttttaa 1450  
aaattacact tataagagta taatcttgaa atgggtagca gccactgtcc 1500  
attacctatc gtaaacattg gggcaattta ataacagcat taaaatagtt 1550  
gtaaactcta atcttatact tattgaagaa taaaagatat ttttatgatg 1600  
agagtaacaa taaagtattc atgatttttc acatacatga atgttcattt 1650  
aaaagtttaa tcctttgagt gtctatgcta tcaggaaagc acattatttc 1700  
catatttggg ttaattttgc ttttattata ttggtctagg aggaaggagc 1750  
tttggagaat ggaactcttg aggactttag ccagggtgat ataataaagg 1800  
tacttttgtg ctgcattaaa ttgcttgga agtgtaaca ttatattata 1850  
taagagtatc ctttatgaaa ttttgaattt gtataacaga tgcattagat 1900  
attcatttta tataatggcc acttaaaata agaacattta aaatataaac 1950  
tatgaagatt gactatcttt tcaggaaaaa agctgtatat agcacaggga 2000  
accctaactc tgggtaattc tagtataaaa caaattatac ttttatttaa 2050  
attcccttg tagcaaatct aattgccaca tggtgcccta tatttcatag 2100  
tatttattct ctatagtaac tgcttaagtg cagctagctt ctagatttag 2150  
actatataga atttagatat tgtattgttc gtcattataa tatgctacca 2200  
catgtagcaa taattacaat attttattaa aataaatatg tgaaatattg 2250  
tttcatgaaa gacagatttc caaatctctc ttctcttctc tgtactgtct 2300  
acctttatgt gaagaaatta atttatgcc attgccaggt 2340

<211> 140  
 <212> PRT  
 <213> Homo sapiens

<400> 395

Met	Phe	Phe	Thr	Ile	Ser	Arg	Lys	Asn	Met	Ser	Gln	Lys	Leu	Ser
1				5					10					15
Leu	Leu	Leu	Leu	Val	Phe	Gly	Leu	Ile	Trp	Gly	Leu	Met	Leu	Leu
				20					25					30
His	Tyr	Thr	Phe	Gln	Gln	Pro	Arg	His	Gln	Ser	Ser	Val	Lys	Leu
				35					40					45
Arg	Glu	Gln	Ile	Leu	Asp	Leu	Ser	Lys	Arg	Tyr	Val	Lys	Ala	Leu
				50					55					60
Ala	Glu	Glu	Asn	Lys	Asn	Thr	Val	Asp	Val	Glu	Asn	Gly	Ala	Ser
				65					70					75
Met	Ala	Gly	Tyr	Ala	Asp	Leu	Lys	Arg	Thr	Ile	Ala	Val	Leu	Leu
				80					85					90
Asp	Asp	Ile	Leu	Gln	Arg	Leu	Val	Lys	Leu	Glu	Asn	Lys	Val	Asp
				95					100					105
Tyr	Ile	Val	Val	Asn	Gly	Ser	Ala	Ala	Asn	Thr	Thr	Asn	Gly	Thr
				110					115					120
Ser	Gly	Asn	Leu	Val	Pro	Val	Thr	Thr	Asn	Lys	Arg	Thr	Asn	Val
				125					130					135
Ser	Gly	Ser	Ile	Arg										
				140										

<210> 396  
 <211> 2639  
 <212> DNA  
 <213> Homo sapiens

<400> 396

cgcgccggg ccgcccgggt gagcgtgccg aggcggctgt ggcgcaggct 50  
 tccagcccc accatgccgt ggcccctgct gctgctgctg gccgtgagt 100  
 ggcccagac aaccgggcca tgcttccccg ggtgccaatg cgaggtggag 150  
 accttcggcc ttttcgacag cttcagcctg actcgggtgg attgtagcgg 200  
 cctgggcccc cacatcatgc cggtgcccat ccctctggac acagcccact 250  
 tggacctgtc ctccaaccgg ctggagatgg tgaatgagtc ggtgttggcg 300  
 gggccgggct acacgacgtt ggctggcctg gatctcagcc acaacctgct 350  
 caccagcatc tcacccactg cttctccccg cttctgctac ctggagtcgc 400

ttgacctcag ccacaatggc ctgacagccc tgccagccga gagcttcacc 450  
agctcacccc tgagcgacgt gaaccttagc cacaaccagc tccgggaggt 500  
ctcagtgtct gccttcacga cgcacagtca gggccgggca ctacacgtgg 550  
acctctccca caacctcatt caccgcctcg tgccccaccc caccagggcc 600  
ggcctgcctg cgcccaccat tcagagcctg aacctggcct ggaaccggct 650  
ccatgccgtg cccaacctcc gagacttgcc cctgcgctac ctgagcctgg 700  
atgggaaccc tctagctgtc attggctcgg gtgccttcgc ggggctggga 750  
ggccttacac acctgtctct ggccagcctg cagaggctcc ctgagctggc 800  
gcccagtggc ttccgtgagc taccgggcct gcaggctctg gacctgtcgg 850  
gcaaccccaa gcttaactgg gcaggagctg aggtgttttc aggctgagc 900  
tccctgcagg agctggacct ttcgggcacc aacctggtgc ccctgcctga 950  
ggcgtgctc ctccacctcc cggcactgca gagcgtcagc gtgggcccagg 1000  
atgtgcggtg ccggcgctg gtgcgggagg gcacctaccc ccggaggcct 1050  
ggctccagcc ccaagggtgcc cctgcactgc gtagacaccc gggaatctgc 1100  
tgccaggggc cccaccatct tgtgacaaat ggtgtggccc agggccacat 1150  
aacagactgc tgtcctgggc tgcctcaggt cccgagtaac ttatgttcaa 1200  
tgtgccaaaca ccagtgggga gcccgcaggc ctatgtggca gcgtcaccac 1250  
aggagtgtg ggcctaggag aggccttgga cctgggagcc acacctagga 1300  
gcaaagtctc acccctttgt ctacgttgct tcccaaacc atgagcagag 1350  
ggacttcgat gccaaaccag actcgggtcc cctcctgctt cccttcccca 1400  
cttatccccc aagtgccttc cctcatgcct gggccggcct gaccgcgaat 1450  
gggcagaggg tgggtgggac ccctgctgc agggcagagt tcagggtccac 1500  
tgggctgagt gtccccttgg gcccatggcc cagtcactca ggggcgagtt 1550  
tcttttctaa catagccctt tctttgcat gaggccatga ggcccgttc 1600  
atccttttct atttcctag aaccttaatg gtagaaggaa ttgcaaagaa 1650  
tcaagtccac ctttctcatg tgacagatgg ggaaactgag gccttgagaa 1700  
ggaaaaaggc taatctaagt tctgcgggc agtggcatga ctggagcaca 1750  
gcctcctgcc tcccagcccc gaccaatgc actttcttgt ctctctaat 1800  
aagccccacc ctccccgcct gggctcccct tgctgcctt gcctgttccc 1850

cattagcaca ggagtagcag cagcaggaca ggcaagagcc tcacaagtgg 1900  
gactctgggc ctctgaccag ctgtgcgga tgggctaagt cactctgccc 1950  
ttcggagcct ctggaagctt agggcacatt ggttcagcc tagccagttt 2000  
ctcacctgg gttgggggcc ccagcatcc agactggaaa cctaccatt 2050  
ttcccctgag catcctctag atgctgcccc aaggagtgc tgcagttctg 2100  
gagcctcatc tggctgggat ctccaagggg cctcctggat tcagtcccca 2150  
ctggccctga gcacgacagc cttcttacc ctcccaggaa tgccgtgaaa 2200  
ggagacaagg tctgcccagc ccatgtctat gctctacccc cagggcagca 2250  
tctcagcttc cgaacctgg gctgtttcct tagtcttcat ttataaaaag 2300  
ttgttgccct tttaacggag tgtcactttc aaccggcctc ccctaccct 2350  
gctggccggg gatggagaca tgtcatttgt aaaagcagaa aaagggtgca 2400  
tttgttcaact tttgtaatat tgcctgggc ctgtgttggg gtgttggggg 2450  
aagctgggca tcagtggcca catgggcac aggggctggc cccacagaga 2500  
ccccacaggg cagtgaagtc tgtcttcccc cacctgccta gcccatcatc 2550  
tatctaaccg gtccttgatt taataaacac tataaaagggt ttaaaaaaaaa 2600  
aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 2639

<210> 397

<211> 353

<212> PRT

<213> Homo sapiens

<400> 397

Met	Pro	Trp	Pro	Leu	Leu	Leu	Leu	Leu	Ala	Val	Ser	Gly	Ala	Gln
1				5					10					15
Thr	Thr	Arg	Pro	Cys	Phe	Pro	Gly	Cys	Gln	Cys	Glu	Val	Glu	Thr
				20					25					30
Phe	Gly	Leu	Phe	Asp	Ser	Phe	Ser	Leu	Thr	Arg	Val	Asp	Cys	Ser
				35					40					45
Gly	Leu	Gly	Pro	His	Ile	Met	Pro	Val	Pro	Ile	Pro	Leu	Asp	Thr
				50					55					60
Ala	His	Leu	Asp	Leu	Ser	Ser	Asn	Arg	Leu	Glu	Met	Val	Asn	Glu
				65					70					75
Ser	Val	Leu	Ala	Gly	Pro	Gly	Tyr	Thr	Thr	Leu	Ala	Gly	Leu	Asp
				80					85					90

Leu Ser His Asn	Leu Leu Thr Ser Ile	Ser Pro Thr Ala Phe	Ser
95	100	105	
Arg Leu Arg Tyr	Leu Glu Ser Leu Asp	Leu Ser His Asn Gly	Leu
110	115	120	
Thr Ala Leu Pro	Ala Glu Ser Phe Thr	Ser Ser Pro Leu Ser	Asp
125	130	135	
Val Asn Leu Ser	His Asn Gln Leu Arg	Glu Val Ser Val Ser	Ala
140	145	150	
Phe Thr Thr His	Ser Gln Gly Arg Ala	Leu His Val Asp Leu	Ser
155	160	165	
His Asn Leu Ile	His Arg Leu Val Pro	His Pro Thr Arg Ala	Gly
170	175	180	
Leu Pro Ala Pro	Thr Ile Gln Ser Leu	Asn Leu Ala Trp Asn	Arg
185	190	195	
Leu His Ala Val	Pro Asn Leu Arg Asp	Leu Pro Leu Arg Tyr	Leu
200	205	210	
Ser Leu Asp Gly	Asn Pro Leu Ala Val	Ile Gly Pro Gly Ala	Phe
215	220	225	
Ala Gly Leu Gly	Gly Leu Thr His Leu	Ser Leu Ala Ser Leu	Gln
230	235	240	
Arg Leu Pro Glu	Leu Ala Pro Ser Gly	Phe Arg Glu Leu Pro	Gly
245	250	255	
Leu Gln Val Leu	Asp Leu Ser Gly Asn	Pro Lys Leu Asn Trp	Ala
260	265	270	
Gly Ala Glu Val	Phe Ser Gly Leu Ser	Ser Leu Gln Glu Leu	Asp
275	280	285	
Leu Ser Gly Thr	Asn Leu Val Pro Leu	Pro Glu Ala Leu Leu	Leu
290	295	300	
His Leu Pro Ala	Leu Gln Ser Val Ser	Val Gly Gln Asp Val	Arg
305	310	315	
Cys Arg Arg Leu	Val Arg Glu Gly Thr	Tyr Pro Arg Arg Pro	Gly
320	325	330	
Ser Ser Pro Lys	Val Pro Leu His Cys	Val Asp Thr Arg Glu	Ser
335	340	345	
Ala Ala Arg Gly	Pro Thr Ile Leu		
350			

<210> 398

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 398

ccctgccagc cgagagcttc acc 23

<210> 399

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 399

ggttggtgcc cgaaaggtcc agc 23

<210> 400

<211> 44

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 400

caaccccaag cttaactggg caggagctga ggtgttttca ggcc 44

<210> 401

<211> 1571

<212> DNA

<213> Homo sapiens

<400> 401

gatggcgcag ccacagcttc tgtgagattc gatttctccc cagttcccct 50

gtgggtctga ggggaccaga agggtagct acgttggtt tctggaagg 100

gaggctatat gcgtcaattc cccaaaacaa gttttgacat ttcccctgaa 150

atgtcattct ctatctattc actgcaagt cctgctgttc caggccttac 200

ctgctgggca ctaacggcgg agccaggatg gggacagaat aaaggagcca 250

cgacctgtgc caccaactcg cactcagact ctgaactcag acctgaaatc 300

ttctcttcac gggaggcttg gcagtttttc ttactcctgt ggtctccaga 350

tttcaggcct aagatgaaag cctctagtct tgccttcagc cttctctctg 400

ctgcgtttta tctcctatgg actccttcca ctggactgaa gacactcaat 450

ttgggaagct gtgtgatcgc cacaaacctt caggaaatac gaaatggatt 500

ttctgagata cggggcagtg tgcaagccaa agatggaaac attgacatca 550



gaatcttaag gaggactgag tctttgcaag acacaaagcc tgcgaatcga 600  
 tgctgcctcc tgcgccatth gctaagactc tatctggaca gggatattta 650  
 aaactaccag acccctgacc attatactct ccggaagatc agcagcctcg 700  
 ccaattcctt tcttaccatc aagaaggacc tccggtcttc tcatgcccac 750  
 atgacatgcc attgtgggga ggaagcaatg aagaaatata gccagattct 800  
 gagtcacttt gaaaagctgg aacctcaggc agcagttgtg aaggctttgg 850  
 gggaactaga cattcttctg caatggatgg aggagacaga ataggaggaa 900  
 agtgatgctg ctgctaagaa tattcgaggt caagagctcc agtcttcaat 950  
 acctgcagag gaggcatgac ccaaaccac catctcttta ctgtactagt 1000  
 cttgtgctgg tcacagtgtg tcttatttat gcattacttg cttccttgca 1050  
 tgattgtctt tatgcatccc caatcttaat tgagaccata cttgtataag 1100  
 atttttgtaa tatctttctg ctattggata tattttattag ttaatatatt 1150  
 tattttattt ttgctattta atgtatttat ttttttactt ggacatgaaa 1200  
 ctttaaaaaa attcacagat tatattttata acctgactag agcaggtgat 1250  
 gtattttttat acagtaaaaa aaaaaaacct tgtaaattct agaagagtgg 1300  
 ctaggggggt tattcatttg tattcaacta aggacatatt tactcatgct 1350  
 gatgctctgt gagatatttg aaattgaacc aatgactact taggatgggt 1400  
 tgtggaataa gttttgatgt ggaattgcac atctacctta caattactga 1450  
 ccatccccag tagactcccc agtcccataa ttgtgtatct tccagccagg 1500  
 aatcctacac ggccagcatg tatttctaca aataaagttt tctttgcata 1550  
 ccaaaaaaaaa aaaaaaaaaa a 1571

<210> 402

<211> 261

<212> PRT

<213> Homo sapiens

<400> 402

Met	Arg	Gln	Phe	Pro	Lys	Thr	Ser	Phe	Asp	Ile	Ser	Pro	Glu	Met
1				5					10				15	
Ser	Phe	Ser	Ile	Tyr	Ser	Leu	Gln	Val	Pro	Ala	Val	Pro	Gly	Leu
				20					25				30	
Thr	Cys	Trp	Ala	Leu	Thr	Ala	Glu	Pro	Gly	Trp	Gly	Gln	Asn	Lys
				35					40				45	

Gly	Ala	Thr	Thr	Cys	Ala	Thr	Asn	Ser	His	Ser	Asp	Ser	Glu	Leu	50	55	60
Arg	Pro	Glu	Ile	Phe	Ser	Ser	Arg	Glu	Ala	Trp	Gln	Phe	Phe	Leu	65	70	75
Leu	Leu	Trp	Ser	Pro	Asp	Phe	Arg	Pro	Lys	Met	Lys	Ala	Ser	Ser	80	85	90
Leu	Ala	Phe	Ser	Leu	Leu	Ser	Ala	Ala	Phe	Tyr	Leu	Leu	Trp	Thr	95	100	105
Pro	Ser	Thr	Gly	Leu	Lys	Thr	Leu	Asn	Leu	Gly	Ser	Cys	Val	Ile	110	115	120
Ala	Thr	Asn	Leu	Gln	Glu	Ile	Arg	Asn	Gly	Phe	Ser	Glu	Ile	Arg	125	130	135
Gly	Ser	Val	Gln	Ala	Lys	Asp	Gly	Asn	Ile	Asp	Ile	Arg	Ile	Leu	140	145	150
Arg	Arg	Thr	Glu	Ser	Leu	Gln	Asp	Thr	Lys	Pro	Ala	Asn	Arg	Cys	155	160	165
Cys	Leu	Leu	Arg	His	Leu	Leu	Arg	Leu	Tyr	Leu	Asp	Arg	Val	Phe	170	175	180
Lys	Asn	Tyr	Gln	Thr	Pro	Asp	His	Tyr	Thr	Leu	Arg	Lys	Ile	Ser	185	190	195
Ser	Leu	Ala	Asn	Ser	Phe	Leu	Thr	Ile	Lys	Lys	Asp	Leu	Arg	Leu	200	205	210
Ser	His	Ala	His	Met	Thr	Cys	His	Cys	Gly	Glu	Glu	Ala	Met	Lys	215	220	225
Lys	Tyr	Ser	Gln	Ile	Leu	Ser	His	Phe	Glu	Lys	Leu	Glu	Pro	Gln	230	235	240
Ala	Ala	Val	Val	Lys	Ala	Leu	Gly	Glu	Leu	Asp	Ile	Leu	Leu	Gln	245	250	255
Trp	Met	Glu	Glu	Thr	Glu										260		

<210> 403

<211> 28

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 403

ctcctgtggt ctccagattt caggccta 28

<210> 404  
<211> 26  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 404  
agtcctcctt aagattctga tgtcaa 26

<210> 405  
<211> 998  
<212> DNA  
<213> Homo sapiens

<400> 405  
ccgttatcgt cttgcgctac tgctgaatgt ccgtcccga ggaggaggag 50  
aggcttttgc cgctgaccca gagatggccc cgagcgagca aattcctact 100  
gtccggctgc gcggctaccg tggccgagct agcaaccttt cccctggatc 150  
tcacaaaaac tcgactccaa atgcaaggag aagcagctct tgctcggttg 200  
ggagacggtg caagagaatc tgccccctat aggggaatgg tgcgcacagc 250  
cctagggatc attgaagagg aaggctttct aaagctttgg caaggagtga 300  
caccgccat ttacagacac gtagtgtatt ctggaggctg aatggtcaca 350  
tatgaacatc tccgagaggt tgtgtttggc aaaagtgaag atgagcatta 400  
tcccctttgg aaatcagtca ttggagggat gatggctggt gttattggcc 450  
agtttttagc caatccaact gacctagtga aggttcagat gcaaattggaa 500  
ggaaaaagga aactggaagg aaaaccattg cgatttcgtg gtgtacatca 550  
tgcatttgca aaaatcttag ctgaaggagg aatacgaggg ctttgggcag 600  
gctgggtacc caatatacaa agagcagcac tggatgaatat ggagattta 650  
accacttatg atacagtga acactacttg gtattgaata caccacttga 700  
ggacaatatc atgactcacg gtttatcaag tttatgttct ggactggtag 750  
cttctattct gggaacacca gccgatgtca tcaaagcag aataatgaat 800  
caaccacgag ataaacaagg aaggggactt ttgtataaat catcgactga 850  
ctgcttgatt caggctgttc aaggtgaagg attcatgagt ctatataaag 900  
gctttttacc atcttggtg agaatgaccc cttggtcaat ggtgttctgg 950  
cttacttatg aaaaaatcag agagatgagt ggagtcagtc cattttaa 998

<210> 406  
 <211> 323  
 <212> PRT  
 <213> Homo sapiens

<400> 406

Met	Ser	Val	Pro	Glu	Glu	Glu	Glu	Arg	Leu	Leu	Pro	Leu	Thr	Gln
1				5					10					15
Arg	Trp	Pro	Arg	Ala	Ser	Lys	Phe	Leu	Leu	Ser	Gly	Cys	Ala	Ala
				20					25					30
Thr	Val	Ala	Glu	Leu	Ala	Thr	Phe	Pro	Leu	Asp	Leu	Thr	Lys	Thr
				35					40					45
Arg	Leu	Gln	Met	Gln	Gly	Glu	Ala	Ala	Leu	Ala	Arg	Leu	Gly	Asp
				50					55					60
Gly	Ala	Arg	Glu	Ser	Ala	Pro	Tyr	Arg	Gly	Met	Val	Arg	Thr	Ala
				65					70					75
Leu	Gly	Ile	Ile	Glu	Glu	Gly	Phe	Leu	Lys	Leu	Trp	Gln	Gly	
				80					85					90
Val	Thr	Pro	Ala	Ile	Tyr	Arg	His	Val	Val	Tyr	Ser	Gly	Gly	Arg
				95					100					105
Met	Val	Thr	Tyr	Glu	His	Leu	Arg	Glu	Val	Val	Phe	Gly	Lys	Ser
				110					115					120
Glu	Asp	Glu	His	Tyr	Pro	Leu	Trp	Lys	Ser	Val	Ile	Gly	Gly	Met
				125					130					135
Met	Ala	Gly	Val	Ile	Gly	Gln	Phe	Leu	Ala	Asn	Pro	Thr	Asp	Leu
				140					145					150
Val	Lys	Val	Gln	Met	Gln	Met	Glu	Gly	Lys	Arg	Lys	Leu	Glu	Gly
				155					160					165
Lys	Pro	Leu	Arg	Phe	Arg	Gly	Val	His	His	Ala	Phe	Ala	Lys	Ile
				170					175					180
Leu	Ala	Glu	Gly	Gly	Ile	Arg	Gly	Leu	Trp	Ala	Gly	Trp	Val	Pro
				185					190					195
Asn	Ile	Gln	Arg	Ala	Ala	Leu	Val	Asn	Met	Gly	Asp	Leu	Thr	Thr
				200					205					210
Tyr	Asp	Thr	Val	Lys	His	Tyr	Leu	Val	Leu	Asn	Thr	Pro	Leu	Glu
				215					220					225
Asp	Asn	Ile	Met	Thr	His	Gly	Leu	Ser	Ser	Leu	Cys	Ser	Gly	Leu
				230					235					240
Val	Ala	Ser	Ile	Leu	Gly	Thr	Pro	Ala	Asp	Val	Ile	Lys	Ser	Arg
				245					250					255

Ile Met Asn Gln Pro Arg Asp Lys Gln Gly Arg Gly Leu Leu Tyr		
	260	270
Lys Ser Ser Thr Asp Cys Leu Ile Gln Ala Val Gln Gly Glu Gly		
	275	285
Phe Met Ser Leu Tyr Lys Gly Phe Leu Pro Ser Trp Leu Arg Met		
	290	300
Thr Pro Trp Ser Met Val Phe Trp Leu Thr Tyr Glu Lys Ile Arg		
	305	315
Glu Met Ser Gly Val Ser Pro Phe		
	320	

<210> 407

<211> 31

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 407

cgcggatccc gttatcgtct tgcgctactg c 31

<210> 408

<211> 34

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 408

gcggaattct taaaatggac tgactccact catc 34

<210> 409

<211> 1487

<212> DNA

<213> Homo sapiens

<400> 409

cggaacgcgtg ggcgcgggac gccggcaggg ttgtggcgca gcagtctcct 50

tcctgcgcgc gcgcctgaag tcggcggtggg cgtttgagga agctgggata 100

cagcatttaa tgaaaaatth atgcttaaga agtaaaaatg gcaggcttcc 150

tagataatth tcgttgccca gaatgtgaat gtattgactg gaggtagaga 200

agaaatgctg tggcatctgt tgctgcaggt atattgtttt ttacaggctg 250

gtggataatg attgatgcag ctgtggtgta tcctaagcca gaacagttga 300

accatgcctt tcacacatgt ggtgtattth ccacattggc tttcttcatg 350

ataaatgctg tatccaatgc tcaggtgaga ggtgatagct atgaaagcgg 400  
 ctgttttagga agaacaggtg ctcgagtttg gcttttcatt ggtttcatgt 450  
 tgatgtttgg gtcacttatt gcttccatgt ggattctttt tggtgcatat 500  
 gttacccaaa atactgatgt ttatccggga ctagctgtgt tttttcaaaa 550  
 tgcacttata ttttttagca ctctgatcta caaatttgga agaaccgaag 600  
 agctatggac ctgagatcac ttcttaagtc acattttcct tttgttatat 650  
 tctgtttgta gataggtttt ttatctctca gtacacattg ccaaattggag 700  
 tagattgtac attaaatggt ttgtttcttt acatttttat gttctgagtt 750  
 ttgaaatagt tttatgaaat ttctttattt ttcatgcat agactgttaa 800  
 tatgtatata atacaagact atatgaattg gataatgagt atcagttttt 850  
 tattcctgag atttagaact tgatctactc cctgagccag gggtacatca 900  
 tcttgtcatt ttagaagtaa ccactcttgt ctctctggct gggcacggtg 950  
 gctcatgcct gtaatcccag cactttggga ggccgaggcg ggccgattgc 1000  
 ttgagggtcaa gtgtttgaga ccagcctggc caacatggcg aaaccccatc 1050  
 tactaaaaat acaaaaatta gccaggcatg gtggtgggtg cctgtaatcc 1100  
 cagctacctg ggaggctgag gcaggagaat cgcttgaacc cggggggcag 1150  
 aggttgcagt gagctgagtt tgcgccactg cactctagcc tggggggagaa 1200  
 agtgaaactc cctctcaaaa aaaagaccac tctcagtatc tctgatttct 1250  
 gaagatgtac aaaaaaatat agcttcatat atctggaatg agcactgagc 1300  
 cataaaagggt tttcagcaag ttgtaactta ttttggccta aaaatgaggt 1350  
 ttttttggtg aagaaaaaat atttgttcct atgtattgaa gaagtgtact 1400  
 tttatataat gattttttta atgcccagaag gactagtttg aaagcttctt 1450  
 ttaaaaagaa ttctctaat atgactttat gtgagaa 1487

<210> 410

<211> 158

<212> PRT

<213> Homo sapiens

<400> 410

Met	Ala	Gly	Phe	Leu	Asp	Asn	Phe	Arg	Trp	Pro	Glu	Cys	Glu	Cys
1				5					10				15	

Ile	Asp	Trp	Ser	Glu	Arg	Arg	Asn	Ala	Val	Ala	Ser	Val	Val	Ala
				20				25					30	

Gly	Ile	Leu	Phe	Phe	Thr	Gly	Trp	Trp	Ile	Met	Ile	Asp	Ala	Ala	
				35					40					45	
Val	Val	Tyr	Pro	Lys	Pro	Glu	Gln	Leu	Asn	His	Ala	Phe	His	Thr	
				50					55					60	
Cys	Gly	Val	Phe	Ser	Thr	Leu	Ala	Phe	Phe	Met	Ile	Asn	Ala	Val	
				65					70					75	
Ser	Asn	Ala	Gln	Val	Arg	Gly	Asp	Ser	Tyr	Glu	Ser	Gly	Cys	Leu	
				80					85					90	
Gly	Arg	Thr	Gly	Ala	Arg	Val	Trp	Leu	Phe	Ile	Gly	Phe	Met	Leu	
				95					100					105	
Met	Phe	Gly	Ser	Leu	Ile	Ala	Ser	Met	Trp	Ile	Leu	Phe	Gly	Ala	
				110					115					120	
Tyr	Val	Thr	Gln	Asn	Thr	Asp	Val	Tyr	Pro	Gly	Leu	Ala	Val	Phe	
				125					130					135	
Phe	Gln	Asn	Ala	Leu	Ile	Phe	Phe	Ser	Thr	Leu	Ile	Tyr	Lys	Phe	
				140					145					150	
Gly	Arg	Thr	Glu	Glu	Leu	Trp	Thr								
				155											

<210> 411  
 <211> 20  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 411  
 gtttgaggaa gctgggatac 20

<210> 412  
 <211> 20  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 412  
 ccaaactcga gcacctgttc 20

<210> 413  
 <211> 40  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 413

atggcaggct tcctagataa ttttcgttg ccagaatgtg 40

<210> 414

<211> 1337

<212> DNA

<213> Homo sapiens

<400> 414

gttgatggca aacttctca aaggaggggc agagcctgcg cagggcagga 50

gcagctggcc cactggcggc ccgcaacact ccgtctcacc ctctgggccc 100

actgcatcta gaggagggcc gtctgtgagg ccactacccc tccagcaact 150

gggaggtggg actgtcagaa gctggcccag ggtggtggtc agctgggtca 200

gggacctacg gcacctgctg gaccacctcg ccttctccat cgaagcaggg 250

aagtgggagc ctcgagccct cgggtggaag ctgaccccaa gccacccttc 300

acctggacag gatgagagtgc tcaggtgtgc ttcgcctcct ggccctcatc 350

tttgccatag tcacgacatg gatgtttatt cgaagctaca tgagcttcag 400

catgaaaacc atccgtctgc cacgctggct ggagcctcg cccaccaagg 450

agatccaggt taaaaagtac aagtgtggcc tcatcaagcc ctgccagcc 500

aactactttg cgttttaaat ctgcagtggg gccgccaacg tcgtgggccc 550

tactatgtgc tttgaagacc gcatgatcat gagtcctgtg aaaaacaatg 600

tgggcagagg cctaaacatc gccctggtga atggaaccac gggagctgtg 650

ctgggacaga aggcatTTga catgtactct ggagatgtta tgcacctagt 700

gaaattcctt aaagaaattc cgggggggtgc actggtgctg gtggcctcct 750

acgacgatcc agggaccaa atgaacgatg aaagcaggaa actcttctct 800

gacttgggga gttcctacgc aaaacaactg ggcttcggg acagctgggt 850

cttcatagga gccaaagacc tcaggggtaa aagccccctt gagcagttct 900

taaagaacag ccagacaca aacaaatacg agggatggcc agagctgctg 950

gagatggagg gctgcatgcc cccgaagcca ttttaggggtg gctgtggctc 1000

ttcctcagcc aggggcctga agaagctcct gcctgactta ggagtcagag 1050

cccggcaggg gctgaggagg aggagcaggg ggtgctgctg ggaaggtgct 1100

gcaggtcctt gcacgctgtg tcgcgcctct cctcctcgga aacagaaccc 1150

tcccacagca catcctaccc ggaagaccag cctcagaggg tccttctgga 1200



accagctgtc tgtggagaga atgggggtgct ttcgtcaggg actgctgacg 1250  
gctggctcctg aggaaggaca aactgccag acttgagccc aattaaattt 1300  
tatttttgcg ggttttgaaa aaaaaaaaaa aaaaaaa 1337

<210> 415

<211> 224

<212> PRT

<213> Homo sapiens

<400> 415

Met	Arg	Val	Ser	Gly	Val	Leu	Arg	Leu	Leu	Ala	Leu	Ile	Phe	Ala	1	5	10	15
Ile	Val	Thr	Thr	Trp	Met	Phe	Ile	Arg	Ser	Tyr	Met	Ser	Phe	Ser	20	25	30	
Met	Lys	Thr	Ile	Arg	Leu	Pro	Arg	Trp	Leu	Ala	Ala	Ser	Pro	Thr	35	40	45	
Lys	Glu	Ile	Gln	Val	Lys	Lys	Tyr	Lys	Cys	Gly	Leu	Ile	Lys	Pro	50	55	60	
Cys	Pro	Ala	Asn	Tyr	Phe	Ala	Phe	Lys	Ile	Cys	Ser	Gly	Ala	Ala	65	70	75	
Asn	Val	Val	Gly	Pro	Thr	Met	Cys	Phe	Glu	Asp	Arg	Met	Ile	Met	80	85	90	
Ser	Pro	Val	Lys	Asn	Asn	Val	Gly	Arg	Gly	Leu	Asn	Ile	Ala	Leu	95	100	105	
Val	Asn	Gly	Thr	Thr	Gly	Ala	Val	Leu	Gly	Gln	Lys	Ala	Phe	Asp	110	115	120	
Met	Tyr	Ser	Gly	Asp	Val	Met	His	Leu	Val	Lys	Phe	Leu	Lys	Glu	125	130	135	
Ile	Pro	Gly	Gly	Ala	Leu	Val	Leu	Val	Ala	Ser	Tyr	Asp	Asp	Pro	140	145	150	
Gly	Thr	Lys	Met	Asn	Asp	Glu	Ser	Arg	Lys	Leu	Phe	Ser	Asp	Leu	155	160	165	
Gly	Ser	Ser	Tyr	Ala	Lys	Gln	Leu	Gly	Phe	Arg	Asp	Ser	Trp	Val	170	175	180	
Phe	Ile	Gly	Ala	Lys	Asp	Leu	Arg	Gly	Lys	Ser	Pro	Phe	Glu	Gln	185	190	195	
Phe	Leu	Lys	Asn	Ser	Pro	Asp	Thr	Asn	Lys	Tyr	Glu	Gly	Trp	Pro	200	205	210	
Glu	Leu	Leu	Glu	Met	Glu	Gly	Cys	Met	Pro	Pro	Lys	Pro	Phe	215	220			

<210> 416  
<211> 21  
<212> DNA  
<213> Artificial Sequence  
  
<220>  
<223> Synthetic oligonucleotide probe  
  
<400> 416  
gccatagtca cgacatggat g 21  
  
<210> 417  
<211> 18  
<212> DNA  
<213> Artificial Sequence  
  
<220>  
<223> Synthetic oligonucleotide probe  
  
<400> 417  
ggatggccag agctgctg 18  
  
<210> 418  
<211> 26  
<212> DNA  
<213> Artificial Sequence  
  
<220>  
<223> Synthetic oligonucleotide probe  
  
<400> 418  
aaagtacaag tgtggcctca tcaagc 26  
  
<210> 419  
<211> 24  
<212> DNA  
<213> Artificial Sequence  
  
<220>  
<223> Synthetic oligonucleotide probe  
  
<400> 419  
tctgactcct aagtcaggca ggag 24  
  
<210> 420  
<211> 24  
<212> DNA  
<213> Artificial Sequence  
  
<220>  
<223> Synthetic oligonucleotide probe  
  
<400> 420  
attctctcca cagacagctg gttc 24  
  
<210> 421

<211> 46  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 421  
gtacaagtgt ggcctcatca agccctgccc agccaactac tttgcg 46

<210> 422  
<211> 1701  
<212> DNA  
<213> Homo sapiens

<220>  
<221> unsure  
<222> 1528  
<223> unknown base

<400> 422  
gagactgcag agggagataa agagagaggg caaagaggca gcaagagatt 50  
tgtcctgggg atccagaaac ccatgatacc ctactgaaca ccgaatcccc 100  
tggaagccca cagagacaga gacagcaaga gaagcagaga taaatacact 150  
cacgccagga gctcgctcgc tctctctctc tctctctcac tcctccctcc 200  
ctctctctct gctgtccta gtctcttagt cctcaaattc ccagtccct 250  
gcaccccttc ctgggacact atgttgttct ccgccctcct gctggaggtg 300  
atgttgatcc tggctgcaga tgggggtcaa cactggacgt atgagggcc 350  
acatggtcag gaccattggc cagcctctta ccctgagtgt ggaaacaatg 400  
cccagtcgcc catcgatatt cagacagaca gtgtgacatt tgaccctgat 450  
ttgcctgctc tgcagcccca cggatatgac cagcctggca ccgagccttt 500  
ggacctgcac aacaatggcc acacagtgc actctctctg ccctctaccc 550  
tgtatctggg tggacttccc cgaaaatatg tagctgcca gctccacctg 600  
cactgggggc agaaaggatc ccagggggg tcagaacacc agatcaacag 650  
tgaagccaca tttgcagagc tccacattgt acattatgac tctgattcct 700  
atgacagctt gagtgaggct gctgagaggc ctcagggcct ggctgtcctg 750  
ggcactcctaa ttgaggtggg tgagactaag aatatagctt atgaacacat 800  
tctgagtcac ttgcatgaag tcaggcataa agatcagaag acctcagtgc 850  
ctcccttcaa cctaagagag ctgctcccca aacagctggg gcagtacttc 900

cgctacaatg gctcgctcac aactccccct tgctaccaga gtgtgctctg 950  
 gacagttttt tatagaaggt cccagatttc aatggaacag ctggaaaagc 1000  
 ttcaggggac attgttctcc acagaagagg agccctctaa gcttctggta 1050  
 cagaactacc gagcccttca gcctctcaat cagcgcacatg tctttgcttc 1100  
 tttcatccaa gcaggatcct cgtataccac aggtgaaatg ctgagtctag 1150  
 gtgtaggaat cttgggtggc tgtctctgcc ttctcctggc tgtttatttc 1200  
 attgctagaa agattcggaa gaagaggctg gaaaaccgaa agagtgtggt 1250  
 cttcacctca gcacaagcca cgactgaggc ataaattcct tctcagatac 1300  
 catggatgtg gatgacttcc cttcatgcct atcaggaagc ctctaaaatg 1350  
 ggggtgtagga tctggccaga aacactgtag gagtagtaag cagatgtcct 1400  
 ccttccccctg gacatctctt agagaggaat ggacccaggc tgtcattcca 1450  
 ggaagaactg cagagccttc agcctctcca aacatgtagg aggaaatgag 1500  
 gaaatcgctg tgttggttaat gcagaganca aactctgttt agttgcaggg 1550  
 gaagtttggg atatacccca aagtcctcta cccctcact tttatggccc 1600  
 tttccctaga tatactgcgg gatctctcct taggataaag agttgctgtt 1650  
 gaagttgtat atttttgatc aatatatttg gaaattaaag tttctgactt 1700  
 t 1701

<210> 423  
 <211> 337  
 <212> PRT  
 <213> Homo sapiens

<400> 423  
 Met Leu Phe Ser Ala Leu Leu Leu Glu Val Ile Trp Ile Leu Ala  
 1 5 10 15  
 Ala Asp Gly Gly Gln His Trp Thr Tyr Glu Gly Pro His Gly Gln  
 20 25 30  
 Asp His Trp Pro Ala Ser Tyr Pro Glu Cys Gly Asn Asn Ala Gln  
 35 40 45  
 Ser Pro Ile Asp Ile Gln Thr Asp Ser Val Thr Phe Asp Pro Asp  
 50 55 60  
 Leu Pro Ala Leu Gln Pro His Gly Tyr Asp Gln Pro Gly Thr Glu  
 65 70 75  
 Pro Leu Asp Leu His Asn Asn Gly His Thr Val Gln Leu Ser Leu  
 80 85 90

Pro Ser Thr Leu Tyr Leu Gly Gly Leu Pro Arg Lys Tyr Val Ala	95	100	105
Ala Gln Leu His Leu His Trp Gly Gln Lys Gly Ser Pro Gly Gly	110	115	120
Ser Glu His Gln Ile Asn Ser Glu Ala Thr Phe Ala Glu Leu His	125	130	135
Ile Val His Tyr Asp Ser Asp Ser Tyr Asp Ser Leu Ser Glu Ala	140	145	150
Ala Glu Arg Pro Gln Gly Leu Ala Val Leu Gly Ile Leu Ile Glu	155	160	165
Val Gly Glu Thr Lys Asn Ile Ala Tyr Glu His Ile Leu Ser His	170	175	180
Leu His Glu Val Arg His Lys Asp Gln Lys Thr Ser Val Pro Pro	185	190	195
Phe Asn Leu Arg Glu Leu Leu Pro Lys Gln Leu Gly Gln Tyr Phe	200	205	210
Arg Tyr Asn Gly Ser Leu Thr Thr Pro Pro Cys Tyr Gln Ser Val	215	220	225
Leu Trp Thr Val Phe Tyr Arg Arg Ser Gln Ile Ser Met Glu Gln	230	235	240
Leu Glu Lys Leu Gln Gly Thr Leu Phe Ser Thr Glu Glu Glu Pro	245	250	255
Ser Lys Leu Leu Val Gln Asn Tyr Arg Ala Leu Gln Pro Leu Asn	260	265	270
Gln Arg Met Val Phe Ala Ser Phe Ile Gln Ala Gly Ser Ser Tyr	275	280	285
Thr Thr Gly Glu Met Leu Ser Leu Gly Val Gly Ile Leu Val Gly	290	295	300
Cys Leu Cys Leu Leu Leu Ala Val Tyr Phe Ile Ala Arg Lys Ile	305	310	315
Arg Lys Lys Arg Leu Glu Asn Arg Lys Ser Val Val Phe Thr Ser	320	325	330
Ala Gln Ala Thr Thr Glu Ala	335		

<210> 424

<211> 18

<212> DNA

<213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe  
  
 <400> 424  
 gtaaagtcgc tggccagc 18  
  
 <210> 425  
 <211> 18  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Synthetic oligonucleotide probe  
  
 <400> 425  
 cccgatctgc ctgctgta 18  
  
 <210> 426  
 <211> 24  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Synthetic oligonucleotide probe  
  
 <400> 426  
 ctgcactgta tggccattat tgtg 24  
  
 <210> 427  
 <211> 45  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Synthetic oligonucleotide probe  
  
 <400> 427  
 cagaaaccca tgatacccta ctgaacaccg aatcccctgg aagcc 45  
  
 <210> 428  
 <211> 1073  
 <212> DNA  
 <213> Homo sapiens  
  
 <400> 428  
 aatttttcac cagagtaaac ttgagaaacc aactggacct tgagtattgt 50  
  
 acattttgcc tcgtggaccc aaaggtagca atctgaaaca tgaggagtac 100  
  
 gattctactg ttttgtcttc taggatcaac tcggtcatta ccacagctca 150  
  
 aacctgcttt gggactccct cccacaaaac tggtccgga tcagggaaca 200  
  
 ctaccaaacc aacagcagtc aatcaggtc tttccttctt taagtctgat 250  
  
 accattaaca cagatgctca cactggggcc agatctgcat ctgttaaadc 300

ctgctgcagg aatgacacct ggtacccaga cccacccatt gaccctggga 350  
 ggggtgaatg tacaacagca actgcaccca catgtgttac caatttttgt 400  
 cacacaactt ggagcccagg gcactatcct aagctcagag gaattgccac 450  
 aaatcttcac gagcctcatc atccattcct tgttcccgga aggcatcctg 500  
 cccaccagtc aggagggggc taatccagat gtccaggatg gaagccttcc 550  
 agcaggagga gcaggtgtaa atcctgccac ccagggaacc ccagcaggcc 600  
 gcctcccaac tcccagtggc acagatgacg actttgcagt gaccaccct 650  
 gcaggcatcc aaaggagcac acatgccatc gaggaagcca ccacagaatc 700  
 agcaaatgga attcagtaag ctgtttcaaa ttttttcaac taagctgcct 750  
 cgaatttggt gatacatgtg aatctttatc attgattata ttatggaata 800  
 gattgagaca cattggatag tcttagaaga aattaattct taatttacct 850  
 gaaaatattc ttgaaatttc agaaaatatg ttctatgtag agaatcccaa 900  
 cttttaaaaa caataattca atggataaat ctgtctttga aatataacat 950  
 tatgtgcct ggatgatatg catattaaaa catatttga aaactggaaa 1000  
 aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 1050  
 aaaaaaaaaa aaaaaaaaaa aaa 1073

<210> 429  
 <211> 209  
 <212> PRT  
 <213> Homo sapiens

<400> 429  
 Met Arg Ser Thr Ile Leu Leu Phe Cys Leu Leu Gly Ser Thr Arg  
 1 5 10 15  
 Ser Leu Pro Gln Leu Lys Pro Ala Leu Gly Leu Pro Pro Thr Lys  
 20 25 30  
 Leu Ala Pro Asp Gln Gly Thr Leu Pro Asn Gln Gln Gln Ser Asn  
 35 40 45  
 Gln Val Phe Pro Ser Leu Ser Leu Ile Pro Leu Thr Gln Met Leu  
 50 55 60  
 Thr Leu Gly Pro Asp Leu His Leu Leu Asn Pro Ala Ala Gly Met  
 65 70 75  
 Thr Pro Gly Thr Gln Thr His Pro Leu Thr Leu Gly Gly Leu Asn  
 80 85 90  
 Val Gln Gln Gln Leu His Pro His Val Leu Pro Ile Phe Val Thr

	95	100	105
Gln Leu Gly Ala	Gln Gly Thr Ile Leu Ser Ser Glu Glu Leu Pro		
	110	115	120
Gln Ile Phe Thr	Ser Leu Ile Ile His Ser Leu Phe Pro Gly Gly		
	125	130	135
Ile Leu Pro Thr	Ser Gln Ala Gly Ala Asn Pro Asp Val Gln Asp		
	140	145	150
Gly Ser Leu Pro	Ala Gly Gly Ala Gly Val Asn Pro Ala Thr Gln		
	155	160	165
Gly Thr Pro Ala	Gly Arg Leu Pro Thr Pro Ser Gly Thr Asp Asp		
	170	175	180
Asp Phe Ala Val	Thr Thr Pro Ala Gly Ile Gln Arg Ser Thr His		
	185	190	195
Ala Ile Glu Glu	Ala Thr Thr Glu Ser Ala Asn Gly Ile Gln		
	200	205	

<210> 430

<211> 1257

<212> DNA

<213> Homo Sapien

<400> 430

```

ggagagaggc gcgcgggtga aaggcgcatt gatgcagcct gcggcggcct 50
cggagcgcgg cggagccaga cgctgaccac gttcctctcc tcggtctcct 100
ccgcctccag ctccgcgctg cccggcagcc gggagccatg cgaccccagg 150
gccccgccgc ctccccgcag cggtccgcg gcctcctgct gtcctgctg 200
ctgcagctgc ccgcgccgtc gagcgccctc gagatcccca aggggaagca 250
aaaggcgcag ctccggcaga gggagggtgt ggacctgtat aatggaatgt 300
gcttacaagg gccagcagga gtgcctggtc gagacgggag ccctggggcc 350
aatgttattc cgggtacacc tgggatccca ggtcgggatg gattcaaagg 400
agaaaagggg gaatgtctga gggaaagctt tgaggagtcc tggacacca 450
actacaagca gtgttcattg agttcattga attatggcat agatcttggg 500
aaaattgcgg agtgtacatt tacaagatg cgttcaaata gtgctctaag 550
agttttgttc agtggctcac ttcggctaaa atgcagaaat gcatgctgtc 600
agcgttggtg ttccacattc aatggagctg aatgttcagg acctcttccc 650
attgaagcta taatttattt ggaccaagga agccctgaaa tgaattcaac 700

```



aattaatatt catcgcaactt cttctgtgga aggactttgt gaaggaattg 750  
gtgctggatt agtggatggt gctatctggg ttggcacttg ttcagattac 800  
ccaaaaggag atgcttctac tggatggaat tcagtttctc gcatcattat 850  
tgaagaacta ccaaaataaa tgctttaatt ttcatttgct acctcttttt 900  
ttattatgcc ttggaatggt tcacttaaat gacattttta ataagtttat 950  
gtatacatct gaatgaaaag caaagctaaa tatgtttaca gaccaaagt 1000  
tgatttcaca ctgtttttta atctagcatt attcattttg cttcaatcaa 1050  
aagtggtttc aatatttttt ttagttgggtt agaatacttt cttcatagtc 1100  
acattctctc aacctataat ttggaatatt gttgtggtct tttgtttttt 1150  
ctcttagtat agcattttta aaaaaatata aaagctacca atctttgtac 1200  
aatttgtaaa tgtaagaat tttttttata tctgttaaatt aaaaattatt 1250  
tccaaca 1257

<210> 431  
<211> 243  
<212> PRT  
<213> Homo Sapien

<400> 431  
Met Arg Pro Gln Gly Pro Ala Ala Ser Pro Gln Arg Leu Arg Gly  
1 5 10 15  
Leu Leu Leu Leu Leu Leu Leu Gln Leu Pro Ala Pro Ser Ser Ala  
20 25 30  
Ser Glu Ile Pro Lys Gly Lys Gln Lys Ala Gln Leu Arg Gln Arg  
35 40 45  
Glu Val Val Asp Leu Tyr Asn Gly Met Cys Leu Gln Gly Pro Ala  
50 55 60  
Gly Val Pro Gly Arg Asp Gly Ser Pro Gly Ala Asn Val Ile Pro  
65 70 75  
Gly Thr Pro Gly Ile Pro Gly Arg Asp Gly Phe Lys Gly Glu Lys  
80 85 90  
Gly Glu Cys Leu Arg Glu Ser Phe Glu Glu Ser Trp Thr Pro Asn  
95 100 105  
Tyr Lys Gln Cys Ser Trp Ser Ser Leu Asn Tyr Gly Ile Asp Leu  
110 115 120  
Gly Lys Ile Ala Glu Cys Thr Phe Thr Lys Met Arg Ser Asn Ser  
125 130 135

Ala	Leu	Arg	Val	Leu	Phe	Ser	Gly	Ser	Leu	Arg	Leu	Lys	Cys	Arg	
				140					145					150	
Asn	Ala	Cys	Cys	Gln	Arg	Trp	Tyr	Phe	Thr	Phe	Asn	Gly	Ala	Glu	
				155					160					165	
Cys	Ser	Gly	Pro	Leu	Pro	Ile	Glu	Ala	Ile	Ile	Tyr	Leu	Asp	Gln	
				170					175					180	
Gly	Ser	Pro	Glu	Met	Asn	Ser	Thr	Ile	Asn	Ile	His	Arg	Thr	Ser	
				185					190					195	
Ser	Val	Glu	Gly	Leu	Cys	Glu	Gly	Ile	Gly	Ala	Gly	Leu	Val	Asp	
				200					205					210	
Val	Ala	Ile	Trp	Val	Gly	Thr	Cys	Ser	Asp	Tyr	Pro	Lys	Gly	Asp	
				215					220					225	
Ala	Ser	Thr	Gly	Trp	Asn	Ser	Val	Ser	Arg	Ile	Ile	Ile	Glu	Glu	
				230					235					240	

Leu Pro Lys

<210> 432

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 432

aggacttgcc ctcaggaa 18

<210> 433

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 433

cgcaggacag ttgtgaaaat a 21

<210> 434

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 434

atgacgctcg tcgaaggcca c 21

<210> 435  
<211> 19  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 435  
cccacctgta ccaccatgt 19

<210> 436  
<211> 24  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 436  
actccaggca ccatctgttc tccc 24

<210> 437  
<211> 19  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 437  
aagggctggc attcaagtc 19

<210> 438  
<211> 19  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 438  
tgacctggca aaggaagaa 19

<210> 439  
<211> 21  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 439  
cagccaccct ccagtccaag g 21

<210> 440  
<211> 19

<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 440  
gggtcgtgtt ttggagaga 19

<210> 441  
<211> 20  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 441  
ctggccctca gagcaccaat 20

<210> 442  
<211> 25  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 442  
tcctccatca cttcccctag ctcca 25

<210> 443  
<211> 24  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 443  
ctggcaggag ttaaagttcc aaga 24

<210> 444  
<211> 18  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 444  
aaaggacacc gggatgtg 18

<210> 445  
<211> 26  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 445  
agcgtacact ctctccaggc aaccag 26

<210> 446  
<211> 22  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 446  
caattctgga tgaggtggta ga 22

<210> 447  
<211> 20  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 447  
caggactgag cgcttggtta 20

<210> 448  
<211> 21  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 448  
caaagcgcca agtaccggac c 21

<210> 449  
<211> 18  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 449  
ccagacctca gccaggaa 18

<210> 450  
<211> 18  
<212> DNA  
<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 450  
ccctagctga ccccttca 18

<210> 451  
<211> 23  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 451  
tctgacaagc agttttctga atc 23

<210> 452  
<211> 26  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 452  
ctctccccct cccttttcct ttgttt 26

<210> 453  
<211> 18  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 453  
ctctggtgcc cacagtga 18

<210> 454  
<211> 21  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 454  
ccatgcctgc tcagccaaga a 21

<210> 455  
<211> 23  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 455  
caggaaatct ggaaacctac agt 23

<210> 456  
<211> 20  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 456  
ccttgaaaag gacccagttt 20

<210> 457  
<211> 22  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 457  
atgagtcgca cctgctgttc cc 22

<210> 458  
<211> 18  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 458  
tagcagctgc ccttggtta 18

<210> 459  
<211> 22  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 459  
aacagcaggt gcgactcatc ta 22

<210> 460  
<211> 23  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 460  
tgctaggcga cgacaccag acc 23

<210> 461  
<211> 18  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 461  
tggacacgtg gcagtgga 18

<210> 462  
<211> 19  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 462  
tcatgtctc gtccattc 19

<210> 463  
<211> 27  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 463  
caccatttgt ttctctgtct ccccatc 27

<210> 464  
<211> 18  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 464  
ccggcatcct tggagtag 18

<210> 465  
<211> 20  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 465  
tccccattag cacaggagta 20

<210> 466



<211> 23  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 466  
aggctcttgc ctgtcctgct gct 23

<210> 467  
<211> 18  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 467  
gccagagtc ccacttgt 18

<210> 468  
<211> 19  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 468  
actgctccgc ctactacga 19

<210> 469  
<211> 20  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 469  
aggcatcctc gccgtcctca 20

<210> 470  
<211> 19  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 470  
aaggccaagg tgagtccat 19

<210> 471  
<211> 20  
<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 471

cgagtgtgtg cgaaacctaa 20

<210> 472

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 472

tcagggtcta catcagcctc ctgc 24

<210> 473

<211> 19

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 473

aaggccaagg tgagtccat 19

<210> 474

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 474

cctactgagg agccctatgc 20

<210> 475

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 475

tccaggtgga cccacttca gg 22

<210> 476

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 476

gggaggctta taggccaat ctgg 24

<210> 477

<211> 50

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 477

ggcttcagca gcaogtgtga agtcgaagtc gcagtcacag atatcaatga 50

-230-

-1-